

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

**THIS PAGE BLANK (USPTO)**

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number  
**WO 01/53455 A2**

(51) International Patent Classification<sup>7</sup>: **C12N**

[US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).  
**LIU, Chenchua** [CN/US]; 1125 Ranchero Way #14, San  
Jose, CA 95117 (US). **DRMANAC, Radoje, T.** [YU/US];  
850 East Greenwich Place, Palo Alto, CA 94303 (US).

(21) International Application Number: PCT/US00/35017

(22) International Filing Date:

22 December 2000 (22.12.2000)

(74) Agent: **ELRIFI, Ivor, R.**; Mintz, Levin, Cohn, Ferris,  
Glovsky, and Popeo, P.C., One Financial Center, Boston,  
MA 02111 (US).

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

09/471,275	23 December 1999 (23.12.1999)	US
09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(63) Related by continuation (CON) or continuation-in-part  
(CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/596,196 (CIP)
Filed on	17 June 2000 (17.06.2000)
US	09/653,274 (CIP)
Filed on	31 August 2000 (31.08.2000)

(84) Designated States (*regional*): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian  
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European  
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,  
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,  
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished  
upon receipt of that report

(71) Applicant (*for all designated States except US*): **HYSEQ,  
INC.** [US/US]; 670 Almanor Avenue, Sunnyvale, CA  
94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **TANG, Y., Tom**

*For two-letter codes and other abbreviations, refer to the "Guidance  
Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.*

WO 01/53455 A2

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

## NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by  
5 such polynucleotides, along with uses for these polynucleotides and proteins, for example  
in therapeutic, diagnostic and research methods.

### 2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines,  
10 such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured  
rapidly over the past decade. The now routine hybridization cloning and expression  
cloning techniques clone novel polynucleotides "directly" in the sense that they rely on  
information directly related to the discovered protein (i.e., partial DNA/amino acid  
15 sequence of the protein in the case of hybridization cloning; activity of the protein in the  
case of expression cloning). More recent "indirect" cloning techniques such as signal  
sequence cloning, which isolates DNA sequences based on the presence of a now  
well-recognized secretory leader sequence motif, as well as various PCR-based or low  
stringency hybridization-based cloning techniques, have advanced the state of the art by  
20 making available large numbers of DNA/amino acid sequences for proteins that are  
known to have biological activity, for example, by virtue of their secreted nature in the  
case of leader sequence cloning, by virtue of their cell or tissue source in the case of  
PCR-based techniques, or by virtue of structural similarity to other genes of known  
biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications  
25 in, for example, diagnostics, forensics, gene mapping; identification of mutations  
responsible for genetic disorders or other traits, to assess biodiversity, and to produce  
many other types of data and products dependent on DNA and amino acid sequences.

### 3. SUMMARY OF THE INVENTION

30 The compositions of the present invention include novel isolated polypeptides, novel  
isolated polynucleotides encoding such polypeptides, including recombinant DNA



molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

5           The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

10           The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO:  
15 1-739. The polypeptides sequences are designated SEQ ID NO: 740-1478. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

20           The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-739 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by  
25 SEQ ID NO:1-739. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-739 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

          The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence  
30 information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or represents the sequence information of SEQ ID NO:1-739.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-739; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 739; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1- 739. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-739; (b) a nucleotide sequence encoding any one of the

amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-739; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein,

and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The

invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

#### 4. DETAILED DESCRIPTION OF THE INVENTION

##### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The  
5 term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ  
10 line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably  
15 linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

20 The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or  
25 RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of  
30 oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid

which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of  
5 nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50  
10 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or  
15 amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from  
20 chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989,  
25 Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or  
30 represents the sequence information of that sequence of SEQ ID NO:1-739. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-



mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because  $4^{20}$  possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully  
5 matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

10 Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ( $1 \div 4^{25}$ ) times the increased probability for mismatch at each nucleotide position ( $3 \times 25$ ). The probability that an eighteen mer with a single mismatch can be detected in an  
15 array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

20 The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously  
25 linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

30 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to

naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may  
5 be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides  
10 may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the  
15 polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*,  
20 conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine,  
25 serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions,  
30 deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may  
5 change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

10 The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological  
15 macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic  
20 acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect,  
25 or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation.

Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of  
30 glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134

-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or  
5 provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS),  
10 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium  
15 pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result  
20 in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the  
25 substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no  
30 more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment,

by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower  
5 percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are  
10 considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying  
15 hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal  
20 integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of  
25 nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and  
30 the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

#### 4.2 NUCLEIC ACIDS OF THE INVENTION

5 Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-739 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:740-1478; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of  
10 any one of SEQ ID NO:740-1478. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-739 ; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide  
15 recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 740-1478. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic  
20 domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or  
25 partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known  
30 methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification



and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-739 can be obtained by screening appropriate cDNA or genomic DNA  
5 libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-739 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-739 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and  
10 sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including  
15 nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

20 Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-739, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or  
25 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on  
30 unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-739, a representative fragment thereof, or a nucleotide sequence at least 90%

5 identical, preferably 95% identical, to SEQ ID NO:1-739 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

10 The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-739, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a  
15 FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

20 The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences  
25 which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably  
30 constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the

nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

15 In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed

20 mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of

25 template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid

30 and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-739, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide.

In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell.

Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be  
5 a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the  
10 recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably  
15 linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene)  
20 pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in  
25 Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the  
30 protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV  
5 immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a  
10 promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\alpha$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a  
15 leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a  
20 structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus*  
25 *subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived  
30 from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example,

pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### 4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-739, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:740-1478 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-739 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding

region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences  
5 which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO:1-739), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid  
10 molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or  
15 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase  
20 the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil,  
25 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil,  
30 beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,



pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### 4.4 RIBOZYMES AND PNA MOIETIES

5 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a  
10 mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO:1-739). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a  
15 SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences  
20 complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the  
25 base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the  
30 deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to

allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

5 PNA's of the invention can be used in therapeutic and diagnostic applications. For example, PNA's can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNA's of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial  
10 restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNA's of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by  
15 the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity.  
20 PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite  
25 coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively,  
30 chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### 4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If

linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a

suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations

of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties  
5 of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a  
10 simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the  
15 identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively  
20 selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial  
25 xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International  
30 Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:740-1478 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-739 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-739 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:740-1478 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:740-1478 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:740-1478.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the



disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane  
5 bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

10 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an  
15 identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide  
20 synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies  
25 against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein.  
30 As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein

which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present  
5 invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in  
10 which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a  
15 full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but  
20 are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity  
25 include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial  
30 libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models

that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

5 In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:740-1478.

10 The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

15 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

25 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other

30

immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

#### **4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY**

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST

(Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al.,  
5 Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S.,  
10 et al., J. Mol. Biol. 215:403-410 (1990).

#### 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide  
15 according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate  
20 that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

25 In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more  
30 domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into

pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction  
5 may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a  
10 ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation,  
15 restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to  
20 complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding  
25 a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of  
30 normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states

involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression



by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a

tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are  
5 contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting  
10 sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance  
15 with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 20 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi,  
25 Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No.  
30 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in

disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

5 Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased  
10 protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to  
15 express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed  
20 or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals,  
25 preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals,  
30 are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

#### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

#### 4.10.1 RESEARCH USES AND UTILITIES

5       The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease  
10   states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known  
15   sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or  
20   potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

25       The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which  
30   the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of

course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic

compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions  
5 of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;  
10 Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node  
15 cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- $\gamma$ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto.  
20 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and  
25 Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986;  
30 Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John

Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.



It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia  
5 inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type,  
10 expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the  
15 culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

20 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to  
25 create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present  
30 invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune

disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

*In vitro* cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. *Proc. Natl. Acad. Sci, U.S.A.*, 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., *Blood*, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

- Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative

disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

5           Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a  
10 tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or  
15 ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo*  
20 for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

          The compositions of the present invention may also be useful for proliferation of  
25 neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and  
30 localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager

syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the

polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and  
5 murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by  
10 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and  
15 persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing  
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that  
25 destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration  
30 of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a



subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or

eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient  
5 by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic  
10 acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation  
15 signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and  $\beta_2$   
20 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene  
25 encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome  
30 tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology

154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may

also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be  
5 measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

10

#### 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial  
15 cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well  
20 as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell  
25 population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:  
30 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the

migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

#### 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a

polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer  
5 may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and  
10 pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast  
15 cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in  
20 the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and  
25 Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant  
30 cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

*In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in



Boyden Chamber assays as described in Pilkington et al., *Anticancer Res.*, 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., *Intl. J. Dev. Biol.*, 40: 1189-97 (1999) and Li et al., *Clin. Exp.*

5 Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### 4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor,  
10 receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation,  
15 cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without  
20 limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those  
25 described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer et al., *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein et al., *J. Exp. Med.*  
30 169:149-160 1989; Stoltenborg et al., *J. Immunol. Methods* 175:59-68, 1994; Stitt et al., *Cell* 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

5        Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in  
10    Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

15

#### 4.10.13        DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in  
20    solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One  
25    may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or  
30    modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3)

combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or  
5 compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.  
10 Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of  
15 particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997);  
20 Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay  
25 are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin  
30 or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity

of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

5       The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding  
10       partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for  
15       receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression  
20       library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides,  
25       oligonucleotides or organic molecules.

      The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host  
30       cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins

involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

#### 5           **4.10.15           ANTI-INFLAMMATORY ACTIVITY**

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells  
10 involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic  
15 inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or  
20 material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or  
25 inflammatory disease, an antiproliferative agent such as for acute or chronic myleogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

#### **4.10.16           LEUKEMIAS**

Leukemias and related disorders may be treated or prevented by administration of  
30 a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not

limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B.

5 Lippincott Co., Philadelphia).

#### 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or  
10 polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention  
15 include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- 20 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by  
25 human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or  
30 amyotrophic lateral sclerosis;

- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody

binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

- 5           In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and
- 10           including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

15           **4.10.18           OTHER ACTIVITIES**

- A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without
- 20           limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of
- 25           dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells
- 30           in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related



diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is

5 cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for

10 diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a

15 predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence

20 of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which

25 an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the

30 present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences

of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

#### 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

#### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01  $\mu\text{g/kg}$  to 100 mg/kg of body weight, with the preferred dose being about 0.1  $\mu\text{g/kg}$  to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

#### 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity

of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers

to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions.

When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in  
5 fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The  
10 liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic  
15 compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

#### 20 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These  
25 pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered  
30 orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the

pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon



dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The

5 compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing  
10 and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic  
15 fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active  
20 ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the  
25 compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives,  
30 for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological

effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

5           The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T  
10 cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to  
15 bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

          The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other  
20 pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the  
25 art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

          The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the  
30 patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each

individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g to about 100 mg (preferably about 0.1  $\mu$ g to about 10 mg, more preferably about 0.1  $\mu$ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

25       The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically

30       well-defined, such as bone or dermal collagen. Further matrices are comprised of pure

proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients

of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating

concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the  $IC_{50}$  as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the  $LD_{50}$  (the dose lethal to 50% of the population) and the  $ED_{50}$  (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between  $LD_{50}$  and  $ED_{50}$ . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the  $ED_{50}$  with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%.

In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu\text{g/kg}$  to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu\text{g/kg}$  to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

#### 4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

#### 4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}'$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG<sub>1</sub>, IgG<sub>2</sub>, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.



Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 4, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

10

#### 5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide

primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D.

- 5 Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

### 5.13.2 Monoclonal Antibodies

- The term "monoclonal antibody" (MAb) or "monoclonal antibody composition",  
10 as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a  
15 particular epitope of the antigen characterized by a unique binding affinity for it.

- Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing  
20 antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

- The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human  
25 mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse  
30 myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or

survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures

such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

20

### 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536

30

(1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found  
5 neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The  
10 humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

### 5.13.3 Human Antibodies

15 Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol  
20 Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human  
25 B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be  
30 made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely

inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to

prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene  
5 encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a  
10 light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody  
15 that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

#### 5.13.4 $F_{ab}$ Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of  
20 single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that  
25 contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

30

#### 5.13.5 Bispecific Antibodies



Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan).

Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as  
5 homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.  $F(ab')_2$  bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science  
10 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate  $F(ab')_2$  fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The  $Fab'$  fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the  $Fab'$ -TNB derivatives is then  
15 reconverted to the  $Fab'$ -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other  $Fab'$ -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally,  $Fab'$  fragments can be directly recovered from *E. coli* and  
20 chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody  $F(ab')_2$  molecule. Each  $Fab'$  fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and  
25 normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol.  
30 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the  $Fab'$  portions of two different antibodies by gene fusion. The antibody

homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ( $V_H$ ) connected to a light-chain variable domain ( $V_L$ ) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the  $V_H$  and  $V_L$  domains of one fragment are forced to pair with the complementary  $V_L$  and  $V_H$  domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc $\gamma$ R), such as Fc $\gamma$ RI (CD64), Fc $\gamma$ RII (CD32) and Fc $\gamma$ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

25

#### 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in

30

vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, 5 for example, in U.S. Patent No. 4,676,980.

### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For 10 example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 15 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

20

### 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments 25 thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, 30 modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcun,

croton, saponaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

5           Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl)  
10 hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid  
15 (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

          In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the  
20 circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

#### 4.14 COMPUTER READABLE SEQUENCES

          In one application of this embodiment, a nucleotide sequence of the present  
25 invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these  
30 categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to

create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-739 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-739 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for

commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

#### 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

#### 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.



In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample.

5 Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise  
10 contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying  
15 for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available  
20 hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described  
25 method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein  
30

extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

25

#### 4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of

30

the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

#### 4.18 SCREENING ASSAYS

5           Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-739, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- 10           (a)     contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b)     determining whether the agent binds to said protein or said nucleic acid.

             In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a

15   polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

             Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide

20   of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

             Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for

25   a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

             Compounds identified via such methods can include compounds which modulate

30   the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds

identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard  
5 assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling  
10 techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected  
15 or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In  
20 Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be  
25 randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA.  
30 Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or

can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

#### 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-739. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO:1-739 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection

of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes.

5 Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein  
10 may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of  
15 chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science  
20 (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

#### 25 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to  
30 those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated  
5 herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be  
10 purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound  
15 to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem.  
20 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond  
25 joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

30 More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M

1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC),  
5 dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

10 It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The  
15 oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA  
20 probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of  
25 Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

30 One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6,



incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 µl of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI\*\*), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

#### 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm<sup>2</sup>, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate

(all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

5           Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

10           The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the  
15           exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon  
20           the scope of the invention are those which appear in the appended claims.

          All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

## 5.0     EXAMPLES

### 5.1     EXAMPLE 1

#### 25           Novel Nucleic Acid Sequences Obtained From Various Libraries

          A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers  
30           specific for the vector sequences which flank the inserts. Clones from cDNA libraries were

spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

5 In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

10

## 5.2 EXAMPLE 2

### Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases  
15 sequences obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-739 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed.  
20 Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 120, gb pri 120, UniGene version 120, and Genpept 120) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of  
25 component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 120, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest  
30 neighbor result showed the closest homologue for each assemblage from Genpept (and

contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for SEQ ID NO: 1-739 are shown in Table 2.

- Tables 1, 2, and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-739. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homologue for each assemblage and contains the translated amino acid sequences for which the assemblage encodes. Table 2 also shows homologues with identifiable functions for SEQ ID NO: 1-739. The polypeptides were predicted using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotides to known polynucleotides (W.R. Pearson, Methods in Enzymology, Vol. 183: pp. 63-98, (1990), herein incorporated by reference). Table 3 shows the predicted amino acid sequence corresponding to the novel nucleic acid contig sequences.

**Table 1 - Tissue Sources**

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	28 46 54 62 95 117 134 175 188-189 324 330 337 356 369 371 378 386 389 396 432 435-436 468 472-473 476-477 483 486 518 538-539 543 545 557 565 571 573 578 582 598 613-614 619 627 632 634 639 687 709
adult brain	GIBCO	ABD003	5 12 46 52 57 66 79 91 97 134 144 148 150 162 164 172 175-176 181 186 193 250 323 325-327 330 334 338 362 367 369 371 378-379 386 388-389 392 396-397 399-401 403 416 422 435 444 449 451 454 461 463-464 468 472-473 483 486 494 506 511 513 516 520 523-524 526 529 533 536-537 539 545 548 552 556 558-559 562-563 565 567 569 573-574 576 579-580 582-584 590 593-594 598 602 606 613-614 619- 621 623-624 627 634 637 641 646 648 659 675 688-689 694 696-698 703 714 729
adult brain	Clontech	ABR001	57 162 164 227 266 316 334 356 367 385 438 468 512 524 528 557 582 590 621 627 631 634 689 714
adult brain	Clontech	ABR006	189 228 385 438 571 584 632 650 677
adult brain	Clontech	ABR008	1 3 5 11-25 31-32 46-47 55-57 59

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			61 65-67 69 75 79 91 103 108 111 113-114 126 132 150 160 162 164 171-172 186 188-189 193 202-203 206 210-212 220 222-224 227-229 233 235-236 243-247 251-252 257 264-266 268 275 313 324 328-331 334-335 338-339 343 346-347 351 355 357 359-361 365 367 370-371 378 380 382 386-389 391 396 399- 400 402 406 413 419-420 423 426 432 434 437-438 442 446 448-449 459-460 465 468 470 472-473 475 481-483 487 489-490 495-497 499 501 503-504 507-509 511 520 524 526 528 532-533 536 539-540 543- 546 551-552 556-557 563 565-567 569 572-573 576-577 579-580 582 584 586 590-591 593 595-597 599- 602 604 610-616 620-621 624-625 627-628 632 634 637-638 641 643- 644 646-647 650 653-657 660-662 668 672 675 677-678 680-681 688- 689 691 693 695-696 698 706-707 709 711 713-727 729 731 733-734 736 738-739
adult brain	Clontech	ABR011	334 476 634 677
adult brain	BioChain	ABR012	379 587
adult brain	Invitrogen	ABR013	334 634
adult brain	Invitrogen	ABT004	3 19 57 62 66 75 110 122 150 160 162 167 171 176 186 197 203 211 230 232 259 328-331 334 369 382 389 394 400 406 417 426 429 442 457 472 483-484 492 511 514 529 531 534 537 540 553 558 562 572 580 582-584 590 604 611 613 615 622 637 639 643-644 648 688-689 692 695
cultured preadipo-cytes	Stratagene	ADP001	16 37-39 66 109 120 141 144 193 273 316 331 333 338 389 415 429 442 444 464-465 475 489 501 511 513 531 534 539-540 545-546 557 583-584 590 596 602 607 613 615 619 622 629 632 634 643
adrenal gland	Clontech	ADR002	4-5 12 48 53 57 162 164 172 186 188 192 196 203 207 213 258 316 330-331 333 339 354 356-357 369 383 385 388 392 395 402 406 411 415 434 454-455 465 468 473 475 477 491 498 501 509 511 517 528- 529 532 537-539 542 545 558 560 565 567 576-577 586 600 606 615 621 624 627 632 634 647 653 660 667 683 689 696 714

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult heart	GIBCO	AHR001	28 39 57 64-65 75 79 89 97-98 108 117 134 144 157 159-160 164-166 169 171 174 184 192-193 203 207 220 243 256 258 266-267 281 314 316 318 328-329 331 338-339 341 346 348 354 356-357 366-367 369 371 377-379 382 385-386 388 393 395-396 399-401 403 415 420 422 425 431-432 435-436 445 451 459 465 472-473 477 483 486 488 490 496 501 503 508 515 519-520 526 528 531 533-534 537-538 540-541 544 546 552 556-557 562-563 566- 571 573 576-581 583-584 586-587 594 602 606 608 611 613-615 618 620-621 626-628 632 634 641 643 646 648 653 659 667 676 678 687 689 696 703-704 708 711 714 729- 730
adult kidney	GIBCO	AKD001	3 28-29 48 56-57 67 79 84 93 106 117 134 138 140 144 156 160-164 168-170 172 177 183 188-189 192- 193 199 203 207 235 251 257 275 319 321-323 328-330 337 346-347 349 354-356 360 367-369 371 375 378-381 383-386 388-389 392 396- 397 399 401 404 407 409 411-412 415-416 420-422 427 432 436-437 439-440 444 451-456 458-459 464- 465 468 470 472-473 477 481 483 486-487 492 496 501 503 505-506 508 511 513-516 518 524 526 529 533 535 537-541 543 545-546 548 552 557 559-560 562-563 565-569 572-574 576-577 579-587 589-591 593-594 602 604-607 613-614 617- 618 620-624 627-628 630 632-635 637-638 640-642 644-645 652 662 664 667-668 677 682 685 687 689 694-696 698 703 716 723 728-729 732 734
adult kidney	Invitrogen	AKT002	92 136 154 160 164 178 271 314 347 353 360 367 376 378-379 386 391 402 409 423 432 449 451 477 490 494 503 526 528 531 534 538-539 541 545-546 559 566 579 584 588 594 602 613 621 624 632 647 652 689
adult lung	GIBCO	ALG001	56-57 67 69 98 113 134 144 164 172 191-192 270 321 328 338 369 371 374 378 380 388-389 396 405 411 416 424 443-444 456 473-474 482- 483 497 508 518 529 531 534 536

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			540 552 556 559 563 568 573 579-580 585-586 588-589 593 601-602 606 612-613 618 634 662 667 685 696 702 726 729-730
lymph node	Clontech	ALN001	28 57 79 113 164 172 179 193 240 325 332 367 378-379 386 388 402 485 526 580 586 603 613-614 621-622 628 634 662 667 686 734
young liver	GIBCO	ALV001	3 24 28 54 60 117 134 137 154 160 193 196 242 273 316 328-329 334 351 354 370-371 388 392 395-396 401 406 411 415 432 435 439 448 454-455 477 483 486-487 495 506 509 514 518 523-524 526 529 531 534 537-538 540 544 548 566 568 571 573 579 587-588 591 594 602 621 641 645 686 713 723
adult liver	Invitrogen	ALV002	3 24 27 56-57 65-66 71 79 92 97 106 134 140 164 192 200 214 220 232 240 242 271-272 291 313 316 328 347 349-350 353 355 357 368-369 371-372 378-379 381-382 385 397 430 435 448 457 459 471-472 475 485 487 502 505-506 511 520 530-531 533-534 537 540-541 543 548 566 574-575 579 582 588 590 612 623 640 648-649 681 687 689 710 714
adult ovary	Invitrogen	AOV001	3 10 14 28 54 56-58 62 65-66 68 73 75 79 98 127 144 154 162 164-165 172-174 182 186 188-189 192-196 206 213 224 234-235 241 243 248 253 261 273 275 289 314 316 321-322 325-327 329-331 333-334 336-338 340 343 345-348 354-357 367 369 371-372 378 382 386 388 395-397 399-402 404 407 411 415-416 419-420 425 427 429 431 435-437 441 444 451 453-459 465 468-470 472-475 481 485 490 494 496 501 503 509-510 513 517-518 522-524 526 528-529 531-534 537-542 545-546 548 552 554 556-557 559-560 562-563 565 567-569 572-579 581-582 584-588 590-591 593-598 602-604 606 611-615 618 620-623 627 629 631-632 635-638 643 647 652-654 657 659 661-662 667 674-675 677-678 682 684 689 693 695-698 703 705-707 714 717-718 723 729 731 738
adult placenta	Clontech	APL001	172 224 239 363 371 392 437 531 534 622 690 696



Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
placenta	Invitrogen	APL002	57 66 122 161 172 241 326 329 334 369 388 407 427 429 436 459 464 506 508 511 539 541 545 566 573 575 590 597 637 648 690
adult spleen	GIBCO	ASP001	28 57 65 78 93 95 117 134 156-157 172 186 188 194 214 273 314 319 331 334 338 344 354 371 374 392 436 457 471-473 478-479 481 483 515 526 528-529 541 548 557 559 563 565 569 573 585-587 603 606 613 615 618 621-622 627 632 634 637 643 654 671 689 696-698 701 712 739
testis	GIBCO	ATS001	3 67 134 160 192 235 327 329 337 342 371 375 378 380-381 396 399 415 431 436 441 451 472 477-478 483 486 494 496 503 522 524 526 531 533-534 538 541-542 546 548 557 568 573 577 579 581 584 594 596 618 641 658 662 689 700 714 729-730
adult bladder	Invitrogen	BLD001	28 57 112 161 164 172 192 194 250 334 354 370 397 404 487 513 526 531 534 545 572 599 602 620 634 651 659 672 689 713 725
bone marrow	Clontech	BMD001	10-11 28 31 54 57 62 75 78-83 88 131-133 135-137 141-143 157 159 164 171-173 176-177 187-189 192 195 200 202 205 207 218 225 282 314-318 325 330 334-335 337 346- 348 367 369 372 378 383 386 388 395 401 405 412-413 416 422 436 442-443 447 449 455 465 472 475 477 503 516 523 528-529 533-534 539 545 551 556 559 563 565-567 571 573-574 576 579-586 594 601- 602 606 613 620-623 628-629 634 638 642-643 646 656 659 666 686 689 691 696 698-699 703 705 714 720 726 729
bone marrow	Clontech	BMD002	2 15 23 35 49 54 57 59 78 81 114 156-157 164 171-172 189-190 202 223 240 325 334 346 357 367 379 381-382 388 397 412 454 465 482 490 509 516 526 535 537 563 566 579 595 600 638 640-641 654-655 676 689 714
adult colon	Invitrogen	CLN001	48 79 94 138 162 167 189 333 368- 369 375 386 404 409 414 435-436 455 470 525 541 548 553 567 603 634 656 659 689 694 721
adult cervix	BioChain	CVX001	3 28 35 54 57 79 83 95 97 113 117 154 162 164 172 176 220 235 248-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			249 321 327 329 333 338 346 348 354 356 362 367-368 371 374-375 378-379 386 388-389 395 401-402 404 407 420 429 431 437 443 451 459 468 475 477 479 483 485 490 493-494 496 506 508 511 517 526 528 531 534 544 550 552 559 566 569 571-573 575-576 581-583 588 590 593-594 604 606 614 622 628 631-635 639 661-662 675 689 692 695 715 718 738
endothelial cells	Strategene	EDT001	3 28 31 39 54 58 65-66 79 89 144 160 173 187 189 191 193 197-199 207 220 230 267 273 314 324 326 329-331 336 347 354 369 372 378- 379 384 386 388 391-394 396-397 399 401 407 420 422 429 431-432 435-437 444 449 451 455 459 465 472 474-475 481-482 486 490 499- 501 503 506 511 513 515-517 520 522-524 528 531-534 538-539 541 545-546 548 550 552 557 559-560 563 565 567 569 571 573 577 579- 580 583-584 587-590 593-594 596- 597 599 602 611 614-615 618 620- 621 624 630 632-634 637-638 642- 643 647-648 651 675 677 680 682 694 696-698 703 708 714 719 724- 725 728-730 734
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	38 41-45 118-121 164 198 292-312
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM003	43 164 295
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	121 164 306 482
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM006	293

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
esophagus	BioChain	ESO002	513 526
fetal brain	Clontech	FBR001	57 468 563 634
fetal brain	Clontech	FBR004	162 186 254 265 491 582
fetal brain	Clontech	FBR006	1-2 5-6 11-12 22-23 49 57 62 73 94 103 114 162 164 172 189 193 203 218 240 244 251-252 259 279 330- 331 334-335 346-347 351 367 378 386 388-389 399 413 420 422 424 434 442 444 448 465 468 470 472- 473 490 496 501 503-504 511 520 524 528 532-533 539 544-546 548 551 553 563 571 573 576 587 591 601 613 615-616 620-621 628 634 641 644 648 653 657 662 672-673 689 691 698 706 714 718 725-728 733 735-739
fetal brain	Clontech	FBRs03	444 587
fetal brain	Invitrogen	FBT002	17 66 157 162 164 186 190 193 250 270 324 331 334-335 338 346 354- 355 374 382 389-390 426 429-430 437 442 453 467 471 475 481 485 491 507-508 513-514 526 528 532 540 544 548 550 552-553 557-558 563 565-566 590 593 602 612 615 637 641 648 654 662 672 676 692 703
fetal heart	Invitrogen	FHR001	57 75 164 547
fetal kidney	Clontech	FKD001	57 164 172 179 188 194 208 218 230 240 250 330 334 369 388 401 413 439 454 465 529 546 550 573 576 581 583 594-596 602 634 648 667 676 689 698 706
fetal kidney	Clontech	FKD002	2 560
fetal kidney	Invitrogen	FKD007	565 596-597
fetal lung	Clontech	FLG001	75 164 355 386 428 455 513 524 528 631 689
fetal lung	Invitrogen	FLG003	30 157 162 169 188 243 253 256 283 330 392 400-401 404 407 424 428 435-436 479 506 508 520 530-531 534 572 578 584 602 611 613 631 654 658 662 676 689 701 716
fetal lung	Clontech	FLG004	371
fetal liver-spleen	Columbia University	FLS001	2-3 5 26 29 31 35 48 54-58 60 62 65 67 70 74-77 79-80 84-87 89 92 96 98-100 104 117 122-130 138 140 144-158 160 162 164 172-173 185- 186 188-189 192-194 196 199-200 207 214 218-219 237-238 241 269 273 280 282 314-316 318-322 324 327 329-331 334-335 337 340 345 348-350 354-358 363-364 367-371

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			373 375 377-380 382-383 385-386 388 394-396 399 402 409 411-412 418 420-422 424 427 431 435-437 440 442 448-451 453 455 459 461 464-465 470 472-473 475 477-478 480-485 488-490 501 503 505-506 509 511-513 515-518 520 522-524 526-534 538-539 541 543-547 549- 550 552-553 556-557 559-564 566- 567 569 571 573 576 578-580 582- 587 589 591-594 596-597 599-600 602 611-615 618 620-625 627-628 631-636 638 641-642 646 648 651 659-660 662-664 667-668 675-678 680-681 684 689-690 696-698 709 714 723 738
fetal liver-spleen	Columbia University	FLS002	15 31-32 39-40 47-49 52 56 60 65 69 72 75 78 84 97-98 100 104 115 123 138 140 144 146 152-153 157 161 164 172-173 182 188 194 196 199 220 241-242 246 249 253 255 266 273-275 280-281 288-291 314- 316 318-319 321-322 324 329-331 336-339 343 347-350 353-354 357- 358 363 367 369-370 372 374 378- 380 382-383 386 388-389 393-397 399 405 407 409-410 412 421 424 432 435 439 448 450-451 453-457 459 461 464-465 470 472-475 477 479-481 483 485 488 490 497 501 503 506 509 511-513 516-518 520 524 527-528 531-532 534 539 541- 546 556 559-560 565-566 569 571 574 576 579 582-586 588 590 597- 599 602-604 606 615 618 620-621 623 625 627 632-634 639 641 644 648 666-668 675-676 681 684 689- 690 696-697 701 703 714 719 723 734-735
fetal liver-spleen	Columbia University	FLS003	60 79 157 190 690
fetal liver	Invitrogen	FLV001	3 27 35 48 50 56-57 66 75 92 94 105 157 161 164 176 189 209 220 243 272 324 328 333 335 353 369- 370 381 392 396 429-430 435 439- 440 442 444 465 471 483 487 502 506 513-514 519 534-535 537 548 554 566 568 576-577 580 582 590 613 621 645 648-649 689
fetal liver	Clontech	FLV002	343
fetal muscle	Invitrogen	FMS001	51 79 97 108-110 166 194 196 266 341 352 380 389 402 407 444 464

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			475 501 513 524 546 552 554 560 570 572 598 605 628 634 649 675 703-704 714 737
fetal muscle	Invitrogen	FMS002	524
fetal skin	Invitrogen	FSK001	31 33 35 48 57 63 67 75 112-114 117 157 162 164 172 178 180 188 196 220 243 254 319 324 328 330 333-334 367 369 371 375 379-383 386 388-389 400 404 407 412 419- 420 429 444 455 472-473 491 499 503 508 511 514 517 522-524 529 531 534 537 540 542 547 552 554 556-557 560 563 565 567 571-572 574 576 579 590 596 599 616 621 625 627 631-632 634 639-640 648 653-654 662 689 708 714
fetal skin	Invitrogen	FSK002	501 537
fetal spleen	BioChain	FSP001	465 729
umbilical cord	BioChain	FUC001	27-28 35 57 68 83 105 136 157 159- 160 164 188 191 225 279 315-316 321 328 334 363 367 369 378-379 383 386 388-389 392 397 406-407 413 415-416 427 440 449 455 458 461 464-465 468 473-475 479 485- 486 488 490 496 514 517 522 524 526 528-529 531 533-534 538 540 546 550 552 556-558 572 582 584- 585 587-588 594-597 602 606 613 616 618-619 631 634 637 651 689 696 698 706 729
fetal brain	GIBCO	HFB001	3 5 22 26 46 53 66 73 94 117 134 139 164 172-173 188-189 212 215 230-231 248 251 262 288-289 316 325 329-331 334 337-338 348 352 365-367 369 371 377-379 385-386 388 392 394 396 400 403 420 422 429 437 444-446 449 451 455 459 461-463 466-468 472-473 475 477 481 483 485-486 488 490-491 496 503-504 506 513 523-524 529 532- 533 539-541 545 548 550 552 557- 560 563 565-566 569 571 576-577 579-580 583-584 586 590 593-594 596-599 601-602 604 606 611 613 615 618 621-623 627-628 634-635 637 641 643 647 662 664-665 667 675 677 680 689 695-697 703 726
macrophage	Invitrogen	HMP001	97 518 532 569
infant brain	Columbia University	IB2002	28 46 56-57 59 67 75 78 109 117 122 129 144 157 162 164-165 172 176 180 190 193 212 220 226 236-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			237 251 261-262 316 318 324 328-330 334-335 337 340 354-356 361 364-365 367 369 371-373 377-380 382 385-386 389 392 395 397 400 411 416 421-422 429 432 436 438 444 448 451 456 464-465 469 471-475 484 486 496 504-506 511 520 524 526 529 531 533-534 537-540 544-546 548 553 556 558 562 565 567 576 579-580 582 584 586 589-590 593 597-598 602 613-614 618 620-621 627-628 632 634 636 641 650 654 659 662 667 683 689 721 730
infant brain	Columbia University	IB2003	46 54 75 109 156 164 220 244 251 314 324-325 331 335 340 361-362 367 369 377-379 400 408 438 442 456 460 464 469 472 496 506 523-524 526 529 538 540 544-545 547 558 560-562 565 567 569 579 584 598 602 613 615 621 627 632 634 637 639 650 738
infant brain	Columbia University	IBM002	262 340 432 436 438 472 531 534 569 613 634
infant brain	Columbia University	IBS001	162 231 283 331 369 385 438 444 472 506 513 523 531 534 580 615 636 689
lung, fibroblast	Strategene	LFB001	28 54 57 65 172 188 233 321 331 340 347 367 369 378-379 388 401 451 459 475 479 503 511 522 524 532 534 559-560 573 580 583 587 597 615 632 634 638 686 689 708
lung tumor	Invitrogen	LGT002	3 7 21 24 26 28 31 54 56-57 62-63 66 92-93 101 109 112 162 164 171-172 176 183 188-189 192-193 196 201-202 223 230 235 259 273-274 316 321 329-331 333-334 338 345 347-348 356 367 369 371-372 378-379 381-382 386 388-390 396 399-404 406 409 416 424-425 427 429 432 436-437 439 451 455-456 459 464-465 467 473 475 484-486 490 499 502-503 506 508 511 513-514 517-518 522 524 526 528 531-532 534-535 538-539 541 543-546 553 557-559 563 567-568 571 573 575-576 579-580 585-588 590-591 593-594 598 601-604 609 611-613 615 621 627-628 631-632 636-637 645 648 651-652 654 662 667 672 677 681 683 689 698 701-702 714 718 724 726 729 734
lymphocytes	ATCC	LPC001	4 31-32 35 57 65-66 70 110 116 156

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			162 164 230 243 250 282 287 326 328-330 334 336 346-347 359 378 386 388 397 407 414 416 419 472 497 520 525 539 545 549 551 582 590 606 615 618 621 631 634 686 692 698 701 714
leukocyte	GIBCO	LUC001	4 7 9-11 23 28 31 35 39 54 65 75- 76 79 90 97 110 117 134 152 157 159 162 164-167 171 173 176 188 193 199 204 207 220 244 253 255 314 316 318 321 324 326 329-330 337-339 346-347 352 354 356 367 369 371 378-379 382 388-389 392 396-397 400-402 405 415-416 420 422 429 432 435-436 443-444 449 454-455 457-459 465 479 481-486 491 497 501 503-504 506 508 511 514 516 520 523-525 529 532-533 535 538-539 545 548 552-554 556 559-560 562-563 565-566 569 571- 573 576 579 581 585-587 590 593- 594 598 600-602 604 606-609 613- 614 618 620-622 624 627 630 632- 634 636 638 643 645 660-662 667 678 682 684 686 689 691 693 696- 698 714 726
leukocyte	Clontech	LUC003	11 54 97 152 164 330 479 546 564- 565 593 613 627 634 646 696 729
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	2 57 67 79 164 171-173 188 193 196 232 321 337 341 346 367 379-380 388 407 427 454 472 477 482 501 520 539 545 552 556 579 588 593 598 611 621 631 648 665 714 730
mammary gland	Invitrogen	MMG001	3 20-21 29 31 54 56-57 63-66 79 94 109 112-113 117 122 125 138 141 154 160 162 164 172 176 186 189 192 204 214 220-221 232 238 251 255 257 273 276-278 324 326 328- 331 333 335 337 341-343 347 354- 355 357 367-371 374-375 379 382- 386 388-392 397 399-400 404 406- 408 410-411 425 431 435-436 444 451 455 457 459 461 464-465 470- 471 475 479 483 485 487-488 491 501 506-508 511 513-519 523-524 526 529 531-532 534-535 537 539- 540 542-545 552-554 557-560 563 566 569 572 577 580 584 587-588 590 597-598 602 604-605 609 611 613 615 624 627 631-634 637 639- 640 643 648-649 654 664 669-670 672-673 676-679 681 689 691-695 697-698 706 714 731 734 737

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
induced neuron cells	Strategene	NTD001	36 57 164 284 388 397 420 481 485 501 524 528-529 539 542 545 560 571 579 582 595 602 620 637 654 667 689 730
retinoid acid induced neuronal cells	Strategene	NTR001	524 584 693
neuronal cells	Strategene	NTU001	36-38 120 204 331 351 354 357 386 388 399 411 442 459 516 533 539 545 565 586 606 615 621 637-638 642 646 648 714 730
placenta	Clontech	PLA003	503 579 690
prostate	Clontech	PRT001	15 40 65 164 187 207 229 337 348 367 375 377-378 395 406 416 428 458 468 476 511 524 526 531 534 538 555 559 563 576 584 597 613 622 624 631 642 667 672 677 684 724 734
rectum	Invitrogen	REC001	57 67 164 260 331 343 370-371 380 382 384 404 409 436 444 475 485 498 513 524 526 540 542 552 554 581 615 619 624 627 634 654 659 671 689 714
salivary gland	Clontech	SAL001	21 84 106-107 152 179 238 246 255 273 287 371 378 383 401 407 420 455 475 477 509 512 515 521 541 548 565 570-571 573-574 589 606 628 634 636 652 689 703 738
skin fibroblast	ATCC	SFB002	192
skin fibroblast	ATCC	SFB003	464
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711
skeletal muscle	Clontech	SKM001	3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738
spinal cord	Clontech	SPC001	10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648 659 688-689 691 693 695
adult spleen	Clontech	SPLc01	478 572
stomach	Clontech	STO001	26 90 164 218 358 369 386 468 475



Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			485 526 532 569 576 579 581 586 603 631 634 677 682 689
thalamus	Clontech	THA002	17 31 57 66 109 127 164 217-218 262 315-316 324 330 357 369 386 388 400 406 435 456 459 464 468- 469 515-516 537 540-541 556 566 574 590 611 622 631 634 644 648 656 677-678 680
thymus	Clontech	THM001	6 15 26 54 79 164 172 187 193 201 264 291 315 329 331 351 356 367 397-398 401 407 412 424 427 429 435-436 443 451 474 478 482 549 563 565 567 569 576 578 581-582 610 615 621 631-632 634 648 662 667 669 679 689 693 696
thymus	Clontech	THMc02	3-6 8 11 16 18 34 58-59 67 132 149 162 164 167 172-173 186 188-189 193 200 203 216 223 232 239 255 263 265 319-320 331 333-334 355 359 370 373 377-380 382 387-390 393 395 398-399 402 404 408 420 427 434 436 467 475-476 503 508 518 524 526 532 540 560 563 565 571-572 576-577 579 582 598 601 603 612-613 615 621 627 632 634 639 641 648 651 657 659 662 672 677-678 684-686 689 696 699 706 714-716 722 726-729 732
thyroid gland	Clontech	THR001	5 29-30 40 54 57 66 72 79 117 144 160 164 166 170 172 176 183 188- 189 208-209 219 230 285-286 314 318 327 331 335 338 344 347 354 363 367 375 377-380 382 384-386 388 393 397 399 401-403 419 422 429 436 442 444 451 456 458-461 464 467-468 470 472-473 476-477 481 488 494 503 508-509 511 516 519-521 524 528-529 533 537-538 543 548 557 559-560 563 565-566 571-574 576 582 585 587 590-591 593-594 596-597 606 614-615 620- 621 623-624 627 631-634 640 650- 651 653 662 667 669-670 675 679 689 708 712 714
trachea	Clontech	TRC001	156 164 171 240 375 378 390 400 422 468 484 565 574 581 585 587 631 654 689 714
uterus	Clontech	UTR001	65 77 79 101 164 220 367 369 451 468 526 530 533 548 554 559 562 568 573 582 594 637 648 689

Table 2 - Nearest Neighbor Results

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
1	1000	gi7021484	Mus musculus	secretory carrier membrane protein 4	567	85
2	10017	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	848	100
3	10020	gi1065967	Caenorhabditis elegans	similar to other protein phosphatases 1, 2A and 2B	325	36
4	10024	G03460	Homo sapiens	Human secreted protein,	439	98
5	10032	Y12505	Homo sapiens	Human 5' EST secreted protein	136	87
6	10042	Y29511	Homo sapiens	Human lung tumour protein SAL-25 1st predicted amino acid sequence.	701	100
7	1006	Y92324	Homo sapiens	Human alpha-2-delta-D polypeptide from splice variant 1.	763	100
8	10064	gi4589375	Homo sapiens	Gab2	425	58
9	1007	gi7018398	Homo sapiens		151	75
10	1008	gi896065	Homo sapiens	protein that is immuno-reactive with anti-PTH polyclonal antibodies	1226	99
11	10088	gi3779244	Homo sapiens	Metallo-protease 1	1512	98
12	10089	gi2947232	Homo sapiens	membrane associated guanylate kinase 2	523	100
13	10091	gi3347863	Mus musculus	cAMP-specific cyclic	223	54

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				nucleotide phosphodiesterase PDE8; MMPDE8		
14	10098	gi6979311	Homo sapiens	cysteine-rich repeat-containing protein S52 precursor	1068	100
15	10102	G01395	Homo sapiens	Human secreted protein,	297	88
16	10103	gi854733	Rattus norvegicus	casein kinase 1 gamma 1 isoform	293	84
17	10104	Y60017	Homo sapiens	Human endometrium tumour EST encoded protein 77.	154	100
18	10108	G03290	Homo sapiens	Human secreted protein,	215	97
19	10110	gi7292299	Drosophila melanogaster	CG1271 gene product	208	46
20	10111	gi4512334	Rattus norvegicus	Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha	822	89
21	10113	Y41694	Homo sapiens	Human PRO382 protein sequence.	633	97
22	10114	gi349075	Rattus norvegicus	calmodulin-binding protein	531	99
23	10116	gi162981	Bos taurus	endozepine-related protein precursor	937	87
24	10121	gi8979743	Canis familiaris	Band4.1-like5 protein	643	100
25	10126	Y99420	Homo sapiens	Human PRO1486 (UNQ755) amino acid sequence	607	100
26	1013	gi804750	Homo sapiens	protein tyrosine	614	73

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Access- ion No.	Species	Description	Smith - Water man Score	% Identity
				phosphatase		
27	10136	W02105	Homo sapiens	Human L-asparaginase.	1243	98
28	10142	Y35924	Homo sapiens	Extended human secreted protein sequence,	862	89
29	10148	gi3334982	Homo sapiens	R27216_1	329	98
30	1015	G02485	Homo sapiens	Human secreted protein,	120	72
31	10154	gi10798804	Homo sapiens	sperm antigen	2607	98
32	10175	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	536	100
33	10196	gi553621	Homo sapiens	profilaggrin	346	39
34	10198	gi1419016	Mus musculus	odorant receptor	281	53
35	10200	Y57903	Homo sapiens	Human transmembrane protein HTMPN-27.	448	100
36	10208	gi4062492	Escherichia coli		505	100
37	10212	gi882529	Escherichia coli	ORF_f141	625	96
38	10213	gi4062778	Escherichia coli	Hypothetical protein HI0761	773	98
39	10214	gi6693832	Rattus norvegicus	opioid growth factor receptor	661	44
40	10227	G01360	Homo sapiens	Human secreted protein,	384	100
41	10236	gi1651257	Escherichia coli		373	100
42	10241	gi2769262	Escherichia coli	catabolite gene activator protein	178	96
43	10245	gi1789539	Escherichia coli	orf, hypothetical protein	679	98
44	10246	gi882492	Escherichia coli	ORF_o179	488	97
45	10247	gi1742149	Escherichia coli	Sn-glycerol-3-phosphate	323	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				transport system permease protein UgpA.		
46	10282	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	521	96
47	1031	gi6435130	Mus musculus	putative E1-E2 ATPase	990	86
48	1040	gi854124	Homo sapiens	Human giant larvae homologue	471	63
49	1043	gi3882285	Homo sapiens	KIAA0782 protein	154	61
50	1051	gi178216	Homo sapiens	anion exchange protein 1	172	100
51	1053	Y76748	Homo sapiens	Human protein kinase homologue, PKH-1.	180	92
52	1062	gi965014	Mus musculus	ADAM 4 protein precursor	492	65
53	1063	gi2393880	Drosophila melanogaster	A-kinase anchor protein DAKAP550	580	60
54	1066	gi2746788	Caenorhabditis elegans	contains similarity to transacylases	607	35
55	107	G00357	Homo sapiens	Human secreted protein,	183	77
56	1071	gi9105937	Xylella fastidiosa	Acetylglutamate kinase	505	36
57	1085	R95913	Homo sapiens	Neural thread protein.	257	55
58	1086	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	387	58
59	1088	gi4589642	Homo sapiens	KIAA0999 protein	873	99
60	109	gi763431	Homo sapiens	KIAA0999 protein	360	85
61	1095	Y94907	Homo sapiens	Human secreted	701	97

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein clone cal06_19x protein sequence		
62	1102	Y07096	Homo sapiens	Colon cancer associated antigen precursor sequence.	1982	100
63	1105	Y84907	Homo sapiens	A human proliferation and apoptosis related protein.	983	91
64	1108	gi1398903	Mus musculus	Ca <sup>2+</sup> dependent activator protein for secretion	1307	89
65	1109	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74	2400	99
66	1113	gi1657462	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-E	1348	94
67	1117	Y32169	Homo sapiens	Human growth-associated protease inhibitor heavy chain precursor.	2831	97
68	1118	gi3063517	Homo sapiens		1138	98
69	1125	gi8248285	Homo sapiens	sphingosine kinase type 2 isoform	1290	98
70	1132	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence	437	59
71	1143	gi45806	Homo sapiens	prepro-major	209	40

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		77		basic protein homolog		
72	1146	gi182395	Homo sapiens	focal adhesion kinase	131	87
73	1161	W90962	Homo sapiens	Human CSGP-2 protein.	931	100
74	117	W69428	Homo sapiens	Human secreted protein bp537_4.	159	93
75	1170	gi34339	Homo sapiens		586	87
76	1175	gi7960243	Homo sapiens	SNARE protein kinase SNAK	308	100
77	118	gi5360093	Homo sapiens	NY-REN-18 antigen	178	96
78	1183	gi292037	Homo sapiens	helix-loop-helix phosphoprotein	361	91
79	1193	gi1899186	Rattus norvegicus	polysialyltransferase	171	76
80	1195	gi1399462	Homo sapiens	serine/threonine-protein kinase PRP4h	208	71
81	1198	gi181535	Homo sapiens	defensin precursor	150	71
82	1201	gi5668935	Rattus norvegicus	plasma membrane Ca <sup>2+</sup> ATPase isoform 1kb	244	73
83	1207	gi6224868	Homo sapiens	TANK binding kinase TBK1	716	86
84	1210	gi179646	Homo sapiens	complement component C1s	242	61
85	1211	gi1483187	Homo sapiens		296	65
86	1214	gi7800638	Streptococcus pneumoniae	PspA	121	37
87	123	Y44810	Homo sapiens	Human Aspartic Protease-2 (NHAP-2).	218	93
88	1259	gi2116672	Homo sapiens	EAR-1r	128	70
89	1266	gi7243125	Homo sapiens	KIAA1372 protein	403	53
90	1270	gi1289445	Homo sapiens	diacylglycerol kinase epsilon DGK	125	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
91	1290	gi14293 71	Drosophila melanogaster	ubiquitin- specific protease	470	41
92	1291	Y66755	Homo sapiens	Membrane-bound protein PRO1185.	993	100
93	1296	gi96520 87	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	1183	99
94	1299	gi73003 98	Drosophila melanogaster	CG7683 gene product	397	40
95	1317	gi36951 15	Rattus norvegicus	CL1AA	216	100
96	132	gi18717 1	Homo sapiens	12- lipoxxygenase	176	97
97	1330	Y12482	Homo sapiens	Human 5' EST secreted protein	65	44
98	1336	gi10798 814	Homo sapiens	MLTK-beta	2366	99
99	135	gi45609 0	Homo sapiens	effector cell protease receptor 1	190	74
100	1356	gi19305 7	Mus musculus	envelope polyprotein precursor	131	36
101	1369	gi45865 7	Homo sapiens	glucocorticoid receptor alpha-2	596	89
102	1392	gi84935 19	Mus musculus	nuclear localization signal binding protein	145	59
103	1408	gi31270 51	Rattus norvegicus	potassium channel regulatory protein KChAP	176	84
104	141	gi64536 13	Mus musculus	putative protein kinase	204	33
105	1424	gi29825 01	Homo sapiens	neuropathy target esterase	769	100
106	143	W50033	Homo sapiens	Human immunity related factor.	1201	98
107	1431	gi10644	Heterodera	hypothetical	133	36



SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		565	glycines	esophageal gland cell secretory protein 10		
108	1441	gi3044086	Myxococcus xanthus	unknown	149	32
109	1444	gi7248381	Homo sapiens	adaptor protein p130Cas	1615	97
110	1447	Y65168	Homo sapiens	Human 5' EST related polypeptide	403	97
111	1457	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	227	77
112	1471	G02532	Homo sapiens	Human secreted protein,	97	59
113	1473	gi6062874	Homo sapiens	candidate tumor suppressor protein DICE1	581	100
114	1474	Y64896	Homo sapiens	Human 5' EST related polypeptide	197	100
115	1483	gi436218	Homo sapiens	KIAA0037	295	76
116	1486	gi5852834	Homo sapiens	bridging integrator-2	133	64
117	149	gi3327162	Homo sapiens	KIAA0674 protein	2243	98
118	1503	gi1736785	Escherichia coli	.	1270	97
119	1506	gi4062298	Escherichia coli	YhhI protein	612	90
120	1513	gi4062346	Escherichia coli	.	556	94
121	1514	gi216609	Escherichia coli	PhoQ protein	661	90
122	1523	gi5712756	Rattus norvegicus	calcium transporter CaT1	1178	90
123	1527	gi1853980	Mus musculus	glucocorticoid receptor interacting protein 1	171	84
124	1536	Y17227	Homo sapiens	Human secreted	452	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein (clone yal-1).		
125	154	gi8515090	Pinus taeda	putative arabinogalactan protein	81	40
126	1544	gi3879933	Caenorhabditis elegans	Similarity to Xenopus F-spondin precursor (PIR Acc. No. comes from this gene	134	34
127	1554	gi6523817	Homo sapiens	SlR protein	255	84
128	1555	gi6635205	Homo sapiens	beta-ureidopropionase	210	90
129	1556	Y39286	Homo sapiens	Phosphodiesterase 10 (PDE10) clone FB93a.	161	61
130	1564	gi8977945	Streptomyces coelicolor A3(2)	putative secreted serine protease	231	45
131	1576	gi3025828	Rattus norvegicus	signal transducer and activator of transcription 4	183	97
132	1578	gi5106572	Homo sapiens	transcriptional activator SRCAP	758	98
133	1579	gi8575527	Homo sapiens	toll-like receptor 8	595	99
134	158	gi406058	Mus musculus	protein kinase	168	70
135	1580	gi63340	Gallus gallus	c-Rnil	231	90
136	1588	gi2217931	Homo sapiens	PKU-alpha	127	92
137	1589	gi1272422	Mus musculus	Phosphoinositide 3-kinase	720	99
138	159	gi2224629	Homo sapiens	KIAA0344	215	43
139	1600	gi1016012	Rattus norvegicus	neural cell adhesion protein BIG-2 precursor	543	93
140	161	gi6649583	Homo sapiens	kidney and liver proline	1651	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				oxidase 1		
141	1612	gi406113	Rattus norvegicus	protein kinase I	125	89
142	1615	gi219992	Homo sapiens	phSR2	150	78
143	1620	gi5714636	Homo sapiens	serine/threonine protein kinase Kp78 splice variant CTAK75a	126	71
144	1644	Y13352	Homo sapiens	Amino acid sequence of protein PRO228.	2542	100
145	1647	Y99444	Homo sapiens	Human PRO1575 (UNQ781) amino acid sequence	704	100
146	1650	gi3789765	Homo sapiens	transmembrane receptor UNC5C	271	100
147	1663	W75258	Homo sapiens	Fragment of human secreted protein encoded by gene 26.	163	96
148	1665	gi10432431	Homo sapiens	secreted modular calcium-binding protein	1428	99
149	1671	gi6708169	Mus musculus	inositol phosphatase eSHIPD183	169	97
150	1672	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	1030	99
151	1678	gi6063017	Homo sapiens	tousled-like kinase 1	132	86
152	1680	gi3510603	Homo sapiens	nuclear receptor co-repressor N-CoR	278	80
153	1692	gi1546084	Homo sapiens	farnesol receptor HRR-1	165	100
154	1698	gi520469	Oryctolagus cuniculus	597 aa protein related to	177	94

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Access- ion No.	Species	Description	Smith - Water man Score	% Identity
				Na/glucose cotransporters		
155	1702	gi10432 382	Homo sapiens		519	95
156	1704	Y91668	Homo sapiens	Human secreted protein sequence encoded by gene 73	214	75
157	1708	gi30807 57	Mus musculus	growth factor independence- 1B	457	78
158	1716	gi29653	Homo sapiens	putative oncogene	220	92
159	173	gi34524 73	Rattus norvegicus	serine/threo- nine protein kinase TAO1	699	100
160	1731	Y27581	Homo sapiens	Human secreted protein encoded by gene No. 15.	774	100
161	1732	gi96520 87	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	1025	98
162	174	Y35923	Homo sapiens	Extended human secreted protein sequence,	1691	100
163	1740	Y53014	Homo sapiens	Human secreted protein clone fn189_13 protein sequence	337	60
164	1748	gi77702 37	Homo sapiens	PRO2822	218	93
165	1751	gi89798 25	Homo sapiens		306	50
166	1755	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone	1184	62

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				3TW).		
167	1762	gi7380947	Homo sapiens	Gem-interacting protein	1545	99
168	1776	gi5912265	Homo sapiens	hypothetical protein	224	100
169	1777	Y70461	Homo sapiens	Human membrane channel protein-11 (MECHP-11).	413	95
170	1781	R26060	Homo sapiens	Growth Factor Receptor Bound protein GRB-1.	398	98
171	1796	gi10312169	Homo sapiens	serine carboxypeptidase 1 precursor protein	1381	99
172	180	gi3002527	Homo sapiens	neuronal thread protein AD7c-NTP	477	61
173	182	gi7385131	Homo sapiens	HBV pX associated protein-8; XAP-8	2066	82
174	1820	G03249	Homo sapiens	Human secreted protein,	370	97
175	1822	gi473969	Oryctolagus cuniculus	one of the members of sodium-glucose cotransporter family	1048	90
176	1829	gi10440355	Homo sapiens	FLJ00012 protein	310	96
177	1832	gi165650	Oryctolagus cuniculus	phosphorylase kinase beta-subunit	146	96
178	1834	W75132	Homo sapiens	Human secreted protein encoded by gene 11 clone HCENJ40.	423	47
179	1837	gi60369	Saimiriine herpesvirus 2	ORF 48~EDLF5~sim. to EBV BRRF2	615	71

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
180	1859	gi9989696	Homo sapiens	ROR2 protein	645	87
181	1880	gi7340847	Mus musculus	chondroitin 4-sulfotransferase	275	40
182	1881	gi7573291	Homo sapiens		298	100
183	1890	gi3149950	Homo sapiens	ST1C2	183	94
184	1899	gi2143260	Homo sapiens	Phosphoinositide 3-kinase	346	98
185	19	gi1808582	Homo sapiens	U2AF1-RS2	224	46
186	192	G03192	Homo sapiens	Human secreted protein,	267	86
187	1922	gi485858	Mus musculus	IB3/5-polypeptide	1206	78
188	1945	gi37261	Homo sapiens		1402	97
189	195	W67863	Homo sapiens	Human secreted protein encoded by gene 57 clone HFEBF41.	551	98
190	1957	gi406738	Homo sapiens	Shb	263	44
191	1969	Y41701	Homo sapiens	Human PRO708 protein sequence.	975	98
192	1970	gi3979817	Caenorhabditis elegans	Weak similarity to Human tyrosine-protein kinase CSK	254	49
193	1973	G00796	Homo sapiens	Human secreted protein,	365	98
194	1985	gi4558637	Homo sapiens	Putative homolog of hypoxia inducible factor three alpha	1420	99
195	1986	gi4455015	Homo sapiens	host cell factor homolog	367	50

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				LCP		
196	2	G02532	Homo sapiens	Human secreted protein,	106	85
197	2004	gi10503935	Homo sapiens	type A calpain-like protease	961	100
198	2023	gi1651341	Escherichia coli	.	1075	97
199	2025	Y71069	Homo sapiens	Human membrane transport protein, MTRP-14.	540	100
200	2038	gi8572543	Homo sapiens	membrane-associated lectin type-C	686	98
201	2041	gi37400	Homo sapiens	trk-2h polypeptide	228	89
202	2043	W75096	Homo sapiens	Human secreted protein encoded by gene 40 clone HNEDJ57.	290	38
203	2068	G03394	Homo sapiens	Human secreted protein,	595	97
204	2072	gi2116552	Rattus norvegicus	cationic amino acid transporter 3	1025	85
205	2076	gi157409	Drosophila melanogaster	fat protein	369	39
206	2078	gi1054940	Gallus gallus	CSH-PTP2	605	94
207	2084	gi9663128	Homo sapiens	hypothetical protein	874	99
208	2088	gi10567590	Homo sapiens	sodium bicarbonate cotransporter-like protein	609	100
209	2089	gi1789001	Escherichia coli	putative ATP-binding component of a transport system	961	98
210	2097	Y70460	Homo sapiens	Human membrane channel	258	96

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein-10 (MECHP-10) .		
211	2108	gi3207508	Rattus norvegicus	hexokinase	767	74
212	2111	gi6330233	Homo sapiens	KIAA1176 protein	3710	99
213	2118	W74797	Homo sapiens	Human secreted protein encoded by gene 68 clone HKIXR69.	156	96
214	2134	gi1780991	Homo sapiens	branched chain acyl-CoA oxidase	209	97
215	2146	gi7688148	Homo sapiens	hypothetical protein	1038	100
216	2149	gi2280485	Homo sapiens	KIAA0376	917	100
217	2153	gi1842429	Rattus norvegicus	ankyrin binding cell adhesion molecule neurofascin	592	88
218	2155	gi6526791	Homo sapiens	Eps15R	1126	100
219	2161	gi7300427	Drosophila melanogaster	CG7709 gene product	200	33
220	2163	Y52296	Homo sapiens	Human isomerase homologue-3 (HIH-3) .	186	91
221	2173	W34526	Homo sapiens	hTCP protein fragment.	164	93
222	2178	gi3360512	Rattus norvegicus	Citron-K kinase	299	94
223	2180	Y74008	Homo sapiens	Human prostate tumor EST fragment derived protein #195.	261	41
224	2184	gi53041	Mus musculus		130	41
225	2186	gi401774	Homo sapiens	ribosomal protein S6 kinase 3	142	64
226	2190	gi577295	Homo sapiens	The ha1225 gene product is related to human alpha-	176	100



SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				glucosidase.		
227	2210	gi2055392	Rattus norvegicus	transmembrane receptor UNC5H1	620	90
228	2214	gi7861733	Homo sapiens	low density lipoprotein receptor related protein-deleted in tumor	1360	98
229	2223	gi7959189	Homo sapiens	KIAA1464 protein	884	99
230	223	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	300	77
231	2233	gi7839587	Homo sapiens	organic anion transporting polypeptide 14	1092	99
232	2237	gi10440400	Homo sapiens	FLJ00033 protein	1212	99
233	2251	gi5923786	Homo sapiens	zinc metallo-protease ADAMTS6	277	44
234	2256	W63698	Homo sapiens	Human secreted protein 18.	516	100
235	2259	gi4678722	Homo sapiens	hypothetical protein	387	36
236	2262	Y33741	Homo sapiens	Beta-secretase.	793	99
237	2265	gi7018545	Homo sapiens	hypothetical protein	608	94
238	2271	gi4186183	Homo sapiens	unknown	684	53
239	2273	gi7243035	Homo sapiens	KIAA1327 protein	1031	100
240	2280	gi5809678	Homo sapiens	sperm membrane protein BS-63	342	95
241	2286	gi6224691	Homo sapiens	Na <sup>+</sup> /sulfate cotransporter SUT-1	1221	99
242	2291	gi207621	Rattus norvegicus	uromodulin	345	50
243	2292	gi7296304	Drosophila melanogaster	CG5274 gene product	272	35
244	2294	Y28503	Homo sapiens	HGFH3 Human Growth Factor	320	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				Homologue 3.		
245	2296	W88799	Homo sapiens	Polypeptide fragment encoded by gene 45.	223	86
246	2303	gi7110160	Homo sapiens	guanine nucleotide exchange factor	1212	99
247	2306	gi6434874	Mus musculus	calcium/calmodulin dependent protein kinase kinase alpha	576	84
248	2309	Y95433	Homo sapiens	Human calcium channel SOC-2/CRAC-1 C-terminal polypeptide.	1203	99
249	2313	gi7300943	Drosophila melanogaster	CG4677 gene product	689	79
250	2318	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	202	59
251	2329	G01772	Homo sapiens	Human secreted protein,	311	84
252	2330	Y41729	Homo sapiens	Human PRO1071 protein sequence.	886	99
253	2342	gi3786430	Caenorhabditis elegans		268	42
254	2350	gi930104	Homo sapiens	protein-tyrosine phosphatase	571	79
255	2359	gi9392591	Homo sapiens	CC chemokine CCL28	679	99
256	2361	gi1666689	Mus musculus	alpha-NAC, muscle-specific form gp220	357	41
257	2374	G03172	Homo sapiens	Human secreted protein,	112	78
258	2387	gi1399197	Homo sapiens	pyruvate dehydrogenase kinase isoform 4	201	85
259	2401	G01757	Homo sapiens	Human	612	99

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
260	2409	gi181123	Homo sapiens	cleavage signal 1 protein	194	86
261	2431	gi7018547	Homo sapiens	hypothetical protein	473	50
262	2432	gi4826496	Homo sapiens		327	39
263	2467	G03667	Homo sapiens	Human secreted protein,	640	97
264	2471	gi7688148	Homo sapiens	hypothetical protein	1284	91
265	2478	gi790819	Homo sapiens	polycystic kidney disease-associated protein	615	90
266	2484	gi3327080	Homo sapiens	KIAA0633 protein	1747	99
267	249	G03793	Homo sapiens	Human secreted protein,	139	65
268	2490	gi6467371	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	757	98
269	25	G03203	Homo sapiens	Human secreted protein,	137	65
270	2504	gi4097712	Homo sapiens	HBV associated factor	166	74
271	2506	gi2072784	Homo sapiens	Na <sup>+</sup> /nucleoside cotransporter	201	95
272	2507	gi5924007	Homo sapiens		335	38
273	2510	gi7717385	Homo sapiens	beta-site APP-cleaving enzyme 2, EC 3.4.23.	383	89
274	2523	gi339709	Homo sapiens		150	96
275	253	gi36615	Homo sapiens	serine/threonine protein kinase	391	77
276	2533	gi45896	Homo sapiens	KIAA0985	191	61

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		14		protein		
277	2536	gi2088685	Caenorhabditis elegans	strong similarity to the CDC2/CDX subfamily of ser/thr protein kinases	419	55
278	2544	gi1002425	Mus musculus	YSPL-1 form 2	280	80
279	2568	Y41738	Homo sapiens	Human PRO541 protein sequence.	379	49
280	2580	gi3004482	Rattus norvegicus	putative integral membrane transport protein	382	49
281	2593	gi7300049	Drosophila melanogaster	CG4525 gene product	582	50
282	2600	gi4530437	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	334	90
283	2625	gi8099652	Homo sapiens	toll-like receptor 9 form A	761	96
284	2641	gi148019	Escherichia coli	tolA	692	100
285	2667	gi1750387	Pseudomonas aeruginosa	Carbamoyl-phosphate synthetase large subunit	143	76
286	2670	gi4883437	Mus musculus	RNA binding protein	139	92
287	2673	Y66656	Homo sapiens	Membrane-bound protein PRO943.	1869	98
288	2676	gi3885978	Mus musculus	mismatch-specific thymine-DNA glycosylate	123	88
289	2680	gi6453438	Homo sapiens	hypothetical protein	465	82
290	2682	gi18417	Mus musculus	GATA-5	527	77

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		56		cardiac transcription factor		
291	2684	gi9844920	Homo sapiens	nicotinic acetylcholine receptor subunit alpha 10	294	88
292	2695	gi1789764	Escherichia coli	putative transport	879	98
293	2697	gi349229	Escherichia coli	peripheral membrane protein	936	99
294	2698	gi4062194	Escherichia coli	.	737	100
295	2700	gi529240	Escherichia coli	homoserine kinase	578	100
296	2704	gi1552831	Escherichia coli	hypothetical	420	100
297	2712	gi1789672	Escherichia coli	putative ATP-binding component of a transport system	262	100
298	2716	gi4062409	Escherichia coli	Transmembrane protein dppC	382	100
299	2719	gi304976	Escherichia coli	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar	921	95
300	2724	gi145856	Escherichia coli	nmpC	647	97
301	2725	gi1789473	Escherichia coli	putative transport protein	312	100
302	2728	gi1805561	Escherichia coli		222	97
303	2729	gi43248	Escherichia coli		655	91
304	2744	gi396299	Escherichia coli	similar to E. coli pyruvate formate-lyase activating enzyme	675	100
305	2749	gi1742648	Escherichia coli	.	592	100
306	2752	gi40622	Escherichia	Sensor kinase	357	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		36	coli	CitA		
307	2762	gi1787795	Escherichia coli	putative LACI-type transcriptional regulator	342	100
308	2764	gi1799743	Escherichia coli	putative LACI-type transcriptional regulator	151	84
309	2768	gi405964	Escherichia coli	yohG	534	94
310	2774	gi4062338	Escherichia coli	.	387	97
311	2790	gi4062338	Escherichia coli	.	420	86
312	2800	gi1789805	Escherichia coli	putative transport	572	100
313	2811	gi5305333	Mus musculus	protein kinase Myak-S	421	49
314	2827	gi10047251	Homo sapiens	KIAA1588 protein.	531	97
315	2830	G02872	Homo sapiens	Human secreted protein,	185	62
316	2836	gi191175	Cricetulus sp.	cAMP-dependent protein kinase alpha-catalytic subunit	1677	97
317	2851	gi558846	Homo sapiens	BCL2/adeno-virus E1B 19kD-interacting protein 3	220	61
318	2856	gi3882211	Homo sapiens	KIAA0745 protein	232	93
319	2866	gi6329708	Homo sapiens	KIAA1119 protein	1331	91
320	2874	gi2853033	Mus musculus	tousled-like kinase	203	82
321	2882	gi10185134	Schizosaccharomyces pombe	hypothetical zinc-finger protein	318	42
322	2886	G03797	Homo sapiens	Human secreted protein,	140	69
323	2899	gi4240325	Homo sapiens	KIAA0918 protein	170	53

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
324	2906	Y94988	Homo sapiens	Human secreted protein vll_1,	1738	100
325	2920	gi9453735	Homo sapiens		1926	100
326	2925	gi6434876	Homo sapiens	CDK4-binding protein p34SEI1	1210	100
327	2930	gi3941320	Schistosoma japonicum	myosin	208	28
328	2934	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-7).	642	63
329	2955	G01165	Homo sapiens	Human secreted protein,	528	99
330	2967	gi7263960	Homo sapiens		466	100
331	2980	gi4589530	Homo sapiens	KIAA0943 protein	1849	94
332	2994	G03812	Homo sapiens	Human secreted protein,	124	61
333	2996	gi9857400	Homo sapiens	tumor endothelial marker 1 precursor	2666	98
334	2999	Y66697	Homo sapiens	Membrane-bound protein PRO1383.	2254	100
335	3	gi6289072	Homo sapiens	JM24 protein	930	100
336	3008	Y45219	Homo sapiens	Human CASB47 protein.	557	92
337	3013	gi5262678	Homo sapiens	hypothetical protein	1747	100
338	3041	Y73335	Homo sapiens	HTRM clone 1850120 protein sequence.	1315	99
339	306	gi4868443	Mesocricetus auratus	Mx-interacting protein kinase PKM	1867	95
340	3061	gi433338	Homo sapiens	protein-tyrosine kinase	3934	94

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
341	309	Y76145	Homo sapiens	Human secreted protein encoded by gene 22.	1313	99
342	3095	gi7300159	Drosophila melanogaster	CG14899 gene product	190	57
343	3098	gi532056	Homo sapiens	protein-tyrosine-phosphatase	2641	86
344	3105	gi285987	Homo sapiens	mitochondrial outer membrane protein 19	192	71
345	3118	gi9929935	Macaca fascicularis	hypothetical protein	180	61
346	3124	gi8131903	Mus musculus	transient receptor potential-related protein	226	100
347	3126	Y02370	Homo sapiens	Polypeptide identified by the signal sequence trap method.	261	100
348	3166	gi7290860	Drosophila melanogaster	CG1531 gene product	534	42
349	3175	gi6649583	Homo sapiens	kidney and liver proline oxidase 1	1752	95
350	3176	gi7208438	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1048	95
351	3188	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	243	57
352	3191	gi7105926	Homo sapiens	calcium channel alpha2-delta3 subunit	300	96
353	3208	gi10334774	Homo sapiens	MUCDHL-FL	613	98
354	3226	Y87209	Homo sapiens	Human secreted protein sequence	3147	99



SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
355	3235	gi6715135	Homo sapiens	Fanconi anemia, complementation group F	1947	99
356	3257	gi5441615	Canis familiaris	zinc finger protein	326	42
357	3282	G03002	Homo sapiens	Human secreted protein,	211	61
358	3289	gi3288457	Homo sapiens	PI3-kinase	5832	97
359	3296	gi7770139	Homo sapiens	PRO1722	293	64
360	3298	gi2198815	Ambystoma tigrinum	electrogenic Na <sup>+</sup> bicarbonate cotransporter; NBC	1278	52
361	3303	gi4028015	Homo sapiens	potassium channel	1881	92
362	3305	gi5902966	Homo sapiens	very large G-protein coupled receptor-1	1770	100
363	3308	gi219944	Homo sapiens	The first in-frame ATG codon is located at nucleotides NPPase.	3967	86
364	3325	gi3510234	Homo sapiens	R31237_1, partial CDS	192	94
365	3341	W78899	Homo sapiens	Human UNC-5 homologue UNC5H-1.	1614	90
366	3342	gi1478205	Mus musculus	PNG protein	341	70
367	3350	gi2739460	Bos taurus	regulator of G-protein signaling 7	2263	98
368	3372	gi7671663	Homo sapiens		375	79
369	338	Y84322	Homo sapiens	A human cardiovascular system associated protein kinase-3.	2606	100
370	3383	gi10441	Homo sapiens	protein	1127	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		382		kinase		
371	3395	gi530823	Homo sapiens	epidermal growth factor receptor kinase substrate	402	47
372	3405	Y29332	Homo sapiens	Human secreted protein clone pe584_2 protein sequence.	1220	94
373	3408	gi3334741	Homo sapiens	shal-type potassium channel	2888	90
374	345	gi4539527	Homo sapiens	NAALADase L protein	600	72
375	346	Y95434	Homo sapiens	Human calcium channel SOC-3/CRAC-2 C-terminal polypeptide.	1802	99
376	3470	gi9798452	Homo sapiens	putative capacitative calcium channel	277	100
377	3482	gi3818572	Homo sapiens	cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase	2353	96
378	3492	gi1665825	Homo sapiens		3878	99
379	3530	gi505100	Homo sapiens	KIAA0066	3637	100
380	3533	Y32169	Homo sapiens	Human growth-associated protease inhibitor heavy chain precursor.	2860	99
381	3545	gi6624133	Homo sapiens		449	98
382	3549	gi1469193	Homo sapiens	The KIAA0135 gene is related to	5374	99

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				pim-1 oncogene.		
383	3595	gi6330190	Homo sapiens	KIAA1169 protein	1893	100
384	3601	gi808915	Homo sapiens	tumor necrosis factor receptor type 1 associated protein	992	99
385	3612	gi5305448	Mus musculus	SH2-B PH domain containing signaling mediator 1 gamma isoform	1439	92
386	3613	Y32194	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 266775.	1438	100
387	3621	gi897849	Mus musculus	ubiquitinating enzyme E2-230 kDa	393	68
388	3624	R47858	Homo sapiens	Human LDL receptor Domains 1 and 2.	2895	100
389	3625	Y57949	Homo sapiens	Human transmembrane protein HTMPN-73.	1868	100
390	3626	W69342	Homo sapiens	Secreted protein of clone CJ424_9.	442	94
391	3627	gi6537136	Homo sapiens	putative organic anion transporter	982	92
392	3630	Y06886	Homo sapiens	HWHHJ20 polypeptide.	1109	91
393	3642	gi4886467	Homo sapiens	hypothetical protein	570	52
394	3645	gi9588402	Homo sapiens		598	98
395	3647	Y12050	Homo sapiens	Human 5' EST secreted protein	517	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
396	3653	Y70018	Homo sapiens	Human Protease and associated protein-12 (PPRG-12).	2232	99
397	3676	W67818	Homo sapiens	Human secreted protein encoded by gene 12 clone HMSJJ74.	338	100
398	3677	gi32093	Homo sapiens	HGMP07J	650	52
399	3681	Y48443	Homo sapiens	Human prostate cancer-associated protein 140.	803	93
400	3682	gi4691726	Homo sapiens	ARF GTPase-activating protein GIT1	2435	91
401	3688	gi6693824	Homo sapiens	ubiquitin-specific protease	1995	99
402	3689	Y94927	Homo sapiens	Human secreted protein clone ck213_12 protein sequence	530	81
403	3690	gi1871612	Oryctolagus cuniculus	ryanodine receptor	594	95
404	3706	gi6002714	Homo sapiens	membrane-type serine protease 1	2630	94
405	3714	gi2695708	Homo sapiens	SPOP	553	81
406	3720	gi9309293	Homo sapiens	asc-type amino acid transporter 1	566	95
407	3726	gi10440381	Homo sapiens	FLJ00026 protein	1023	69
408	373	gi5714696	Mus musculus	alpha 2 delta calcium channel subunit	243	95
409	3788	gi6911219	Homo sapiens	type II membrane serine protease	841	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
410	3789	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	1084	95
411	3790	gi1524088	Homo sapiens	Polio virus receptor protein	1508	99
412	3801	gi6723675	Homo sapiens	mitotic kinase-like protein-1	2035	99
413	3803	gi968973	Homo sapiens	mitotic kinase-like protein-1	332	86
414	3820	gi1770478	Homo sapiens	NK receptor	1988	99
415	3831	gi2781386	Homo sapiens		1493	99
416	3837	gi9367840	Homo sapiens	neuronal apoptosis inhibitory protein 2	2243	99
417	385	gi1526978	Homo sapiens	ryanodine receptor 2	149	96
418	3856	gi995654	Homo sapiens	interleukin-11 receptor	147	100
419	386	gi4960038	Mus musculus	T2K protein kinase homolog	669	66
420	3861	Y74129	Homo sapiens	Human prostate tumor EST fragment derived protein #316.	842	98
421	3883	gi6635205	Homo sapiens	beta-ureidopropionase	1576	100
422	3898	gi37231	Homo sapiens	DNA topoisomerase II	8436	99
423	3921	gi8648881	Homo sapiens	putative organic anion transporter	131	100
424	3932	gi8575775	Homo sapiens	KRAB zinc finger protein	1935	99
425	3934	gi4689128	Homo sapiens	SIH003	127	92
426	3963	gi3212996	Homo sapiens		339	64
427	3974	G03790	Homo sapiens	Human	232	63

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
428	3983	gi181971	Homo sapiens	vascular endothelial growth factor	433	85
429	3999	gi1657464	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-G	484	75
430	4001	gi6572230	Homo sapiens		329	100
431	4009	gi2143260	Homo sapiens	phosphoinositide 3-kinase	521	99
432	401	gi6572379	Homo sapiens		1372	56
433	4020	gi2815624	Homo sapiens	tumor necrosis factor superfamily member LIGHT	1252	100
434	4024	Y21166	Homo sapiens	Human bcl2 proto-oncogene mutant protein fragment 14.	84	40
435	4040	Y57285	Homo sapiens	Human GPCR protein (HGPRP) sequence (clone ID 2214673).	1726	99
436	4057	W74873	Homo sapiens	Human secreted protein encoded by gene 145 clone HFXHL79.	531	100
437	4066	G03714	Homo sapiens	Human secreted protein,	92	70
438	4067	gi8331760	Homo sapiens	LU1 protein	1077	92
439	4078	Y57900	Homo sapiens	Human transmembrane protein HTPN-24.	996	100
440	4120	gi18715	Homo sapiens	mitogen-	927	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		39		activated protein kinase phosphatase 4		
441	4123	gi5360125	Homo sapiens	NY-REN-58 antigen	140	100
442	4130	gi6289072	Homo sapiens	JM24 protein	604	100
443	4133	gi8575527	Homo sapiens	toll-like receptor 8	755	100
444	4166	gi6118555	Homo sapiens	DEAD-box protein abstrakt	2512	100
445	4167	gi3800830	Rattus norvegicus	putative four repeat ion channel	615	93
446	4172	gi7209676	Homo sapiens	potassium channel Kv8.1	369	100
447	4185	gi5305405	Homo sapiens	Na <sup>+</sup> /H <sup>+</sup> exchanger isoform 2	1769	100
448	4197	gi2811122	Xenopus laevis	NaDC-2	524	69
449	4203	Q89840_aa1	Homo sapiens	Human death associated protein DAP-3.	198	97
450	4262	gi5901478	Marmota marmota	olfactory receptor	209	92
451	4276	gi32456	Homo sapiens	protein-tyrosine phosphatase	3270	99
452	4283	R41231	Homo sapiens	GAT-2 transporter gene.	477	100
453	4331	gi3171912	Homo sapiens	RAMP2	443	98
454	4340	gi8118223	Homo sapiens	unknown	1330	100
455	4351	gi1754515	Rattus norvegicus	aminopeptidase -B	2050	92
456	4354	Y57906	Homo sapiens	Human transmembrane protein HTPN-30.	1402	100
457	4385	gi5596433	Homo sapiens	candidate tumor suppressor protein NOC2	509	97

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
458	4388	W78140	Homo sapiens	Human secreted protein encoded by gene 15 clone HSDES04.	100	94
459	4405	Y48226	Homo sapiens	Human prostate cancer-associated protein 12.	1246	99
460	441	gi291536	Bovine herpesvirus 1	BICP4	106	35
461	4417	gi6562533	Homo sapiens	sialin	939	100
462	4419	gi1841555	Homo sapiens	NG5	146	33
463	4443	gi496139	Mus musculus	AMPA selective glutamate receptor	262	94
464	4470	gi7248381	Homo sapiens	adaptor protein p130Cas	2592	100
465	4482	gi7329979	Homo sapiens	apoptosis regulator	2071	100
466	4487	gi6706659	Homo sapiens		405	100
467	4491	gi9837341	Homo sapiens	CamKI-like protein kinase	1044	100
468	4492	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	586	99
469	4497	gi6179740	Homo sapiens	paraneoplastic cancer-testis-brain antigen	352	37
470	4502	gi6329742	Homo sapiens	KIAA1124 protein	327	100
471	4519	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence	1563	100
472	4526	Y08008	Homo sapiens	Human HLIG-1 protein.	4023	99
473	4547	gi4589562	Homo sapiens	KIAA0959 protein	4165	99
474	4554	gi1381029	Mus musculus		1164	77



SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
475	4555	gi2792366	Homo sapiens	unknown protein IT12	4461	99
476	457	Y70551	Homo sapiens	Human latent transforming growth factor-beta binding protein 3 (I).	1825	100
477	4571	gi5360115	Homo sapiens	NY-REN-45 antigen	869	100
478	4613	Y05868	Homo sapiens	Human Toll protein PRO358.	2413	100
479	4614	Y27129	Homo sapiens	Human bone marrow-derived polypeptide (clone OAF038-Leu).	1815	100
480	4622	G03789	Homo sapiens	Human secreted protein,	173	53
481	4667	gi7673638	Danio rerio	Deddl	446	48
482	4670	gi402649	Homo sapiens	c-rel	2309	100
483	4683	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2234	99
484	4698	Y73470	Homo sapiens	Human secreted protein clone yd141_1 protein sequence	746	100
485	4724	gi6456846	Homo sapiens	hypothetical protein	1101	99
486	4734	gi3334982	Homo sapiens	R27216_1	1151	80
487	4814	gi6274473	Homo sapiens	pregnancy-induced growth inhibitor	1348	100
488	4819	Y07825	Homo sapiens	Human secreted protein fragment #4 encoded from	117	67

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				gene 28.		
489	4821	Y81498	Homo sapiens	Human foetal bone-derived growth factor-like protein.	1200	100
490	4851	gi56894 91	Homo sapiens	KIAA1077 protein	4364	99
491	4872	gi59119 53	Homo sapiens	hypothetical protein	3723	99
492	4902	B08917	Homo sapiens	Human secreted protein sequence encoded by gene 27	717	100
493	5006	gi43577 4	Homo sapiens	receptor tyrosine kinase isoform FLT4 long, FLT41 {C-terminal}	385	100
494	5007	Y93951	Homo sapiens	Amino acid sequence of a Brainiac-5 polypeptide.	804	100
495	5027	gi35487 91	Homo sapiens	R33590_1	1606	100
496	5029	gi56895 27	Homo sapiens	KIAA1095 protein	5722	99
497	5033	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	166	66
498	5040	Y95019	Homo sapiens	Human secreted protein vq1_1,	258	92
499	5061	gi13044 34	Pseudorabies virus	EP0	85	38
500	5081	gi40380 81	Homo sapiens	vascular endothelial cell growth inhibitor	134	100
501	5129	gi31691 58	Homo sapiens	BC269730_2	2340	99
502	5139	gi40628 56	Homo sapiens	HEXIM1 protein	293	47
503	5174	gi93685	Homo sapiens	140up gene	576	90

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		40		product		
504	524	G00329	Homo sapiens	Human secreted protein,	565	100
505	5291	Y92515	Homo sapiens	Human OXRE-12.	1271	98
506	5335	gi7296158	Drosophila melanogaster	CG3862 gene product	753	46
507	5346	Y94987	Homo sapiens	Human secreted protein vj1_1,	849	100
508	5379	gi7144506	Homo sapiens	cytokine-inducible SH2-containing protein	1353	99
509	5441	gi8096551	Homo sapiens	similar to mouse Ehm2	1516	100
510	549	Y22113	Homo sapiens	Human ZSMF-3 protein sequence.	294	62
511	5542	Y76267	Homo sapiens	Fragment of human secreted protein encoded by gene 11.	1066	100
512	5560	G03790	Homo sapiens	Human secreted protein,	103	36
513	5696	gi7920398	Homo sapiens	PTOV1	1904	91
514	5704	B08930	Homo sapiens	Human secreted protein sequence encoded by gene 2	987	100
515	5758	W18878	Homo sapiens	Human protein kinase C inhibitor, IPKC-1.	368	100
516	5760	gi6562176	Homo sapiens	hypothetical protein	425	100
517	5763	Y41706	Homo sapiens	Human PRO381 protein sequence.	441	100
518	5787	Y57907	Homo sapiens	Human transmembrane protein HTPN-31.	952	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
519	5823	gi9800242	rat cytomegalovirus Maastricht	pr5	153	36
520	5886	gi1781037	Mus musculus	neuronal tyrosine threonine phosphatase 1	1135	52
521	5924	W69221	Homo sapiens	Human parotid secretory protein.	710	96
522	5960	Y91529	Homo sapiens	Human secreted protein sequence encoded by gene 79	1300	99
523	5962	W69784	Homo sapiens	Protein Kinase C Inhibitor-like Protein (IPKC-2).	395	100
524	5969	Y79141	Homo sapiens	Human haemopoietic stem cell regulatory protein SCM113.	1205	79
525	5976	gi780310	Homo sapiens	natural killer associated transcript 4	1808	91
526	6002	gi2104553	Homo sapiens		4367	67
527	6008	Y66765	Homo sapiens	Membrane-bound protein PRO1384.	822	100
528	6020	gi1911548	Homo sapiens	cytochrome c-like polypeptide	322	50
529	6036	W71362	Homo sapiens	Human cytokine/steroid receptor protein.	353	51
530	6070	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	626	100
531	6075	gi10732648	Homo sapiens	angiopoietin-like protein	2164	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				PP1158		
532	6106	gi2217970	Homo sapiens	p40	1349	96
533	6420	W82000	Homo sapiens	Human adult brain secreted protein dm26_2.	929	100
534	6434	gi10732648	Homo sapiens	angiopoietin-like protein PP1158	2164	100
535	6439	gi189701	Homo sapiens	endothelial cell growth factor	376	100
536	6463	Y41720	Homo sapiens	Human PRO792 protein sequence.	360	82
537	6466	gi4884084	Homo sapiens	hypothetical protein	538	100
538	6508	gi5442030	Homo sapiens	aminopeptidase	2317	96
539	6570	gi5921491	Homo sapiens		1591	99
540	6719	gi31847	Homo sapiens	glypican	1625	87
541	6772	Y65432	Homo sapiens	Human 5' EST related polypeptide	180	53
542	6789	gi537292	Homo sapiens	ICH-1L	1556	100
543	6805	gi4454702	Homo sapiens	HSPC007	634	84
544	6833	gi1890660	Homo sapiens	protein tyrosine phosphatase receptor omicron	5726	87
545	6834	gi5921491	Homo sapiens		1746	88
546	6851	gi2407641	Homo sapiens	neuropilin	3968	98
547	6868	gi6714641	Drosophila melanogaster	MAP kinase phosphatase	218	49
548	6876	Y13138	Homo sapiens	Human secreted protein encoded by 5' EST	414	76
549	688	Y73463	Homo sapiens	Human secreted protein clone	701	98

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				yk199_1 protein sequence		
550	6897	gi58151 80	Homo sapiens	unknown	509	97
551	690	gi10645 186	Homo sapiens	meningioma- expressed antigen 5s splice variant	522	100
552	6909	W78149	Homo sapiens	Human secreted protein encoded by gene 24 clone HSVBF78.	485	100
553	6924	Y35923	Homo sapiens	Extended human secreted protein sequence,	514	99
554	6937	G03798	Homo sapiens	Human secreted protein,	281	70
555	6951	gi51185 7	Homo sapiens	prostate- specific antigen	364	95
556	7008	G03200	Homo sapiens	Human secreted protein,	548	98
557	7009	Y22213	Homo sapiens	Human V201 protein sequence.	856	100
558	7057	gi60036 54	Homo sapiens	brain specific membrane- anchored protein BSMAP	1814	100
559	7098	W27291	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
560	7114	gi32121 10	Homo sapiens	prefoldin subunit 1	534	98
561	712	gi45586 41	Homo sapiens	P85B HUMAN; PTDINS-3- KINASE P85- BETA	470	74
562	7215	gi48683 66	Homo sapiens	delta-6 fatty acid desaturase	2437	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
563	7244	Y12445	Homo sapiens	Human 5' EST secreted protein	428	100
564	7248	gi311376	Homo sapiens	Humig	633	100
565	7252	gi5689531	Homo sapiens	KIAA1097 protein	5240	100
566	7292	gi5106998	Homo sapiens	HSPC040 protein	580	100
567	7306	Y32201	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2057886.	1974	95
568	7338	Y73880	Homo sapiens	Human prostate tumor EST fragment derived protein #67.	1566	100
569	736	gi10178317	Homo sapiens		1468	100
570	737	G00851	Homo sapiens	Human secreted protein,	522	98
571	740	W85610	Homo sapiens	Secreted protein clone eh80_1.	1115	87
572	7400	Y93948	Homo sapiens	Amino acid sequence of a lectin ss3939 polypeptide.	1982	98
573	7415	gi3043670	Homo sapiens	KIAA0573 protein	2392	100
574	7429	Y40864	Homo sapiens	A human glutathione-S-transferase (hGST) protein.	1183	99
575	7458	Y53643	Homo sapiens	A bone marrow secreted protein designated BMS6.	554	99
576	7516	gi4468311	Homo sapiens		1146	99
577	7526	gi4138922	Homo sapiens	promyelocytic leukemia zinc finger	3571	99

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				protein; kruppel-like zinc finger protein; PLZF		
578	7571	G02915	Homo sapiens	Human secreted protein,	209	100
579	7614	W74726	Homo sapiens	Human secreted protein fg949_3.	1879	100
580	7663	gi5912548	Homo sapiens		1634	100
581	7686	gi4929711	Homo sapiens	CGI-121 protein	870	100
582	7714	gi388765	Homo sapiens	phospholipase D	4428	99
583	7724	G03933	Homo sapiens	Human secreted protein,	570	100
584	7834	gi8919166	Homo sapiens	mesenchymal stem cell protein DSC92	1133	100
585	7855	Y48505	Homo sapiens	Human breast tumour-associated protein 50.	684	100
586	7870	Y13372	Homo sapiens	Amino acid sequence of protein PRO223.	2559	100
587	7871	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93	768	100
588	7892	gi34659	Homo sapiens	macrophage inflammatory protein-2alpha precursor	532	100
589	7927	gi32575	Homo sapiens		183	91
590	7944	gil657458	Sus scrofa	calcium/calmodulin-dependent protein kinase II isoform gamma-B	2744	100
591	7947	G01131	Homo sapiens	Human	574	96



SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Acces- sion No.	Species	Description	Smith - Water man Score	% Identity
				secreted protein,		
592	800	gi30214 28	Homo sapiens	neutral sphingomyelina se	167	68
593	8055	gi49296 37	Homo sapiens	CGI-84 protein	1038	100
594	8082	gi46790 14	Homo sapiens	HSPC014	715	100
595	8127	gi99556 93	Homo sapiens	twisted gastrulation protein	905	95
596	8174	gi55322 94	Homo sapiens	MUM2	767	100
597	8178	gi45305 87	Homo sapiens	TADA1 protein	1132	100
598	8215	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
599	8263	Y48371	Homo sapiens	Human prostate cancer- associated protein 68.	713	98
600	827	gi31723 37	Cavia porcellus	phospholipase B	955	73
601	828	Y29517	Homo sapiens	Human lung tumour protein SAL-82 predicted amino acid sequence.	833	94
602	8294	gi49297 67	Homo sapiens	CGI-149 protein	1085	100
603	8313	gi57714 20	Homo sapiens	group IID secretory phospholipase A2	852	100
604	832	Y86260	Homo sapiens	Human secreted protein HELHN47,	319	78
605	8357	gi41913 58	Mus musculus	claudin-7	164	47
606	8373	gi19452 71	Homo sapiens	protein phosphatase 6	1666	100
607	8379	gi58529	Homo sapiens		1226	100

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		81		cardiotrophin-like cytokine CLC		
608	8380	gi3402216	Homo sapiens	protein	974	100
609	8386	gi386988	Homo sapiens	oncostatin M	1297	99
610	8418	Y70210	Homo sapiens	Human TANGO 130 protein.	722	98
611	8442	G01895	Homo sapiens	Human secreted protein,	490	95
612	8457	G04048	Homo sapiens	Human secreted protein,	450	98
613	8458	W97119	Homo sapiens	S-adenosyl-L-methyltransferase (SAM-MT) protein.	1484	100
614	8469	gi7159799	Homo sapiens		255	100
615	8480	gi4589530	Homo sapiens	KIAA0943 protein	1998	100
616	8521	gi5726235	multiple sclerosis associated retrovirus element	unknown protein U5/2	250	82
617	857	gi9663958	Homo sapiens	cysteinyl leukotriene CysLT2 receptor	612	99
618	8574	gi6841260	Homo sapiens	HSPC305	1049	100
619	8606	gi3367707	Homo sapiens	scrapie responsive protein 1	544	100
620	8632	G01158	Homo sapiens	Human secreted protein,	502	100
621	8646	gi3882249	Homo sapiens	KIAA0764 protein	2175	100
622	8666	Y66196	Homo sapiens	Human bladder tumour EST encoded protein 54.	1080	95
623	8675	gi9963908	Homo sapiens	NPD009	432	96
624	8683	G04018	Homo sapiens	Human	469	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein,		
625	8708	gi1633564	Homo sapiens	C8	364	98
626	8720	gi8248465	Homo sapiens	hepatocellular carcinoma-associated antigen 56A	191	69
627	8756	Y94984	Homo sapiens	Human secreted protein vell_1,	369	97
628	8765	Y00346	Homo sapiens	Fragment of human secreted protein encoded by gene 2.	1068	97
629	8783	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	1051	95
630	8804	Y25426	Homo sapiens	Human SIGIRR protein.	887	100
631	8838	Y99409	Homo sapiens	Human PRO1343 (UNQ698) amino acid sequence	1279	100
632	8851	W74785	Homo sapiens	Human secreted protein encoded by gene 56 clone HSAXS65.	454	100
633	8853	W75116	Homo sapiens	Human secreted protein encoded by gene 60 clone HILCJ01.	245	95
634	8857	gi2565196	Homo sapiens	non-functional folate binding protein	479	74
635	8859	Y02690	Homo sapiens	Human secreted protein encoded by gene 41c lone	600	100

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				HSZAF47.		
636	8901	Y86491	Homo sapiens	Human gene 59-encoded protein fragment,	548	99
637	8907	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone HTSEV09.	2004	99
638	8934	W75088	Homo sapiens	Human secreted protein encoded by gene 32 clone HAGBB70.	421	98
639	8960	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	267	72
640	8979	Y76143	Homo sapiens	Human secreted protein encoded by gene 20.	1374	98
641	8980	Y11433	Homo sapiens	Human 5' EST secreted protein	466	100
642	8986	G02626	Homo sapiens	Human secreted protein,	306	100
643	8987	G02093	Homo sapiens	Human secreted protein,	486	97
644	8995	Y12908	Homo sapiens	Human 5' EST secreted protein	181	100
645	9035	Y71108	Homo sapiens	Human Hydrolase protein-6 (HYDRL-6).	800	100
646	9062	gi88860 05	Homo sapiens	lysophosphatid ic acid acyltransferase- delta	523	100
647	9074	Y25761	Homo sapiens	Human	1366	99

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				secreted protein encoded from gene 51.		
648	9075	Y73336	Homo sapiens	HTRM clone 1852290 protein sequence.	1591	100
649	9098	Y57878	Homo sapiens	Human transmembrane protein HTPN-2.	516	100
650	9109	gi23903	Homo sapiens	63kDa protein kinase	1141	97
651	911	gi32456	Homo sapiens	protein-tyrosine phosphatase	2591	100
652	912	gi1136743	Homo sapiens	human P5	212	46
653	9163	Y34129	Homo sapiens	Human potassium channel K+Hnov28.	377	71
654	9164	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNF1Y77.	1083	99
655	9173	gi6851256	Mus musculus	protein tyrosine phosphatase-like protein PTPLB	631	93
656	9187	Y66721	Homo sapiens	Membrane-bound protein PRO511.	1173	95
657	9190	W40378	Homo sapiens	Human breast cancer protein CH14-2a16-1 from 2.0 kB DNA fragment #2.	792	81
658	9194	Y02781	Homo sapiens	Human secreted protein.	462	70
659	9210	G02994	Homo sapiens	Human secreted protein,	166	80

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
660	9222	G02520	Homo sapiens	Human secreted protein,	186	43
661	9230	gi6706554	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase B	1315	95
662	9258	gi522145	Homo sapiens	B-cell growth factor	120	56
663	9260	G04072	Homo sapiens	Human secreted protein,	138	51
664	9271	gi6690095	Homo sapiens	tetraspanin protein	317	67
665	9272	gi163042	Bos taurus	factor activating exoenzyme S	444	72
666	9275	gi401774	Homo sapiens	ribosomal protein S6 kinase 3	424	81
667	930	G02355	Homo sapiens	Human secreted protein,	167	41
668	9304	gi8979743	Canis familiaris	Band4.1-like5 protein	1493	93
669	9346	gi2738989	Mus musculus	high mobility group protein homolog HMG4	384	89
670	9347	gi36613	Homo sapiens	serine/threonine protein kinase	199	91
671	935	gi5541870	Homo sapiens	QA79 membrane protein, allelic variant airm-1b	334	57
672	9350	gi3327124	Homo sapiens	KIAA0655 protein	757	87
673	9351	W57260	Homo sapiens	Human semaphorin Y.	573	95
674	9356	gi59977	Human endogenous retrovirus	tripartite fusion transcript PLA2L	127	59
675	9363	Y17834	Homo sapiens	Human PRO361 protein sequence.	968	92
676	9366	gi72431	Homo sapiens	KIAA1374	649	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Access- ion No.	Species	Description	Smith - Water man Score	% Identity
		29		protein		
677	9369	G03793	Homo sapiens	Human secreted protein,	222	69
678	9378	gi44683 11	Homo sapiens		163	39
679	9393	gi27389 89	Mus musculus	high mobility group protein homolog HMG4	384	89
680	9444	G01399	Homo sapiens	Human secreted protein,	157	93
681	9467	gi44547 02	Homo sapiens	HSPC007	230	71
682	9486	gi10047 243	Homo sapiens	KIAA1584 protein	605	93
683	949	Y30895	Homo sapiens	Human secreted protein fragment encoded from gene 25.	704	99
684	9499	W36002	Homo sapiens	Human Fchd531 gene product.	2173	96
685	9510	gi16657 99	Homo sapiens		867	83
686	9523	Y53022	Homo sapiens	Human secreted protein clone qf116_2 protein sequence	1252	89
687	9534	Y66670	Homo sapiens	Membrane- bound protein PRO1180.	998	100
688	9539	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	633	100
689	954	G02490	Homo sapiens	Human secreted protein,	160	78
690	9546	gi18112 1	Homo sapiens	chorionic somatomammotro pin	616	96
691	955	gi72431 03	Homo sapiens	KIAA1361 protein	2042	100
692	9551	gi17723	Homo sapiens	ras-related	341	57

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		45		GTP-binding protein		
693	9558	W88403	Homo sapiens	Human adult testis secreted protein ga63_6.	2252	100
694	9561	gi6690017	Herpesvirus papio	NTR	100	30
695	957	Y86260	Homo sapiens	Human secreted protein HELHN47,	319	78
696	9572	gi972940	Mus musculus	Elf-1	806	92
697	9576	gi3249005	Homo sapiens	geminin	448	98
698	9586	gi2887288	Homo sapiens	mRNA cleavage factor I 25 kDa subunit	208	100
699	9587	G00995	Homo sapiens	Human secreted protein,	726	99
700	9592	gi495273	Rattus norvegicus	ribosomal protein S15a	202	78
701	9595	gi7799912	Homo sapiens	UBASH3A protein	453	47
702	9610	Y07875	Homo sapiens	Human secreted protein fragment encoded from gene 24.	574	100
703	9634	Y73325	Homo sapiens	HTRM clone 001106 protein sequence.	820	99
704	9639	G00805	Homo sapiens	Human secreted protein,	155	67
705	9647	G03786	Homo sapiens	Human secreted protein,	196	73
706	9653	gi3882341	Homo sapiens	KIAA0810 protein	523	100
707	9654	G01924	Homo sapiens	Human secreted protein,	469	100
708	9678	Y99376	Homo sapiens	Human PRO1244 (UNQ628) amino	474	100



SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
				acid sequence		
709	9709	Y11825	Homo sapiens	Human 5' EST secreted protein	657	100
710	9722	gi7677422	Mus musculus	GTPase Rab37	189	75
711	9731	Y12424	Homo sapiens	Human 5' EST secreted protein	207	100
712	9742	Y57954	Homo sapiens	Human transmembrane protein HTMPN-78.	484	100
713	9749	gi3687829	Homo sapiens	hT41	386	65
714	9755	gi2055295	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	2583	100
715	9762	G03436	Homo sapiens	Human secreted protein,	176	61
716	9763	gi6180011	Homo sapiens	anaphase-promoting complex subunit 4	1016	100
717	9784	G03570	Homo sapiens	Human secreted protein,	401	96
718	9794	G00803	Homo sapiens	Human secreted protein,	333	69
719	9795	gi2516242	Mus musculus	Rab33B	669	94
720	9798	gi558599	Homo sapiens	ZID, zinc finger protein with interaction domain	605	96
721	9805	Y25881	Homo sapiens	Human secreted protein fragment encoded from gene 61.	566	96
722	9816	gi532056	Homo sapiens	protein-tyrosine-phosphatase	384	100
723	9830	G00857	Homo sapiens	Human	539	96

SEQ ID NO:	SEQ ID NO: in USSN 09/48 8,725	Accession No.	Species	Description	Smith - Water man Score	% Identity
				secreted protein,		
724	9836	G00914	Homo sapiens	Human secreted protein,	527	100
725	9837	gi26620 99	Homo sapiens	KIAA0409	230	67
726	984	Y29517	Homo sapiens	Human lung tumour protein SAL-82 predicted amino acid sequence.	833	94
727	9849	gi72293 05	Homo sapiens	ZNF264, partial cds	140	90
728	9851	gi52625 60	Homo sapiens	hypothetical protein	369	64
729	9859	gi38819 76	Homo sapiens	hypothetical protein	167	93
730	9863	gi72957 07	Drosophila melanogaster	CG15433 gene product	837	78
731	9888	gi33196 77	Homo sapiens		209	72
732	989	gi45571 43	Rattus norvegicus	zinc finger protein RIN ZF	604	92
733	9919	G01843	Homo sapiens	Human secreted protein,	586	100
734	9922	W67869	Homo sapiens	Human secreted protein encoded by gene 63 clone HHGDB72.	551	93
735	9947	W78239	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	251	78
736	9956	Y36203	Homo sapiens	Human secreted protein #75.	273	77
737	9961	Y99357	Homo sapiens	Human PRO1190 (UNQ604) amino acid sequence	650	99
738	9972	Y12149	Homo sapiens	Human 5' EST secreted protein	284	100
739	9977	gi10039	Homo sapiens	osteoblast	822	98

SEQ ID NO:	SEQ ID NO: in USSN 09/488,725	Accession No.	Species	Description	Smith - Waterman Score	% Identity
		439		differentiation promoting factor		

Table 3 - Amino Acids

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	740	2	557	FVGRLLRLGEALRLRPDPSSGGCRLQPALVGTEMSEKENNFPP LPKFIPVKPCFYQNFSD EIPVEHQVLVKRIYRLWMFYCATLGV NLIACLAWWIGGGSGTNFGLAFVWLLLF TPCGYVCWFRPVYKA FRADSSFNMAFFFI FRSPVCPDRHPGDWLLRLGRVRLAVGNW ILPVQPGRCRGHA
2	741	305	838	FLGAGADIFCAYLRMSSKQATSPFACADGEDAMTQDLTSREK EEGSDQHVASHPLHPIMHNKPHSEELPTLVSTIQDADWDSDV LSSQQRMESENNKLC SLYSFRNTSTSPHKPDEGSRDREIMTSV TFGTPERRKGS LADVVDTLKQKKLEEMTRTEQEDSSCMEKLLS KDWKE
3	742	12	1315	EGYLTGRPTRPVAVRGKSTADLRMMGRSPGFAMQHI VGVPHVL VRRGLLGRDLFMTRTLCSPGPSQPGKRPEEVALGLHHRPAL GRALGHSIQQRATSTAKTWDRYEEFVGLNEVREAQGVTEAE KVFMVARGLVREAREDLVHQAKLKEVRDRLDRVSREDSQYLE LATLEHRMLQEEKRLRTAYLRAEDSEREFSLFSAAVRESHEK ERTRAERTKNWSLIGSVLGALIGVAGSTYVNRVRLQELKALLL EAQKGPVSLQEAIREQASSYSRQQRDLHNLMDLRLGVHAAGP GQDSGSQAGSPPTRDRDVLVLSAALKEQLSHSRQVHSCLEGLR EQLDGLEKTCSQMAGVVQLVKSAAHPGLVEPADGAMP SFLEEQ GSMILALSDTEQRLEAQVNRNTIYSTLVTCVTFVATLPVLYML FKAS
4	743	112	745	NLPPLTPQPGPRLAGSGPSHWFSPLSLPVASKAPGTMAQALGE DLVQPPELQDDSSSLGSDSELSGPGPYRQADRYGFIGGSSAEP GPGHPPADLIRQREMKWVEMTSHWEKTMSSRRYKVKMQCRKGI PSALRARCWPLL CGAHVCQKNSPGTYQELAEAPGDPQWMETIG RDLHRQFPLHEMFVSPQGHGQQGLLQVLKAYTLYRPEQG
5	744	99	265	LRGMAAAAAGPAASQRFQSFSDALIDQDPQAALVEGEPFLLP PLPADPPPSSTA

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6	745	210	758	WACFRSAHCSRHLNRNIFMYLYWDKTRSPVCKGPALREERPQP RLKLEDYKDRLKSGEHLNPDQLEAVEKEYEEVLHNLEFAKELQK TFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQ NLQTQEHVQKDFKGGNGAVYLPSELDYLIKFSKLTCPERNES LRQTLEGSTV
7	746	48	450	XAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLD CFVI DNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYD YQAMCKPSSHHSAAQPLVSPISAFILTATRWLLQELVLFLEW SVWGSX*
8	747	1	469	CRGRLAQLEEAATAATMSAGDAVCTGWLKSPPERKLQRYAWR KRWVFLRRGRMSGNPVLEYYRNKHSSKPIRVIDLSECAVWKH VGPSFVRKEFQNNFVIVKTTSTRTFYLVAKTEQEMQVWVHSIS QVCNLGHLEDGAADSMESLSYTRS YLQ
9	748	242	409	IPAVPLTSCVTGVSYSLSVRDYPDPRQGD TVKH YKIRTL\DKRG FYISP\RSTFSTLQ
10	749	1	1146	KDSVLNLIARGKKYGEKTKRVSSRKKPALKC/TSQKQPALKATC DKEDSVPNTATEKKDEQISGTVSSQKQPALKATSDKKDSVSN I PTEIKDGQSGTVSSQKQPAWKATSVKKDSVSN IATEIKDGQI \RGTVSSQRQPALKA\TGDEKDSVSN IAREIKDGEKSGTVSPQ KQSAQKVI FKKKVSLLNIATRITGGWKSGETEYPENLPTLKATI ENKNSVLNTATKMKDVQTSTPEQDLEMASEGEQKRLEEYENNQ PQVKNQIHSRDDLDI IQSSQTVSEGD SLCCNCKNVILLIDQ HEMKCKDCVHLLKIKKTFCLCKRLTELKDNHCEQLRVKIRKLK NKASVLQKRLSEKEEIKSQLKHETLELEKELCSLRFATQQ
11	750	3	892	SPLRYRAGQSGSTISSSSCAMWRCGGRQGLCVLRRLSGGHAHH RAWRWNSNRACERALQYKLGDKIHGFTVNQVTSVPFLFTAVK LTHDDTGARYLHLAREDTNNLFSVQFRTTPMDSTGVPHILEHT VLGCSQKYP CRDPFFKMLNRSLSFMNAFTASDYTL YPFSTQN PKDFQNL LSVYLDATFFPCLRELD FWQEGWRLEHENPSDPQTP LVFKGVVFNEMKGAFTDNERIFSQHLQNRLLPDHTYSVVS GGD PLCIPELTWEQLKQFHATHYHPSNARFFTYGNFPLDQH
12	751	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPGTEATRPTAM SKSLKKKSHWTSKVHESVIGRNPEGQLGFELKGAENGQFPYL GEVKPGKVAYESGSKLVSEELLLEVNETPVAGLTIRDVLA VIK HCKDPLRLKCVKQGESSGLLSVLPGGGTARGAGQ
13	752	144	442	SHRPQPDARQGNAFQCVQKEKMQVSSAEVRIGPMRLTQDPIQ VLLIFAKEDSQSDGFWACDRAGYRCNIARTPESALECFLDKH HEIIVIDHRQTQN
14	753	1	581	FRLAGCGHLLVSLGLLLLLLARS GTRALVCLPCDESKCEEP RN CPGSIVQGVCCCYTCASQRNESC GGTFGIYGTCDRGLRCVIR PPLNGDSLTEYEAGVCEDENWTDQLLGFKPCNENLIAGCNII NGKCECNTIRTC SNPFEPSPQDMCL SALKRIEEKPDCKARC EVQFSPRCPEDSVLIEGYAPP

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
15	754	1	219	FRMAANVGSMFQYWKRFDLQQLQRELDATATVLANRQDESEQS RKRLIEQSREFKKNTPPEVRRVTIVFALKGS
16	755	313	562	ETLSRIMDHPSREKDERQRTTKPMAQRSAHCSRPSGSSSSSG VLMVGNPNFRVGGKIGCGNFGEGLRLGEGLPQVYFPGCGKY
17	756	273	574	GCCKD*HSGVIGRSWAMLFASGGFQVKLYDIEQQQIRNALENI RWASRRSPGMEVGLFSLVGLVCHILKAMRICDVTFSDDGYCS ASELVKARPTVAGM
18	757	3	390	NSRVDDFVSARPKPRPLPRARGMVVVTGREPDSRRQDGAMSSS DAEDDFLEPATPTATQAGHAL/PPAAT/GSFLRLPLTSEGLT SLHACPHCGATKTPCWQPCSVGGTTSPTTPRAGTSSTEMAHTL EMC
19	758	98	461	RALWVGCGSGEACGIGMSGLLTDPEQRAQEPRYPGFVLGLDVG SSVIRCHVYDRAARVCGSSVQKVENLYPQIGWVEIDPDVLWIQ FVAVIKEAVKAAGIQMNQIVGLGISTQRTATFITWN
20	759	100	731	GLAAEQSMQFVKLWCGCSGEFPTRLRRRTPLTEAMEGGPAVCC QDPRAELVERVAIDVTHLEADGGPEPTRNGVDP PPRARAAS VIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAAGPYATGP ASHISPRAWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGKGA YGVVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRRPPP
21	760	2	520	FVYGGKPVTLWPTISSVVPSTFLGLGNYEVEVEAEPDVRGPEIV TMGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILS LLPLKFFPIIVIGIIALILALAIGLGIHFDCSGKYRCRSSFKC IELIARCDGVSDCKDGEDEYRCVRVGGQNAALQVFTAASRKTM
22	761	158	470	SLAMPFGCVTLGDKKNYNQPSVETDRYDLGQVIKTEEFCEIFR AKDKTTGKLHTCKKFQKRDGRKVRKAANEIGILKMVKHPNIL QLVDVFVTRKEYFIFLEL
23	762	1	749	QRRRFRAGLWGGHGLTDGLRRNGGCGCSARVPRVGERLRGHR PDPLCLLLDMLFLSFHAGSWESWCCCLIPADRPWDRGQHWQL EMADTRSVEHTRFEAAVKVIQSLPKNGSFQPTNEMMLKFYSFY KQATEGPKLSRPGFWDPIGRYKWDASSLGDMTKEEAMIAIV EEMKKI IETMPMTEKVEELLRVIGPFYEIVEDKKSGRSSDITS DLGNVLTSTPNAKTVNGKAESSDSGAESSEEEAC
24	763	3	558	SCFKGRTGGRSGSSGDSRRWARCGRHFSASTEPPPLSQPCSA PRSGRRGCAVPSSVTKMLSFRRRTLGRSSMRKHAERLREAQ RAATHIPAAGDSKSIITCRVSLLDGTDVSDLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTSIKKQVKIGSP YCLHLRVKFYSS
25	764	9	424	ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGLHSPGL PLVLVLLALGAGWAQEGSEPVLLGECLVVCPEGRAAAGGPGG AALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVN EGGGFDRAS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
26	765	2	507	EDVKSYYTVHLPQLENINSGETRTISHFHYTTWPDFGVPQSPA SFLNLFKVRRESGSLNPDHGPVVIHRSAGTGRSSTFSVVHTCL VLMEKGDDINIKQVLLNIRKFQMGLI\QTPDQLRFSYMAITEG AKCVKGDSSIQRWKELSKE/DLPPAFDHS PNKIMTEKYNR
27	766	84	852	LNRQRCGDQVLVPGTGLAATLRTLPMFHDDEEHARAGLSEDTL VLPPASRNQRILYTVLECCQLFDSSDMTIAEWVCLAQTIKRHY EQYHGFVVIHGTDTMAFAASMLSFMLENLQKTVILTGAQVPIH ALWSDGRENLLGALLMAGQYVIVEVCLFFQNLFRGNRATKVD ARRFAAFCSPNLLPLATVGADITINRELVRKVDGKAGLVHSS MEQDVGLLRLLYPGIPAALVRAFLQPPLKGVVMEFTFGSGNG
28	767	992	210	LFRLAPGFLRSLARQGYHQIWAFFPLPSGATATWPAASRSRSL AARSLRSPARPGPNDAALLGEHDFRGQGVRAQRFRFSEEPGPG ADGAVLEVHPQIGAGVSLPGILAACKGAEVILSDSSSELPHCL EVCQRSCQMNNLPHLQVVGLTWGHI SWDLLALFPQDIILASDV FFEPEDFEDILATIIYFLMHKNPKVQLWSTYQVRSADWSLEALL YKWDMMKCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKD SL
29	768	23	624	SFIYKHTHRARFGPRATVASEPALTAGPHVSLTASCRVGMWVSC SPSPFLHPTNTLVAVLERDTLGIREVRLFNAVVRWSEAEQORQ QLQVTPENRRKVLGKALGLIRFPLMTIEEFAAGNRARAQGLVW EGSGTQVGIIW/CTEDSAPEFTAESLADAWHIQIGRNLACEDAS T/WAIC*PRPGSVPTVHTARPRLSCLSSCF
30	769	100	2	MASTQDAELAVSRXRATLXPGXQSXXPSQKKK
31	770	158	1957	LLKSCGVLLSGVCIPCEGKGFTVLVIQTAVPQDRPTKSSMRSA AKPWNPAIRAGGHGPDVRPLPAASSGMKSSKSSSTSLAFESRL SRLKRASSEDTLNKP GSTAASGVVRLKKTATAGAI SELTESRL RSGTGAF TTTKRTGIPAPREFSVTVSRERSVPRGPSNPRKSVS SPTSSNTPTPTKHLRTPSTKPKQENEGGEK\VR LSPK/FRELL AEAKAKDSEINRLRSELKKYKEKRTLNAEGTDALGPVNDGTSV SPGDTEPMIRALEEKNKNFQKELSDLEENRVLKEKLIYLEHS PNSEGAASHTGDSSCPTSITQESSFGSP TGNQLSSDIDEYKKN IHGNALRTSGSSSDVT KASLSPDASDFEHITAETPSRPLSST SNPFKSSKCS TAGSSPNSVSEL SLASLTEKIQKMEENHHSTAE ELQATLQELSDQQQM VQELTAENEKLVDEKTILET SFHQHRER AEQLSQENEKLMNLLQERVKNEEPTTQEGKII ELEQKCTGILE QGRFEREKLLNIQQQLTCSLRKVEEENQGALEM IKRLKEENEK LNEFLELERHNNNMMAKTLEECRVTL EGLKMENGSLKSHLQG
32	771	203	514	SQMHLIFVYTLICANFCSCRDTSATPQASATKALRNANLRD ESNHLTDLYRRDETIQVKNGYVQSPRFPNSYPRNLLL TWR LH SQENTRIQLVFDNQFGL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F= Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
33	772	59	713	PFFKMTDLLRSVVTVIDVFYKYTKQDGECGLTSKGELKELLEK ELHPVLKNPDDPDTVDVIMHMLDRDHRRDLDFTEFLLMIFKLT MACNKVLSKEYCKASGSKKHRRGHRHQEESETEDEEDTPGH KSGYRHSWSSEGEHGYSSGHSRGTVKCRHGSNSRRLGRQGNL SSSGNQEGSQKRYHRSSCGHSWSGGKDRHGSSSVELRERINKS HIK
34	773	209	601	VPKISGPDHIDFIPWDQLFMASSSSVTEFLVLGFSSSLGELQLV LFAVFLCLYLIILSGNIIIIISVIHLDSLHTPMYFFLGILSIS EIFYTTVILPKMLINLFSVFRTLSFVSCATQMFYEIVPGTQER
35	774	373	987	DHSTETPGIPAAEPVSHGTGKLERAPTLPGAELPAPAAVPCP TL*VC/LYPQLLGLSVATMVTLTLYFGAHFAVIRRASLEKNPYQ AVHQWGTQQRLLIQHPESGSEGQSLGPLRAFSAGLSLVGLLTL GAVLSAAATVREAQGLMAGGFLCFSLAFCAQVQVVFWRLLHSPT QVEDAMLDITYDLVYEQAMKGTSHVRRQELAAIQ
36	775	102	466	QPGYSEYDKNRGQGMLLNMMCGRQLSAISLCLAVTFAPLFNAQ ADEPEVIPGDSPPAVVSEQGEALPQAQATAIMAGIQPLPEGAAE KARTQIESQLPAGYKPVYLNQLQLLYAARGISCSV
37	776	2	430	RTRAADVYVFSLTGKSRNVSSSTVRRSAVGMSALALFDLLKP NYALATQVEFTDPEIVA EYITYPSPNGHGEVRGYLVKPAKMSG KTPAVVVVHENRGLNPNYIEDVARRVAKAGYIALAPDGLSSVGG YPGNDIKVVSAAA
38	777	106	556	VKQRHGNSLLTTETKTCISRLGVPLSPQRRFQAIRIEEVKLRW FAFLIVLLAGCSSKHDYTNPPWNAKVPVQRAMQWMPISQKAGA AWGVDPLITAI IAIESGGNPNAVSKSNAIGLMQLKASTSGRD VYRRMGWSGEPTTSELKNSSR
39	778	3	892	HAAGIRHEAKPKRSFYAARDLYKYRHQYPNFKDIRYQNDLSNL RFYKNIKIPFKPDGVYIEEVLSKWKG DYKLEHNHTYIQWLFPL REQGLNFYAKELTTYEIEEFKKTKEAIRRFLLAYKMMLEFFGI KLTDKTGNVARAVNWQERFQHLNESQHNYLRITRILKSLGELG YESFKSPLVKFILHEALVENTIPNIKQSALEYFVYTIRDRRER RKLLRFAQKHYPSENFIWGPPEKEQSEGSKAQKMSSPLASSH NSQTSMHKKAKDSKNSSSAVHLNSKTAEDKKVAPKEPV
40	779	123	395	ELQVFQPIGGMSDSGSQLGSMGSLTMKSQLQITVISA LKLENK KNWFGPSPYVEVTVDGQSKKTEKCNNTNSPKWKQPLTVIVTPV SKLH
41	780	173	438	IETLSFVIRNWNTHAMSKPIVMERG VKYRDADKMALIPVKNA TEREALLRKPEWMKIKLPADSTRIQGIKAAMRKNGLHSVCEEAS C
42	781	287	393	PRMVLGKPQTDPTLEWFLSHCHIHKYPSKSTLIPQ
43	782	119	556	GLRISVQERIKACFTESIQTQIAAAEALPD AISRAAMTLVQSL LNGNKILCCGNGTSAANAQHFAASMINRFETERPSLPALALNT DNVVLTAIANDRLHDEVYAKQVRALGHAGDVLLAISTRGNSRD IVKAVEAAVTRDTTIV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
44	783	248	554	KQTQHAPGMMKKYLALALIAPLLISCSTTKKGDITYNEAWVKDT NGFDILMGQFAHNENIENIWFGEVVIAGPKDYVKYTDQYQTRSH INFDDGTITIEPIPGT
45	784	77	311	TDRTALNPGQESAMNRLFSGRSDMPFALLLLAPSLLLLGGLVA WPMVSNIEISFLRLPLNPNIESTFVGVSNNYVRILS
46	785	184	627	KELVDEKSERGRAMDPVSQLASAGTFRVLKEPLAFLRALELLF AIFAFATCGGYSGGLRLSVDVCNKTESNLSIDIAFAYPFRLLHQ VTFEVPTCEGKERQKLALIGDSSSSAEFFVTAVFAFLYSLAA TGRYIFFHNKNRENNRGPL
47	786	3	742	LGTVSYGADTMDEIQSHVRDSYSQMQSQAGGNNTGSTPLRKAQ SSAPKVRKSVSSRIEAVKAIVLCHNVTVPYESRAGVTEETEF AEADQDFSDENRTYQASSPDEVALVQWTESVGLTLVSRDLTSM QLKTPSGQVLSFCILQLFPFTSESKRMGVIVRDESTAETTFYM KGADVAMSPIVQYNDWLEEECGNMAREGLRTLTVVAKKALTEEQ YQDFEVSRLLPGIPSSYDGAFLTLKLVLVPFV
48	787	864	335	EGPHR\RLFQMVKA/LQEPEDPNQILIGYSRGLVVIWDLQGS RVLYHFLSSQQLENIWQDGRLLVSCSDGSYCQW\VSSEA QQPEPLRSLVPYGPFPCKAITRILWLTRQGLPFTIFQGGMPR ASYGDRHCISVIHDGQQTAFDFTSRVIGFTVLTEADPAASRA SGVGAQG
49	788	410	951	KQGLEVRDLHFKEITSGRALLRVACKRPSMVPGGQLQRAGAGA QARITGLSPALWGARVHGWIPELPAGLPPGACLWPLIPACPSR HWGWVSAPVKG/WAQAILGLALCL/RGEHRGLGAGVSKVRSK MDRKVWTETLIEVGMPLLATDTWGLPHSTAVVVSQPPPYLSDH STLELERDPL
50	789	1	437	LSCNSEQALLSLVPVQRELLRRRYQSSPAKPDSSFYKGLGTCP SQLRLSEPPPTPRHLSVASVSHMFPSHRSLCPHLPDFFAAPF PSDNLPTTLQSPFPSPPPATPSDHALILHH\DLNGGPDPLQQ TGQLFGGLVRDIRRRYP
51	790	1	198	SPSSKLVGMMWAGRAGSSRTTSVSLCLP/SAPFGASNLLVNP LEPQNADKIKIKIADLGNACWV
52	791	3	435	RVDPVRVAPRCGDKIKNHMY\KDCGSLKDCASDRCCETSCTL SLGSVCNTGLCCHKCKYAAPGVVCRDLGGICDLPEYCDGKKEE CPNDIYIQDGTPCSASVVCIRGNCSDRDMQCQALFGYQVKDGS PACYRKLNRIGNRFGT
53	792	1	728	PGRPTRPDASLAQ/DPRTMFRIPEFKWSPMHQRLTDLFLAL ETDVHVWRS\HSTKSVMDFVNSNENIIFVHNTIHLISQMVNDI IIACGGILPLLSAATSPTGSKTELENIEVTQGMASAEAVTFLS RLMAMVDVLVFASSLNFSEIEAKNMSSGGLMRQCLKLVCVA VRNCLECRQRQRDRGNKS SHGSSKQPQEVQSVTATAASKTPLE NVPGNLSPIKDPDRLLQDVDINRLRAVVF



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
54	793	2230	990	NSSGVKLLQALGLSPGNGKDHSILHSRNDLEEAFIHFMGKGAA AERFFSDKETFHDIAQVASEFPGAQHYVGGNAALIGQKFAANS DLKVLLCGPVGPKLHELDDNVFVPPESLQEVDEFHLILEYQA GEEWGQLKAPHANRFIFSHDLSNGAMNMLEVFSLSLEEFQPD GGLSGLHMEGQSKELQRKRLLLEVVTSSISDIPTGIPV\HLELG \SMTNRELMSSIV\LQQVFPAVTSGLLNEQELLFLTQSASGPH SSLSSWNGVDPVGMVSDILFWILKEHGRSKSRASDLTRIHFT LVYHILATVDGHWANQLAAVAAGARVAGTQACATETIDTSRVS LRAPQEFMTSHSEAGSRIVLNPKNPVVEWHREGISFHTFPVLV CKDPIRTVGLGDAISAEGLFYSEVHPHY
55	794	249	3	DDSSGWGLEQLVVRWSLALWPRLECSGMISAHCNLC/LGSSD SPASAPRVAGITDVCHHAWLVFVFLVVMGFPHVGHVGLLELL
56	795	2	1176	LGEVLKCCQQGVSSLAFLALFLQRMMDKPLVVLGLPAPTAPSGC LSFWEAKAQLAKSCKVLVDALRHNAAAVPPFGGGSVLRAAEP APHASYGGIVSVETDLLQWCLESGSIPILCPIGETAARRSVLL DSLEVTASLAKALRPTKIIFLNNTGGLRDSSHKVLSNVNLPAD LDLVCNAEWSTKERQQMRLIVDVLRLPHHSSAVITAASTLL TELFNSKGSGLFKNAERMLRVRSLDKLDQGRVLVDLVNASFGK KLRRDYLASLRPLHSIYVSEGYNAAILTMEPVLGGTPYLDK FVVSSSRQGGSGQMLWECLRRDLQTLFWRSRVTNPINPWYFK HSDGGSFNSKQWIFFWGLADIRDSYELVNHAKGLPDSFHKPAS DPGS
57	796	755	374	YHAPALQPGQSKTSLSQEKKNFFRPGAVAHTCNPSTLGGRGGR ITRSGDRDHPG*HGETPSLLKIQKLAGRDGGRL*SQLGRLR QENGVPNGGGGCSEPRLRHCTPAW*QSETISRKKRKKERY
58	797	2	476	FRPIGIIIRQALCSADGHQRRILTLRLGLLVIPFLPASNLFFRV GFVVPSVGGCVMLLFGFG/ALRKHTEKKLIAAVVLGILLS/N DAERLRCAVRGGEWRSE/EAVFRGAVSVCPLSAEVRNCNIGRNL AAKGNQTGAIRYHREAVSLNPKTKSSTREFRPC
59	798	3	711	KIADFGFSNLFTPGQLLKTWCGSPPYAAPFLFEGKEYDGPVKD IWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRIPFFMST ECEHLIRHMLVLDPNKRLSMEQICKHKWMKLGADPNFDRLIA ECQQLKEERQVDPLNEDVLLAMEDMGLDKEQTLQSLRSDAYDH YSAIYSLLCDRHKRHKTLLRLGALPSMPRALGLSSTSQYP\AEQ AGTAMNISVPVQVLINPENQIV
60	799	2	344	AREFLGHRASITWS*ARVHHRFPKAEVA*P/SLLRTDLTEDRT KCCHGDLLECADDRADLVEDIWNQDSISTILIECCEKPLEK SHCIAEVENDEMPADLPSLAADFVESKDV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
61	800	142	594	VPPKMKRGTSLSRRGKPEAPKGS PQINRKSGQEMTAVMQSGR PRSSSTTDAPTGSAMMEIACAAAAAAACLPGEEGTAERIERL EVSSLAQTSSAVASSTDGS IHTDSVDGTPDPQRTKAAIAHLQQ KILKLTQEQIKIAQTARRNRRPGS*KDCTP*KCLRKSDEALNRV LQQI\RVPPKMKRGTSLSRRGKPEAPKGS PQINRKSGQEMTA VMQSGRPRSSSTTDAPTGSAMMEIACAAAAAAACLPGEEGTA ERIERLEVSSLAQTSSAVASSTDGS IHTDSVDGTPDPQRTKAA IAHLQQKILKLTQEQIKIAQTARRNRRPG
62	801	232	1299	MQTIERLVKERDDLMSALVSVRSSLADTQQREASAYEQVKQVL QISEEANFEKTKALIQCDQLRKELERQAERLEKELASQQEKRA IEKDMMKKEITKEREYMGSKMLILSONIAQLEAVEKVTKKI SAINQLEEIQSQLASREMDVTKVC GEMRYQLNKTNMEKDEAEK EHREFRAKTNRDLEIKDQEI EKLRIELDESKQHLEQEQKAAL AREECLRLTELLGESEHQLHLTRQEKDSIQSFSKEAKAQAALQ AQQREQELTQKIQQMEAQHDKTENEQYLLLTSTNTFLTTLKEE CCTLAKKLEQISQKTRSEIAQLSQEKRYTYDKLGLQRRNEEL EEQCVQHGRST*
63	802	3	334	SYPVWNSPLTAEVPPPELLAAAGFFHTGHQDKVRCFFCYGGLQ SWKRGGDPWTEHAKWFPSQFLLRSKGRDFVHSVQETHSOLLG SWDPWEEPEDAAPVAPSPASGYPELPTPRREVQSESAQEPGG VSPAQAQRAWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVS IVFVPCGHLVC\AECAPGLQLCPI\CRSPCGPLRPLWVP
64	803	70	456	MCSYREKKAEPQELLQLDGYTVDYTDPOPGLEGGRAFFNAVKE GDTVIFASDDEQDRILWQAMYRATGQSHKVPPTQVQKLNK GGNVPQLDAPISQFYADRAQKHGMDDEFISSNPCNFDHASLFEM *
65	804	2	1376	KQLIVLGNKVDLLPQDAPGYRQRLRERLWEDCARAGLLAPGH QGPQRVPKDEPQDGENPNPNWSRTVVRDVLISAKTGYGVVEE LISALQRSWRYRGDVYLVGATNAGKSTLFNTLLES DYCTAKGS EADIRATISPPWPGTTLNLLKFPICNPTPYRMFKRHQRLKKDST QAEDLSEQEQNLNVLKKGYYVGRVGRTFLYSEEQKDNIPF EFDADSLAFDMENDPVMGTHKSTKQVELTAQDVKDAHWFYDTP GITKENCILNLLTEKEVNIVLPTQSIVPRTFVLKPGMVFLGA IGRIDFLQGNQSAWFTVVASNILPVHITS LDRADALYQKHAGH TLLQIPMGKKERMAGFPPLVAEDIMLKEGLGASEAVADIKFSS AGWVSVTPNFKDRLHLRGYTPGTVLTVRPPLLPYIVNIKQOR IKKS VAYKTKKPPSLMYNVRKKKGKINV
66	805	1	874	STVASMMHRQETVECLRKFNARRKLKGAILTMLVSRNFSAAK SLNKKSDGGVKPQSNKNLSVSPAQEPAPLQTAMEPQTTVVH NATDGIKGSTESCNNTTTEDEDLKAAPLRTGNGSSVPEGRSSRD RTAPSAGMQPQPSLCSSAMRKQEI IKITEQLIEAINNGDFEAY TKICDPGLTSFEPEALGNLVEGMDFHKFFENLLSKNSKPIHT TILNPHVHVIGEDAACIAYIRLTQYIDGQGRPSNPAKSEE\TR VWH\RR\DGKWLNVHYHCSGAPCPHRCSELSHRGF

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
67	806	3	1714	LPKNVFVLDSSASMVGTKLRQTKDALFTILHDLRPQDRFSII GFSNRKIKVWKDHLISVTPDSIRDGKVYIHMSPTGGTDINGAL QRAIRLLNKYVAHSGIGDRRVSLIVFLTGDGKPTVGETHTLKIL NNTREARGQVCIFTIGIGNDVDFRLLEKLSLENCGLTRRVHE EEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFPNY FNGSEIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPRP QKAGKDVTSRPPGGDGEDTNHIERLWSYLTTKELLSSWLQS DDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRMDGLEE AHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPYQPRIKISKTSV DGDPHFVVDPLSRLTVCFNIDGQPGDILRLVSDHRDSGVTVN GELIGAPAPPNGHKKQRTYLRTITILINKPERSYLEITPSRVI LDGGDRLVLPNQSVVVGSGLEVSVSANANVTVTIQGSIAFV ILIHLYKKPAPFQRHHLGFYIANSEGLSSNCRVFCESGILIQE LTQQSVAVAGR
68	807	2	841	FFLEQVSQYTFAMCSYREKKSEPQELMQLEGYTVDYTDPHPG QGGMFFNAVKEGDTVIFASDDEQDRILWVQAMYRATGQSYKP VPAIQTKLNPKGGTLHADAQLYADRFQKHGMDEFISANPCKL DHAFLFRIILQRQTLDRHLNDSYSLGWFS PGQVFVLD EYCARY GVRGCHRHLCYLAELMEHSENGAVIDPTLLHYSFAFCAS\H VHGNRPDGI GTVSVEEKERFEEIKERLSSLLENQISHFRYCF PFGRPEGALKATLSLLERVLMKDIA
69	808	2	757	DGLLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQ HGGFEPALGLDLLNCSLLLCRGGHPLDLLSVTLASGSRCSF LSVAWGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGR LSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMASPLHR SVSDLPLPLPQPALASPGSPEPLPILSLNGGGP ELAGDWGGAG DAPLSPDPQLSSPPGSPKAAHSPV*KKAPVIPDPM
70	809	3	530	KGVP TLLMAAGSFYDILAITGFNTCLGIAFSTGSTVFNVLRGV LEVIGVATGSVLGGFIQYFPSRDQDKLVCKRTFLVLGLSVLA VFSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW DIFQPLLFLGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI FDYIF
71	810	228	541	LLKEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI SVCSYTS SDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER SHWNFGYWALWSPGNGNGC
72	811	173	404	ICTSTYLQIFPGKPSCFMCKGRMLCIYFILWYLGHYTSLHWNW CRYISDPNVD/ACPDPRNAEVSMTHTVPALMELID
73	812	2	586	LES LPGFKEIVSRGVKVDYLTDPDFPSLSYPNYTLM TGRHCEV HQMIGNYMWDPPTNKSFDIGVNKDSLMLWNGSEPLWVTLTK AKRKVYMYWPGEVEILGVRPTYCLEYKNVPTDINFANAVSD ALDSFKSGRADLAAIYHERIDVEGHYGPASPQRKDALKA\VD TVLK YMTKWIQERGLQDRLNVII

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
74	813	2	348	ARDFHPKQTLDFLRSDMANSKITEEVKRSIAQQYLDLTVA/LE QVDPDAEVDAA PSTTSSCGH*DSHAGS*RVLSLLGD*GPA*TG ANSMAGKLLLVAWLGFDPDFWGKELSDPAFK
75	814	2	366	KQSGDVTCTNCTDGR LAPSC LTCVGHCI FGGYCTMNSKMMPECQ SPPHMTGPRCEEHVFSQHQP GHITS ILI PML*LLLLVLVAGVI FCHKRRVQGA KGFQHQRTNGAMNAQ IANPTYKMY
76	815	420	681	TVENAGRWL*EEAEIQAELERLERVRNLHIRELKRINNEDNSQ FKDHPTLNERYLLHLLGRGGFSEVYKVMYGLFWFFYTINVAR I
77	816	37	428	MCEEFLVMGKGCS CVF* ILLSNPQMWWLNDSPETDNRQESPS QENIDRVSD/MAFVPSAWTASGGVAWGNLGESGSR TGGVRAET LAPRLQV*PAHLRGHPRSNRGQGRPPWKAGKLGKCQEV LFRFA AF
78	817	1	358	FRAMFLAVQHDCRPMDKSAGSGHKSEEKREKMKRTLLKDWKTR LSYFLQNSSTPGKPKTGKSKQQA FIK*VENPELANINS*LLN *KGEL**A*ANIQNLS CRPSPEEAQLWSEAFDE
79	818	1	169	GFFNFSSPKLKGW KINSSSLVLEIRKNILRFLDAERDVSVVKSS FPSKDARHSSVHR*FTQLHWGPPSHTPARP*RGFFNFSSPKLK GWKINSSSLVLEIRKNILRFLDAERDVSVVKSSFPSKDARHSSV HR
80	819	55	310	RIDDQQELKRV T*YSQKEYTKKLHKKCN I IQADIKPDNILDN ESITILKLSDFGSASHVADNDITPSSSQ TTS AASSPPRTLRR
81	820	1	134	SSKEWD*SLAPKHS G*TKNMDCYCI IPTCIGRERCYGT CIGDT V
82	821	187	360	NSSKKLVMEHQWK KYLRNYQRMNLRLITLIGSCGVL*LISTI PTSRLKFLKETGHGT P MEEIPEEELSEDVEQIDHADRELRRGQ NLRCKGIHRLPTHIQVGON
83	822	208	723	KWMLLHSFKIFCLSLYPQL*CPFEFFSHSATIFHEL VYKQTKI ISSNQELIYEGRR LVLEPGR LAQHFPKTTEENPIFVVSREPLN TIGLIYEKISLPKVHPRYDLGDASMAKAITGVV CYACRIAST LLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLGFLVSR
84	823	1	314	GTRKMGPTVSPICLP GTWGDYNLMDGDLGLISGWGRTEKRDRA DRLKAGRSPAAG*RKWEPGRGDPTWEESEEDVHKS KWTRCVDE KGA*C*TDNKRPLRCGVT
85	824	3	302	HELENLIKSAHSYSLY*G*YLHGA*TAEPEASFCPRRGWNRQA GAAGSRMNF R PGLVSSRQLGLPGPPDGPDYTVYYPFHRLAMVT AASRLEREHLTHL
86	825	87	422	PVPLPHPILEVCPGQ*EPQSAISLTA FQVQAGASRASPGPPAP SSSKPGRKAKVASPCPDRPAPPPT*PRPAAAPGSESSPRPPRP RTGRRQQR AHARRAAARTAPWRPSC
87	826	3	289	HEGRRRGWASASQRFLRNWAF LTPSKVRRLKGQKAFGKLPSHS DTSLSLSDLG FHHRFNP NASSSFKPSGTFKFAIQYGTGRVDGILS EDKLT VSGL
88	827	1	101	GRNIMHYPNGHAICIAN GHCIIL*NSHNIKVVV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
89	828	1	535	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQH LFAFLAHTQREAYAPRIFFEASRPPWFTPRSQDCSEYLRFL DRLHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETP RTSDGEKTLIEKMFGGKLRTHIRCLNCTSTSQKVEAFTDLSLA FWPSSS
90	829	1	434	ARDDPRVRLSLSPNFF*LASKLGKQWTPLIILANSLSGTNMGE
91	830	3	782	MHRILKNDRMFTPEELDMSTFIDVEDEKSPQTESCTDSGAENE GSCHSDQMSNDFSNDGVDGEGICLETNSGTEKISKSGLEKNSL IYELFSVMVHSGSAAGGHYACIKSFSDEQWYSFNDQHVSRIT QEDIKKTGGSSGSRGYSSAFASSTNAYMLIYRLKDPARNAK FLEVDEYPEHIKNLVQKERELEEQEKRQREIERNTCKIKLFCL HPTKQVMMED*IEVHKDKTLKEAVEMAYKMDLEEVIPLDCCR L
92	831	2	604	SVMPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHH TLQLGQALNGVYRTTEGRLTARNLSLGLYGRTELLGQEVSRG RDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQKVL DSVQRLEVLQSAWLGPAYPEFEVLKAHADKQSHILWALTGHV QRQRREMAQQHRLRQIERLHTAALPA
93	832	16	690	ITSVDPRVRGNASTGYGKIWLDDVSCDGDSDLWSCRNSGWGN NDCSHSEVGVICSDASDMELRLVGGSSRCAGKVEVNVQGA VGLCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS NSGCAGGEASLWDCIRWEWKQTACHLNMEASLICSARQPRLV GADMPGSGRVEVKHAHTWRSVCDSDFSLHAANVLCRELNCGDA ISLSVGDHFG
94	833	108	727	SNYPSSRFRVAGITGVKLGMRSPITACTIYHKFFCETNLDA YDPYLIAMSSYLAGKVEEQHLRTRDIINVSNRYPNPSGEPL LDSRFWELRDSIVQCELLMLRVLRFQVSFQHPHYLLHYLVSL QNWLNRHSWQRTPVAVTAWALLRDSYHGALCLRFQAQHI AVAVLYLALQVYGVVEVPAEVEA/DEAVGWQIYAMDTEIP
95	834	118	376	RGSRHAVHGWAFLGLFINKESVVMAYLFTTFNAFQGVFIFV FHCALQKKVRSRRGPSQPPLTFPGYPGEGGEGGDSGAPSSPQ
96	835	3	333	ARKDDLPPNMRFHEEKRLDFEWTLKAG*EKG*PSK*NGWEGQ E***TVRD*GIS**VKPQHLS*\ALQMAKRVYTLSSWNCLE DFDQIFWGQKSALAGQWFPEVSIIP
97	836	740	951	GKQQRRETLRRPSPTISVQRAGSPEHSSASH*HSPCPAPGQ RVLPTALCTLMTSKHFHGCPLAGQGRAVTL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
98	837	81	1503	GVCGLPRFCGSIILCHYEMSSSLGASFVQIKFDDLQFFENC GGG SFGSVYRAKWSIQDKEVAVKLLKIEKEAELSVLSHRNI IQF YGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWA TDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGA SRFHNTTHMSLVGTFPWWAPEVIQSLFVSETCDTYSYGVVLW EMLTREVPFKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH QCWEADAKKRPSFKQIIISILESMSNDTSLPDKCNSFLHNKAEW RCEIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLTEQS NTPLLLPLAARMSEESYFESKTEESNSAEMSCQITATSNGE GH GMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQAKQNS SK TTSKRGRGKKNMALGFSDFDLSEGDDDDDDGEEYNDMDNSE
99	838	185	328	MLWETGCSAACRVTVSPTVTFATFSTRGIDAMRPGPSFLWRQQ LSQG*
100	839	1	348	PTLGDQPDLSITRASRPKLCRKNCPNLTITVHDPNSTQ*YY GMSWELRFYIPGFDVGTMTFIQKILVSWSPPKPIGPLTDLGDP MFQKPPNKVDLTVPPPFLVIKDTLQKFEKI
101	840	1	416	SLNNVTLPQAKTEKDFIQLCTPGVIKQEKLGTVYQCASSPGAN MIGNKMSAISVHGVSTSGGQMYHYDMNTASLSQQ*DQKPIFNV IPPIPVGSSENWNRCCQSGDDNLTSLGTLNFPGRVTSFSEFEMES RSVAAQAGVQ
102	841	105	354	RHTQECRCPHTHIHTHSHTHSHTHSHSHSTTPRCSTHTQPP HAQAPALC*S*EDRGQPTWKLCAHRPRLKVIKEGGWLG
103	842	171	347	NYSLSVYLVRQLTAGTLLQKLRAKGIRNPDHSRALSE*HLSSL PHLIWIQVFLALQPS
104	843	2	690	ATYIVDFGFSTTFREGQMLTAFCGMYPYVAPERSLGQACQ*PA RDIQSLSVILYFRNTVGRRTLPFYS/AEASKLQEKILTGRY HAPPLALQLDSL/IKLLMLNARKCPSL*LMKNPWVKSSQKMP LIPYEEPL/RGPPQTIQLMVAMGFQAKNISVAIERKFNPMA TYLILEHTKQERKSTIRELSLPPGVPTSPSPSTELSTFPLSL MRAHREPAFNVQPPEESQ
105	844	2	777	AKQELAKLMRIEDPSLLNSRVLLHHAKAGTTIARQGDQDVS LH FVLWGCLHVVYQRMIDKAEDVCLFVAQPGELVGQLAVLTGEPLI FTLRAQRDCTFLRISKSDFYEMRAQPSVVLSSAHTVAARMS P FVRQMDFAIDWTAVEAGRALYRCSSHRAAQRPRGGDLGVVRP C*PPRPLRQGRSDCTYIVLNGRLRSVIQRGSGKKELVGEYGR GDLIGVVSATPTH*PLAFSRPVPRQLTRIIIPGNPGSGEVFPGA
106	845	3	709	HASGWTPTGTTQTILGQGTAWDTVASTPGTSETTASAEGRRTPGA TRPAAPGTGSWAEGSVKAPAPIPESPPSKSRSMSNTTEGVWEG TRSSVTNRARASKDRREMTTTKADRPREDIEGVRIALDAKKV LGTIGPPALVSETLAWELPQATPVSKQQSQSIGETTPAAGM WTLGTPAADVWILGTPAADVWTSMEAASGECSAAGDLDAATGD RGPQATLSQTPAV*PWGPPG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
107	846	3	406	AGTSGTGDTGPGNTAVSGTPVVS PGATPGAPGSSTPGEADIGN TSFGKSGTPTVSAASTTSSPVSKHTDAASATAVTISGSKPGTP GTPGGATSGGKITPGIA*PTLDQKSPCFSGYGGYFPVNPHQNP CADSL
108	847	1	565	RAHRCCLPLPSLSCEIQIGFS*SSIFPGQ*ACPCSCCRSCRRN WPQSPRCPHPPAPCSLLLSSCLPPPLSCSWRGTS GKPPSQSP AASRSMRPRCSPTSSLRGASCRGPGGSAPAAASGPRCRGCSR SPRRCSRSGCAAASPPRSQRRSPPLSPPPFPTSGTLLLKTSRF GSATRE*SSPRPRRP
109	848	2	987	DDVPPPAPDLYDVPPGLRRPGPTLYDVPRERVLPPPEVADGGV VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSLEVA GPGREPLELEVAVEALARLQQGV SATVAHLLDLGASAGATGSW RSPSEPQEPLVQDLQA AAVQSAVHELLEFARS AVGNAAHTS DR LHAKLSRQLQKMEDVHQT LVAHGQALDAGRGGSGATLEDL DRLVACSRVPEDAKQLAS FLHGNASLLFRRTKATAPGPEGGG TLHPNPTDKTSSIQSRPLSPPKFTSQDSPDQYENSEGGWME DYDYVHLTGRRSF*KTQKELLGKRAA
110	849	84	372	MATDEENVYGLEENAQSRQESTRRLILVGRTGAGKSATGNSIL GQRRFFSRLGATSVTRACTTGSRRWDKCHVEVDTPDIFSSQV SKTDPGCEERX*
111	850	2	47	TLGLRSLTKEGGGGDVAAFEVGTGAAASRALGQCQQLQKLIV IFIGSLCGLCTKCAVSNDLTQQEIQTPEIQQRNA*CDSRVTF NEGGRWWG
112	851	1192	1040	FFFLVETRHHIGQAGLELLTSLIK*SARLGLPKCWDRREPP YLAGFMI
113	852	791	362	RRSPPPPAPPLPSPLSPPPRAPVSPASTMPILLFLIDTSASMN QRSHLGTTYLD TAKGAVETFMKL RARDPASRGDRYMLVTFEPP PYAIKAGWKENHATFMNELKNLQAEGLTTLGQSLRTAFDLLNL NRLVTGIDNYGQVG
114	853	812	348	NCRTYVFCFVLVFRLLFLHGSPLSPSLLSRAGLLCGSAENPTP FLCGITMAAGVSL LALVVRVILSTAILCPSGASRRQRSSEVIEW GTD SGVYRLYCWRVGFLGPGGELRLGLSEARGGRVWGRGEKRC RVWAVRSLRKFGFSVAALRRGIWAG
115	854	93	170	VTPTPPQYYTCS CVLGF IACSI FLQMSLKPVMLLTVALVACL VLFNLSQCWQRDCCSQGLGNLT EPGTNR*GPAAVSWASLPAP SSCR
116	855	1	183	GKAGGAAGLFAKQVQKKFSRAQEK*TRRFKTCQPEERAREER QEGPEIEFGFSFFSLSLY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
117	856	53	2400	PKRLFLFQDVNTLQGGGQPVVTPSVQPSLQPAHPALPQMTSQA PQPSVTGLQAPSALMQVSSLDHSAVSGNAQSFQPYAGMQAY AYPQASAVTSQLOPVRPLYAPPLSQPPHFQSGDMASFLMTEA RQHNTTEIRMAVSKVADKMDHLMTKVEELQKHSAGNSMLIPSMS VTMETSMIMSNIQRIIQENERLKQEILEKSNRIEEQNNDKISEL IERNQRYVEQSNLMMEKRNNSLQTATENTQARVLHAEQEKAKV TEELAAATAQVSHLQLKMTAHQKKETELQMQLTESLKETDLLR GQLTKVQAKLSELQETSEQAQSKFKSEKQNRKQLELKVTSLEE ELTDLRVEKESLEKNLSERKKKSAQERSQAEEDIDEIRKSYQE ELDKLRQLLKKTRVSTDQAAAEQLSLVQAEQTQWEAKCEHLL ASAKDEHLQOYQEVCAQRDAYQQKLVQLQEKSVCFALCLALQA QITALTQNEQHIKELEKNKSQMSGVEAAASDPSEKVKKIMNQ VFQSLRREFELEESYNGRTILGTIMNTIKMVTQLLLNQEQEK EESSEEEEEKAEERPRRPSQEQSASASSGQAPLNRERPER PMVPSEQVVEEAVPLPPQALTTSDGHRRKGDSEAEALSEIKD GSLPPELSCIPSHRVLGPPTSIPPEPLGPVSMDBSEESLAAS PMAAK\PDNPSGK\VCVQGK*APDGPTYKE\SSTRLFPGFQDP E\EGDPLALGLE\SPG\EPQPPQLQGKVDVH*VPPVPHKGAFQ EQEGRFPQFCRE
118	857	1	791	SETAQQIDRLRVKLAKPEGANLFLMAVQDIRVGGRQSNASYQ YTLLSDDLAALREWEKPKIRKKLATLPELADVNSDQDNGAEMN LVYDRDTMARLGIDVQAANSLNNAFQGRQISTYQPMNQYKV VMEVDPRYTQDISALEKMFVINNEGKAIPLSYFAKWQANAPL SVNHQGLSAALTISFNLPTGKSLSDASAAIDRAMSQLGVPSTV RGSFAGPAQVFQETMNSQVILI IAAIATVYIVLGIPYERYVHP PTILL*RPGANLFLMAVQDIRVGGRQSNASYQYTLLSDDLAAL REWEKPKIRKKLATLPELADVNSDQDNGAEMNLVYDRDTMARL GIDVQAANSLNNAFQGRQISTYQPMNQYKVMEVDPRYTQD ISALEKMFVINNEGKAIPLSYFAKWQANAPL SVNHQGLSAAL TISFNLPTGKSLSDASAAIDRAMSQLGVPSTV RGSFAGPAQVF QETMNSQVILI IAAIATVYIVLGIPYERYVHPPTILL
119	858	3	417	IITPDAMGCQKDIAEKIQKQGGDYLFVAVKGNQGRNLKAFEEKF PLKELNNPEHDSYAISEKSHGREEIRLHIVCDVPDELIDFTFE WKGLKKLCVAVSFRSIIAEQKKEPEMTVRYNIS*LGIAGDISV TAISGTDD
120	859	2	373	HYLKMLTQARREVIIANAYFFPGYRFLHALRKAARRGVRIKLI IQGEPDMPIVRVGARLLYNLVKGGVQVFEYRRRPLHGKVALM DDHWATVGSSNLHPVS*SGNLQANVILHVLRVPTLNP
121	860	286	495	CWSKSAAFHSLKATTCIVPVCAGHCSAAW*SLRPTEALAKEV RELK*HTR*LLNPATTRELTSLGRNLNRLKSERERYDKYRTT LTDLTHSLKTPLAVLQSTLRLRSEKMSVSDAEPVMLEQISRI SQQIGYYLHRASMRGGTLLSRELHPVAPLLDNLTSALIKGKPR KGGNVTVFPFTAMYRDGH



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
122	861	2	725	GNTVMFQHLMQKRKHTQWTYGPLTSTLYDLTEIDSSGDEQSLL ELIITTKKREARQILDQTPVKELVSLKWKRYGRPYFCMLGAIY LLYIICFTMCCTIYRPLKPRNTNRTSPRDNLTLLQOKLLQEAYMT PKDDIRLVGELVTVIGAI IILLVEVPDIFRMGVTRFFGQTILG GPFHVLIIITYAFMVLVTMVMRLISASGEVVPMSFALVLGWCNV MYFARGFQMLGPFTIMIQKMIFGDLM
123	862	1	135	EKAAAANIDEVQKSDVSSTGQGVIDKDALGPMMLEVAHLHFS A VF
124	863	2	364	LEVPSEVTPLGFAMQATKTLTLLRTCCLOEFNIMEKNKGWALLG GKDGHLQQLFLLANALLERNQLLAQKVMYLLVPLLNRGNDKHK LTSAGFFVELLRSPVAKRLPSIYSVARFKDWLQD
125	864	1	374	RPAPAPSAAPEEAPSP\GVKGRGMAKRRVPAPVWGGAGGGTKS ARRAAAPDTERSEEGGRAVKEAYPSSRQPPPPSP*PLRCARR CHPNLAPSMPI SNREGKGKRREEKIRPLSPASTHTSARA
126	865	3	364	LQGVHGSSTFCSSLSSDFDPLEYCSKPGDPQQRVDMQPSVTSR PRSLDSEVPTGETQVSSHVHYHRHRHHYKKRFQRHGRKPGPE TGVPQSRPPIPTQPPPEPPSPDQVTRSNAAAP
127	866	2	250	MADPDPRYPRSSIEDDFNYGSSEASDTVHIRMAFLRRVYSILS LQDLLATVTSTDNLAFEDGRTDWLQRPDCVSFKIHVLEPM
128	867	194	375	AGMSVVVPPIGSSYLGLISQEHFPNEFTSGDGKKAHQDFGYF YGSSYVAASDSSRTPLG
129	868	104	339	VAAALTLPQQLSPPGAWGLGLSACFCCAEGFSRLNQQVLSSS LLLLSRTNCPCKYSFLDNLKKLTERRDVPTYPKVR
130	869	2	360	RDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVDL FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGLAAMMLSAEP ELTLAELRQRLIHFSKDVINEAWFPEDQRVLT
131	870	2	105	LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW
132	871	2	466	EAGDADEDEADANSSDCEPEGPVEAEPPQEDSSSQSDSVEDR SEDEEDEHSEEEETSGSSASEESESESESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AESLQPKGYTLATTQVKTPILLL
133	872	1	354	LKNLRELLLEDNQLPQIPSGLPESLTELSTLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSL S FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED
134	873	59	184	MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTPSLG*
135	874	1	210	LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVDFEFGPVFRGSWALLSWSTRP
136	875	131	254	QTPDKKQNDQRNRKRAEPYETSQGSNNFVSTKVLNSNVLR
137	876	84	504	YFTIKGMVELVPASDTLRKIQVEYGVGTGSFKDKPLAEWLKYN PSEEEYEKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTG HMFHIDFGKFLGHAQMFGSFKRDRAPFVLTSDMAYVINGGEKP TIRFQLFVDL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
138	877	3	215	PSPLPSLSLPPPVAPGGQESPSPTAEVESEASPPPARPLPGE ARLAPISEEGKPQLVGRF\QVTSSK\NRLSLFPCSQHPPLSLV LQNLQPLSSLQRAQIQRTV/PGGGPETREALAESDRAEGLGA GVEEEGDDGKEPQVGGSPQPLSHSPVWMNYSYSSLCLSSEES ESSGEDEEFWAEQLSLRQKHLSEVETLQTLQKKEIEDLYSRLG KQPPPGIVAPAAMLSSRRRLSKGSFPTSRRLSLQRSEPPGPG ETA/GHPASIFSLRPLSVD CFSPGPGGLPRGNRPPLPTSPFLT *CSPSPHTAEVESEASPPPARPLPGEARLAPISEEGKPQLVGR FPSDFIQGTG
139	878	1	337	RRFVSQETGNLYIAKVEKSDVGNVTCVVTNTVTNHKVLGPPTP LILRNDGVMGEYEPKIEVQFPETVPTAKGATVKLECFALGNPV PTIIWRRADGKPIARKARRHKS RVGK
140	879	72	917	MLRTCIVLCSQAGPRSRGWQSLSDGGAFLHKTGELTRALLV LRLCAWPLLVTHGLLLQAWSRRLLSGASFLRASVYGQFVA GETAEVKGCVQQLRTLRLPLAVPTEEPDSAAKSGEAWYE GNLGAMLRCDLSRGLLEPPSLAEASLMQLKVLTALTSTRLCKE LASWVRPFGASLELSPERLAEMDSGQNLQVSCLNABQNHRLR ASLSRLHRVAQYARAQHVRLLVDAEYTSLNPAISLLVAALAVR WNSPGEGGPVWNTYQACLKDTF*
141	880	219	308	PHHRIAGDTAIDKNIHQSVSEQIKKNFAK
142	881	182	317	QMTNPFFLCFTTMSNCNFFKGP GPPGEGKDRGPTGESGPRG FP
143	882	177	341	NGIIASFRLRTFIFCFIHIQGCQAGQTIKVQVSFDLLSLMFTF VSPCTNDLIH
144	883	3	1441	KL SVNHRRLTHLTKLMHTVEQATLRISQS FQKTTEFDNSTDIA LKVFFFD SYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNAV AF LYK SIGPLSSSDN FLLKPQNYDNSEEEERVISVISVSM SSNPPTLYELEKITFTLSHRKVTDYRSLCAFWNYSPTDMNGS WSSEGC ELYSNETHTSCRCNHLTHFAILMSSGPGSIGIKDYN I LTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCS LFLAELVFLVGINTNTNKLFC SIIAGLLHYFFLAFAWMCI EG IHLYLIVGVIYNKGFLHKNFYIFGYLSPAVVVGFS AALGYRY YGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFR HTAGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLVHVA SVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNVPC CFGCLR
145	884	1	429	GTREAA PSRFMFLFLLTCELA AEVAAEVEKSSDGPGAAQEPT WLTDPVPAAMEFIAATEVAVIGFFQDLEIPAVPILHSMVQKFP G V SFGISTDSEVLTHYNITGNTICLFR LVDNEQLNLEDEDIESI DATKLSRFIEINSL
146	885	1	156	DETSGLIVREVSIETSRQQVEELFGPEDYWCQCVAWSSAGTTK SRKAYVRIA
147	886	1	121	GTRSIHVKLDVGKLHTQPKLAAQLRMVDDGSGKVEGLPGI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
148	887	128	652	XCGEDGSFTQVQCHTYTGYCWCVTPDGKPI SGSSVQNKT PVCSGSVTDKPLSQGNSGRKDDGSKPTPTMETQPVFDGDEITAPTLWIKHLVIKDSKLNNTNIRNSEKVYSCDQERQSALEEAQQNPREGIVPECAPGGLYKPVQCHQSTGYCWCVLVDGTGRPLPGTSTRYVMPX*
149	888	128	273	VLQLIKSQKFLNKLVLVETEKEKILRKEYVFADSKVSDSKLLKWA VR
150	889	1	948	RRLSLDLQLGPLGRDPPQECSTFSPTDSGEEPGLSPGVQFQRRQNRFRFMSMEDVSKRLSLPMDIRLPQEFQLQLMESPDLPKPLSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLTENLVALKEIRLEHEEGAPCTAIREVSLKLNKLANIVTLHDLIHTDRSLTLVFEYLDSDLKQYLDHCGNLSMHNKVRPRGQGGPILAATCPEAQCGDPLSPFGIRLLRWLKP SHVGKRERAMPSTSPGTGLSALPQEQTHTVCHCLAVGIKPTLNSEHQFPPLSNGSVSYLPKCREASGEARGYE
151	890	3	108	HERHEPSPTALAFGDHP IVQPKQLSFKIIQVNDN
152	891	2	208	ARGPSLLSEFHPGSDRPQERRTSYEPIHGPSPVDHDSLESKRPRLEQASDSHYQGHITGESLPGRVH
153	892	1	116	GTRKEEFSAEENFLILTEMATNHVQVLVEFTKKLPGIF
154	893	74	661	HTHKLVA PRPGLPPTSQWPRDAGRQASGGLPSLSTGPPKGRDGLARGHPAEWLAGSPGNNSPTQGS LPPQLDLYAGALFVHICLWNFYLSTILTLGITALYTIAGMVPAAGRSTQGTCKGVRRPPPTGPREQPRKWPQQEPQKFLPVSLLPGARAPSSN LASTGRGPGCCNLHGRPADAHGGGGCHPDNQR
155	894	55	312	MVNHSLQETSEQNVILQHTLQOQQQMLQOQETIRNGELED TQTKLEKQVSKLEQELQKQRESSAEKLRKMEKCESAAHEADLKRQK*
156	895	38	185	VCPKWC RFLTMLGHCCYFWHVWPAS*ALSAGTPTSRSFSPSP LRSIST
157	896	37	462	MRGPPVLLLQAAPMECFVPQGI PAGSSPEPAPDPPGPHFLRQERSFECRMCGKAFKRSSLSTHLLIHS DTRPYPCQFCGKR FHQKSDMKKHTYIHTGEKPHKCQTQREPTMVLS PADKTNVKAAX*
158	897	3	175	HEQLTNNTATAPSATPVFGQVAASTAPSLFGQQTGITASTAVATPQVISSRFINLDF
159	898	187	677	VSVFKNCPMY*ICIFLT KMFCVLII\*NKF*VHKKPLQEVEIAAITHGALQGLAYLHSHMTMIHRDIKAGNILLTEPGQVKLADFGSASMAS PANSFVGTPYWMAP EVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPTLQSNW

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
160	899	2	1060	RHARPGGGHNSNRKMSLEQEEETQPGRLLGRRDAVPAFIEPN VRFWITERQSFIRRFLOWTELLDPTNVFISVESIENSRLCT NEDVSSPASADQRIQEAWRSLATVHPDSSNLIPKLFRAAFL PFMAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNSY TCKPLERSLLMAGAVASSTFLGVIPOFVQMKYGLTGPWIKRLL PVIIFLVQASGMNVMSRSLESIKGIAVMDKEGNVLGHSRIAGT KAVRETLASRIVLFGTSALIEVFTYFFKRTQYFRKNPGSLWI LKLSCTVLAMGLMVPFSFSIFPQIGQIQYCSLEEKIQSPTEET EIFYHRGV
161	900	3	564	HASGRLEVFYNGTWGSVGRNITTATAGIVCRQLGCGENGVS LAPLSKTGSGFMWDDIQCPKTHISIWQCLSAPWERRISSPAE ETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDSDWLAE AEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL WDCHAKPWGQSDCG
162	901	1099	2	LGDFPQQRQRRPGASDLPPHLAGARQWEVRFRRHLPARTLPP SLRMPEGPPELHLASQFVNEACRALVFGGCVKSSVSRNPEVPF ESSAYRISASARGKELRLILSPLPGAQPPQEPLALVFRFGMSG SFQLVPREELPRHAHLRFYTAPPGPRALCFVDIRRFGRWDLG GKWQPGRGPCVLQEYQQFRENVLRNLADKAFDRPICEALLDQR FFNGIGNYLRAEILYRLKIPPEKARSVLEALQQHRPSPETL SQKIRTKLQNPDLLELCHSVPEVVQLGGRGYGSESEEDFAA FRAWLRCYGMPSLQDRHGRTIWFQGDGPGLAPKGRKSRKK KSKATQLSPEDRVEDALPPSK
163	902	3	335	LTWSACYWRDILRIQLWIAADILLRMLEKALLYSEHQNISNTG LSSQGLLIFAEIIPAIKRTLARLLVIIASLDYGIKPHLGTGM HRVIGLMLLYLIFANAESVIRVIG
164	903	2	135	FFFEMESRSAAQAGVQWCNLSLQALPPRFTPFSCLSLPSSWD Y
165	904	74	645	YECEELAKKLENSQRDGISRNKLALAELEYEDEVCKSSKSNRP KATVFKSPRTPPQRFYSSEHEYSGLNIVRPSTGKIVNELFKEA REHGAVPLNEATRASGDDKSKSFTGGGYRLGSSFCRSEYIYG ENQLQDVQILLKLWSNGFSLDDGELRPYNEPTNAQFLESVKRG VTLIACMPEIQQLMLEIF
166	905	14	1257	WPCGAAPGLTHASERMFTLTMTIQALAPVMGWRKPLKMFSS EMRGHLHHHKCLTKILKVEGQVPDLPSCLPLTDNTRMLASIL INMLYDDLRCDDPERDHFRIKICEEYITGKFDPQMDKNLNAIQT VSGILQGPFDLGNQLLGLKGVMMVALCGSERETDQLVAVEA LIHASTKLSRATFIITNGVSLKQIYKTTKNEKIKIRTLVGLC KLGSAGTDYGLRQFAEGSTEKLAKQCRKWLCNMSIDTRRW AVEGLAYLTLDADVKDDFVQDVPALQAMFELAKTSDKTILYSV ATTLVNCTNSYDVKEVIPQLVQLAKFSKQHVPEEHPKDKKDFI DMRVKRLKAGVISALACMVKADSAILTDQTKELLARVFLALC DNPKDRGTIVAQGGGKALIPLALEGT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
167	906	3	894	VDSVGGGSESRLDSPTSSPGAGTRQLVKASSTGTSSDDFEE RDPDLGDLGNLGSFPGKWTLSAAQTHQLRRLRGPACRECE EAFMVSGETECEEFLTCHKRCLETLLILCGHRRLPARTPLFGV DFLQLPRDFPEEVFFVVTCTAEIEHRALDVQGIYRVSGSRVR VERLCQAFENGRALVELSGNSPHDVSSVLKRFLQELTEPVI HLYDAFISLAKTLHADPGDDPGTPSPSPSEVIRSLKTLVQLPD SNYNTLRHLVAHLFRVAARFMENKMSANNLGIVFGPTL
168	907	1	394	GLHVISLHSDGRHWEDPLSELDSESVSAFLVTETLVFYLFC LADETVVPPDVPSYLSQGTLSDRQETVVRTEGGPQANGHIES NGKASVTVKQSSAVTVSLGAGGGLQVFTGQVPGIRWKGKLG EAH AS
169	908	179	551	KIKHRPEEEPRWAAAGASAGPGAEEVAPPRPGTVAPGANGMT DSATANGDDRDPEIELFVKAGIDGESIGNCPFSQRLFMILWLK GVVFNVTTVDLKRKPADLRNLAPGTHPPFLAFNWYVKT
170	909	1	335	LGFSDGQEARPEEIGWLNNGYNETTGERGDFPGTYVEYIGRKKI SPPTPKPRPPRPLPVAPGSSKTEADVEQQVLYKYRKKPSSSHR PQTPHNGKSKNFLHKQGLKKKKASL
171	910	1	895	RTRGVMELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKE VWDYVTVRKDAYMFWWLYYATNSCKNFSELPLVMWLQGGPGGS STGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY VNGSGAYAKDLAMVASDMMGLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLELYKAIQRTIKCNFAGVALGDSWISPVDSVL SWGPLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYREATELW GKAEMIEQVKGNTORRACLAFSGGYRAHWCCQTSWLH
172	911	553	194	PGWSRSPDLVIRLPRPPKVLGLQYHFFFLRWSL/DSVAQAE VQWHDLRSLQAPPPGFTPFSCLSLPGSWDYRCPPPRPANFLYF **RRGFTVLARMVIS*PRDPPASASQSAGITVLSLFFFEME SCSVAQAGVQWRYLGLSLQALPPGFTPFSCLSLPSWDYRRPPP RPANFFVFLVETGVSPC*PGWSRSPDLVIRLPQPPKVLGLQV
173	912	1761	1	PSMKTGELEKETAPLRKADSSISVLEIHSQKAQIEEDPPEM ETSLDSSEMAKDLSSKTALSTESCTMKGEEKSPKTKKDKRPP ILECLEKLEKSKKTFDKDAQRLSPIPEEVPKSTLESEKPGSP EAAETSPPSNIIDHCEKLASEKEVVEQSTSTVGGQS VKKVDL ETLKEDSEFTKVEDNLDNAQTSGLIEEPSETKGSQKSKFKYK LVPEEETTASENTEITSERQKEGIKLTIRISSRKKKPDSPPKV LEPENKQEKTEKEEEKTNVGRTLRRSPRISRPTAKVAEIRDQK ADKKRGEDEVEEESTALQKTDKKEILKKSEKDTNSKVSKVK PKGKVRWGTGRTRGRWKYSSNDESESGSEKSSAASEEEKE SEEAAILADDEPCKKCGLPNHPHELILLCDSCDSGYHTALPFAP PLMIHPQMGGW\F\CPTFCPTLNLLLLLEKLEDQF\QDL\VAL KKERALPERRK\ERLVYVGI\SIENIIPPQ\EPDFSEDQEEKK KDSKSKANLL\ERRSTRTRKCISYRFDEFDEAIDEAIEDDIK EADGGGVGRGKDITITGHRGKDITILDEER

[illegible]

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
185	924	3	361	KMMI*GLFEIQQCPIGKHCNLFQVLRN/PNRDL/WLVSSFGKS SKGRERMGHHDYYRLRGR/HNPSPDHSYKRNSESERKRKSH *HMSKSQERHNSPSRGRNSDRSGGRCSRSDNGRSRYR
186	925	443	1412	PLSLFARVAGSRVEMPEPPGLGDEGRPLLHPGRREAVGSWVSA FAGDSTPCGPGDLSVPRREPFRLTAL*PHRSPVVRTSLIGLLL GFSVKEELRGVGAARTPLGIR
187	926	2	917	FDKRQHEARIQQMENEIHYLQENLKSMEETQGLTDLQLEADE EKERILAQLRELEKKKKLEDAKSQEQVFGLDKELKKLKKAVAT SDKLATAELTIAKDQLKSLHGTVMKINQERAEELQEAERFSRK AAQAARDLTRAEAEIELLQNLRLQKGEQFRLEMEKTGVGTGAN SQVLEIEKLNEMTERQRTIARLQNVLYLTGSDNKGGFENVLE EIAELRREGSYQNDYISSMADPFKRRGYWFMPPPPSSKVVSH SSQATKDSGVGLKYSASTPVRKPRPGQQDGKEGSQPPPASGYW VYSP
188	927	171	1082	SDASSEFKTRVIVPRPRVPLGSAITENSLESDSQIGQFGVGF YSAFLVADKVIIVTSKHNDTQHIWESDSNEFSVIADPRGNTLG RGTTITLVLKEEASDYLELDTIKNLVKKYSQFINFPIYVWSSK TETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTKKVEK TVWDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFESKESDDPMA YIHFTAEGEVTFKSILFVPTSAPRGLFDEYGSKKSDYIKLYVR RVFITDDFHDMPKYLNFVKGVVDSDDLPLNVSRETLOQHKL KV
189	928	718	275	CGSWMRRALIPPCRGGPSASDRCCSCSPSGFSAGRGRCPVQGC LRPHRVQLLRWGPSPAGQRLSKGFQLLRWGPSPAPEPRK GPFPPDPWPVTAVTVMAGSVPSAQSVDALESPGPLALEGPS SPRNLLWREMSIFLPGIF
190	929	1	550	PGPTPPPRHGSPPHRLIRVETPGPPAPPADERISGPPASSDRL AILEDYADPDFVQETGEGSAGASGAPEKVPENDGYMEPYEAQK MMAEIRGSKETATQPLPLYDTPYEPEEDGATPEGEGAPWPRES RLPEDDERPPEEYDQPWEWKKERISKAFAVDIKVIDLPWPPP VGQLDSSPSLP
191	930	1	562	QFFSLFLRYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVG YSTHMVGKWHLGFYRKECMPTRRGFDTFGSLGSGDYIYTHYK CDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTORVQQILASHN PTKPIFLYIAYQAVHSPQAPGRYFEHYRSIININRRRYAAML SCLDEAINNVTLALK
192	931	3	580	RVRKGRGGERLQSPLRVPQKPERPPLPPKPQFLNSGAYPQKPL RNQGVVRTLSSSAQEDIIRWFKEEQPLRAGYQKTSDTIAPWF HGILTLLKANELLSTGMPSFLIRVSEIRIKGYALSYLESDGC KHFLIDASADAYSFLGVDQLQHATLADLVEYHKEEPITSLGKE LLLYPCGQQDQLPDYLELFE

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
193	932	3	1641	GSLEKALFQLLKVGWQWAEQTRRLQRLDVSLSVARVRSAGPSC QNKGDLVMEALLEGIQNRGHGGFLTSCAEQLQELMKQIDIMV AHKKSEWEGRTHALETCLKIREQELKSLRSQLDVTHKEVGMLH QQVEEHEKIKQEMTMEYKQELKKLHEELCILKRSYEKLQKKQM REFRGNTKNHREDRSEIERLTAKIEEFRQKSLDWEKQRLIYQQ QVSSLEAQKALAEQSEIIQAQLVNRKQKLESVELSSQSEIQH LSSKLERANDTICANELEIERLTMRVNDLVGTSMTVLQEQQQK EEKLRESEKLLLEALQEEKRELKAALQSQENLIHEARIQKEKLQ EKVKATNTQHAVEAISLESVSATCKQLSQELMEKYEELKRMEA HNNEYKAEIKKLKEQILQGEQSYSSALEGMKMEISHLTQELHQ RDITIASTKGSSSDMEKRLRAEMQKAEDKAHEHKEILDQLES LKLENRHLSEMVMKLELGLHECPLVSPSGSIATRFLEEELRS HHILERLDAHIEELKRESEKTVRQFTALK
194	933	159	1053	TGFLGWSQGPSTPTSLSALYPSQVEETGVVLSLEQTEQHSRR PIQRGAPSQKDTNPNGDSLDTGPRILAFILHPPSLSEALAAD PRRFCSPDLRRLGPILDGASVAATPSTPLATRHQPSPSADL PDELPVGTENVHRLFTSGKDEAVETDLIDIAQDADALDLEMLA PYISMDDDFQLNASEQLPRAYHRPLGAVPRPRARSFHGLSPPA LEPSLLPRWGS DPLRLSCSSPSRGDPSASSPMAGARKRTLQAQSS KDEDEGVELLGVRPPKRS P SPEHENFLFPLSLSLFLTG
195	934	3	425	ELQDCFDVHDASWEEQIFWGWHDNDVHIFDTKTQTFQPEIKGG VPPQPRAAHTCAVLGNKGYIFGGRVLQTRMNDLHYLNLDWTW SGRITINGESPKHRSWHTLTPIADDKLFLCGGLNAYNMPPLSDG WIHNVTTHCWK
196	935	2	295	FFFLRTRSHSVTPRWECSDDITAHWQPQWPWGSSDPLTFS/RPQ VVVPFRHTTLCF\ANFFVFCIFCRNRISPWCWGSRTPAWQLI RLPRPPKVLGLQV
197	936	2	737	PREGQVKQGLLGDWFLCACAALQKSRHLLDQVIPPQGQPSWAD QEYRGSFCTRIWQFGRWVEVTTDDRPLCLAGRLCFSRCQREDV FWLPLLEKVYAKVHGSYEHFWAGQVADALVDLTGGLAERNLKG GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGE ARGQHGRAAASVPPTARPQAHCSFLCDWLHSPVRTKWEVSLF SRVVSSVCDLPLLSSSRGTWPFSPPLTS PFH
198	937	3	638	AECLEASIAHYAHRVANSRYTFDGETVTLSPSQGVNQLHGGPE GFDKRRWQIVNQNDRQVLFALSSDDGDQGFPGNLGATVQYRLT DDNRISITYRATVDKPCPVNMTNHVYFNLDGEQSDVRNHLQI LADEYLPVDEGGIPHDGLKSVAGTSFDFRSAKIIASEFLADDD QRKVKGYDHAFLQAKGDGKKVAHVWSADEKLQLKVYT
199	938	69	425	PLSRFLSKESQEDWGMERQSRVMSEKDEYQFQHQGAVELLVFN FLLILTILTIWLFKNHRFRFLHETGGAMVYDKPPKFAMSREQM SQSCSHTAHNASLLTDAGPLSCGESRASCLFL



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
200	939	3	435	DSKEPRLQQLGLLEEEQLRGLGFRQTRGYKSLAGCLGHGPLVL QLLSFTLLAGLLVQVSKVPSSISQEQSRQDAIYQNLTLQKAAV GELSEKSKLQEIYQELTQLKAAVGELPEKSKLQEIYQELTWLK AAVGELPEKSKMQE
201	940	657	469	MQSIAWGHRRDRGESPLGWGQSEASPSALTEAPKAAHTTRLG FLAANNPNHGSQPQDSFLL*
202	941	1	714	FETLSMRGIPHMLALGPQQLLAQDEEGDTLLHLFAARGLRWAA YAAAEVLQVYRRLDIREHKGKTPLLVAAAANQPLIVEDLLNLG AEPNAADHQGRSVLHVAATYGLPGVLLAVLNSGVQVDLEARDF EGLTPLHTAILALNVAMRPSDLCPRVLSQARDRLDCVHMLLQ MGANHTIQVSGDVGGQTLGDCVEWGHLDVRELQANADFASSLL RALEHVTSLLCALRVFCLFLCQL
203	942	3	479	DAWADAWGTMADLDSPPKLSGVQQPSEGVGGGRCSEISAEL IRSLTELQELEAVYERLCGEEKVVERELDALLEQONTIESKMV TLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLA KNRLYQAIQRADDILDLKFCMDGVQTALR
204	943	1	706	AVEFRVPRSGSAYLYSYVTVGELWAFITGWNLLISYVIGTASV ARAWSSAFDNLIGNHISKTLQGSIALHVPVLAEPDFFALGL VLLLTGLLALGASESALVTKVFTGVNLLVLGFVMISGFVKGDV HNWKLTEEDYELAMAEINDTYSLGPLGSGGFVFFGFEGILRGA ATCFYAFVGFDCIATTGEEAQNPQRSIPMGIGISLSVCFLADF AVSSALTLMPYPYQLQPES
205	944	1	852	GFHPNTHYRARAARAGAGSFVGEVSAVDKDFGNPEVRYSF EMVQPDFELHAISGEITNTHQFDRESLMRRRGTA VFSFTVIAT DQGIPQPLKDQATVHVYMKDINDNAPKFLKDFYQATISESAAN LTQVLRVSASDVDEGNGLIHYSIIKGNEERQFAIDSTSGQVT LIGKLDYEATPAYSLVIQAVDSGTIPLNSTCTLNIDILDENDN TPFF/LLNQHFFVDVLENMRIGELGASGTATDS\DSGDIADLY YKFTGTGKHPPTFSISPKHLGVFFLAQK
206	945	3	363	GDCYDLYGGEKFATLAELVQYMEHHGQLKEKNGDVIELKNPL NCADPTSQRWFHGLSGKEAEKLLTEKGKHSFLVRESQSHPG DFVLSVCTGDDKGESNDGKSKVTHVMHCQELK
207	946	218	717	IDSGNQNGNDDKTKNAERNYLNVLPGFEFYITRHSNLSEIHVA FHLCDVDHVKSGNITARDPAIMGLRNILKVCCTHDITTIISPL LLVHDMSEEMTIPWCLRRRELVKCVKGFMEMASWDGGISRT VQFLVPQSISEEMFYQLSNMLPQIFRVSSTLTLSKH
208	947	3	368	SILPALVITILIFMDQQITAVIVNRKENKLKKAAGYHLDLFWV GILMALCSFMGLPWYVAATVISIAHIDSLKMETETSAPGEQPO FLGVREQRVTGIIIVFILTGISVFLAPILKCIPLPV
209	948	2	575	GASRVEAGSANGMLIDGGSQIVKVQGHADGTTINKSGSQDVVQ GSLATNTTINGGRQYVEQSTVETTTIKNGGEQRVYESRALD'TT IEGGTQSLNSKSTAKNTHIYSGGTQIVDNTSTSDVIEVYSGGV LDVRGGTATNVTQHDGAILKTNTNGTTVSGTNSEGAFSIHNHV ADNVLENGGHLIDINAYGS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
210	949	1	296	FFSSIQLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVGTD VPVKELLKTIPKYKVMNDLIPKATEMPRALFSQSSGFKLYF GAMFLLTTITAC
211	950	3	594	SCSGTGTNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGAL EDIRTEFDRELDLGS LNPGKQLFEKMISGLYLGEVLRLILLKM AKAGLLFGGEKSSALHTKGK IETRHVAAMEKYKEGLANTREIL VDLGLEPSEADCI AVQHVC TIVSFRSANLCAAALAILTRLRE NKKVERLRTTVGMDGTLYKIHPQY
212	951	2	2167	FVAIATNGVVPAGGSYYMISRSLGPEFGGAVGLCFYLGTTTFAG AMYILGTIEILLAYLFPAMAI FKAEDASGEAAAMLNMRVYGT CVLTCMATVVFVGKYNKFALVFLGCVILSILAIYAGVIKSA FDPPNFPICLLGNRTLSRHGFVCAKLAWEGNETVTTRLWGLF CSSRFLNATCDEYFTRNNVTEIQGIPGAASGLIKENLWSSYLT KGVIVERSGMTSVGLADGTPIDMDHPYVFSDMTSYFTLLVGIY FPSVTGIMAGSNRSGDLRDAQKSIPTGTILAIATTSVYISSV VLFGACIEGVVLRDKFGEAVNGNLVVGTLAWPSPWVIVIGSFF STCGAGLQSLTGAPRLLQAISR DGIVPFLQVFGHGKANGPTW ALLLTACICEIGILIASLDEVAPILSMFFLMCYMFVNLAACAVQ TLLRTPNWRPRFRYYHWTL SFLGMSLCALMFICSWYYALVAM LIAGLIYKIEYRGAKKEWGDGIRGLSLSAARYALLRLEEGPP HTKNWRPQLLVLRVDQDQNVVHPQLLSLTSQKAGKGLTIVG SVLEGTFLNHPQAQRAEESIRRLMEAEKVKGFCQVVISSNLR DGVSHLIQSGGLGGLQHNTVLVGVWPRNWRQKEDHQTWRNFIEL VRETTAGHLALLVTKNVSMFPGNPERFSEGSIDRWGIGHDGGM LMLVPFLLRHHKVVRCKMRIFTVAQMVDMMHAM
213	952	1	128	FYLRLLSFFCFQEHEKRCWSVDFNLMDPKLLASGSDDAKGTV
214	953	3	244	RNSKAMHRSSCDGPLLSLPSVGRSATHALVQAQLICSGARRGM HAFIVPIRSLQDHTPLPGKPIMLPQGTLPGEPRWPP
215	954	2	609	CGTLILQARAYVGPVLA VVTRTGFTAKGGLVSSILHPRPIN FKFYKHSMKFVAALS VLALLGTIYSIFILYRNRVPLNEIVIRA LDLVTVVPPALPAAMTVCTLYAQSR LRQGFICIHPLRINLG GKLQLVCFDKTGTLTEDGLDVMGVVPLKGQAFPLVPEPRRLP VGPLLRALATCHALSRLQDTPVGDPMDLKM
216	955	292	855	QIEYFRSLLEHHISYVIDEDVKSGRYMELEQRYMDLAENARF EREQLLGVOQHLSNTLKMAEQDNKEAQEMIGALKERSHMERI IESEQKGKAALATLEEYKATVASDQIEMNRLKAQLENEKQKV AELYSIHNSGDKSDIQDLLESVRLDKEKAETLASSLQEDLAHT RNDANRLQDATAKGRG
217	956	2	400	ARYRFTLSARTQVGSGEAVTEES PAPPNEATPTAAPPTLPPTT VGATGAVSSTDATAIAATTEATTVP I IPTVAPTMTATTTT VAT TTTTTAAATTTTESPPTTSGTKIHESAPDEQSIWNVTVL PNS KWA

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
218	957	1	662	LKSTQDEINQARSKLSQLHESRQEAHRSLEQYDQVLDGAHGAS LTDLANLSEGVSLAERGSFGAMDDPFKNKALLFSNNTQELHPD PFQTEDPFKSDPFKGADPFKGDPFQNDPFABEQTTSTDPFGGD PFKESDPFRGSATDDFFKKQTKNDPFTSDPFTKNPSLPSKLD FESSDPFSSSSVSSKGSDFPGTLDPFSGSGSFNSAEGFADFSTI EGRRG
219	958	1	752	RTRGGSGNSSQPSLREGHDKPVFNAGAKPHSSTSSPSVPKTS SRTQKSAVEHKAKKSLSHPSHSRPGPMVT PHNKA KSPGVRQPG SSSSSAPGQPSTGVARPTVSSGPVPRRQNGSSSSGPERSISGS KKPTNDSNPSRRTVSGTCGPGQPASSSGGPGRPISGSVSSARP LGSSRGPGRPVSSPHELRRPVSGLGPPGRSVSGPGRSISGSIP AGRTVSNSVPGRPVSSLGPGQTVSSSGPTIKPKCT
220	959	439	582	RGKGITPRYHLCISDPHNLKICCRVNGEVVQSSNTNQMVFKTE DLIAW
221	960	230	420	VVAVTRWLCENGVSYLKRCVCSACRHGTRCAGEVAAAANNSHC TVGIAFNAKIGGMGNQLTWM
222	961	311	490	GAPPPFVPTLKSDDDTSNFDEPKKNSWSSSPCQLSPSGFSGE ELPFVGFYSYKALGIL
223	962	2	422	FVERLAHLHAACAPRRKVALLLLEVCRDVYAGLARGENQDPLGA DAFLPALTEELIWSPIGDTQLDVEFLMELLDPDELARGEAGYY LTTWFGALHHIAHYQPETDRAPRGLSSEARASLHQWHRRTLH RKDHPRQQDL
224	963	385	844	FWMDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHT LLSCKVQLLGSQECPDSVQRDVLSGGRHTRHVKRKKVTFLEE VTEYYISGDEDRKGPWEFARDGCRFQKRIQETEDAIGYCLTF EHRERMFNRLQGTCTFKGLNVLKQC
225	964	3	166	AASTAYSFFGTVENMAPKVNRPGHTQSADWGSFGGLMGRFEF GIFLKGKEIVK
226	965	1	118	GFVFLPGPMSVGLDFSLPGMEHVYGIPEHADNLRLLKVTE
227	966	1	390	GSECQGTDLDRNCTSDLCVHTASGPEDVALYVGLIAVAVCLV LLLLVLILVYCRKKEGLSDVDADSSILTSGFQPVSIKPSKADN PHLLTIQPDLSSTTTTYYQGS LCP RQDGPSPKFQLTNGHLLSPL G
228	967	1	777	LIYNEDMICWIESRESSNQLKCIQITKAGGLTDEWTINILQSF HNVQQMAIDWLTRNLYFVDHVGDRIFVCNSNGSVCVTLIDLEL HNPKAIAVDPIAGKLFFTDYGNVAKVERCDMDGMNRTRIIDS TEQPAALALDLVNKL VYWDLYLDYVGVDYQGNRHAVIQGR QVRHLYGITVFEDYLYATNSDSYNIVRISRFGTDIHS LKIE NAWGIRIYQKRTQPTVRSHACEVDYGPMPGGCSHICLLSSSYT K
229	968	3	488	SSGNPQPGDSSGGGAGGGLPSPEQEQLSRRLQRLYPVAVNQET PLPRSWSPKDKYNYIGLSQGNLRVHYKGHGKHNKDAASVRATH PIPAACGIYYFEVKIVSKGRDGYMGIGLSAQGVNMNRLPGWDK HSYGYHGDDGHSFCSSGTGQPYGPTFTTTGDVI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
230	969	1	228	FFFFKMGSRSVTQAGVQWCDVSSSQAPPPRFTLFCLSLPSSWDYRCVPPCPANFFVFLVETGFRVSYGLDLTSLTS
231	970	2	119	QLSLARGKVFLCALSFVYFAKALAEGYLKSTITQIERRVDIPS SLVGVIDGSFEIGNLLVITFVSYFGAKLHRPKIIGAGCVIMGV GTLIIAMPQFFMEQKYERYSPSSNSTLSISPCLLESSSQLPV SVMEKSKSKISNECEVDTSSSMWIYVFLGNLLRGIGETPIQPL GIAYLDDFASEDNAAFYIGCVQTVAIIGPIFGFLLGSLCAKLY VDIGFVNL/DHF*VSAQLGTRKGVLCVLCCLLQCSIGRRLSE EHHHSDREKG
232	971	221	1068	QPAGRVEAFCKFHMWAEGMTSLMKAALDLTYPITSMFSGAGFN SSIFSVMFKDQQIEDLWIPYFAITTDITASAMRVHTDGLWRYV RASMSLSGYMPPPLCDPKDGHLLMDGGYINNLPADVARSMGAKV VIAIDVGSRDDETDLTNYGDALSGWLLWKRWNPLATKVVLNM AEIQTRLAYVCCVRQLEVVKSSDYCEYLRPPIDSYSTLDFGKF NEICEVGYQHGRITVFDIWGRSGVLEKMLRDQQGPSKKPASAVL TCPNASFTDLAEIVSRIEPAKPAM
233	972	133	635	LWVMFVSYLILTLHVQTAVLARPGGESIGCDDYLGSDDKVV KCGVCGDNTGQCQVSVGVFKHALTSLGYHRVVEIPEGATKINI TEMYKSNNYLALRSRSGRSIINGNWAIDRPGKYEGGGTMTFTYK RPNEISSTAGESFLAEGPTNEILDVYVSLDVSGLFFGF
234	973	1	420	ISGGTRSAGPLRRNYNFIAAVVEKVAPSVVHVQLWGRNQOWIE VVLQNGARYEAVVKDIDLKLDLAVIKIESNAELPVLMLGRSSD LRAGEFVVALGSPFSLQNTATAGIVSTKQGGKELGMKDSMD YVQIDATINYG
235	974	2	860	PRVRELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHR DLKLENIMVKSSLIDDNNEINLNKIVTDFGLAVKKQSRSEAML QATCGTFPIYMAPEVISAHDYSSQCDIWSIGVVMXMLLRGEPPF LASSEKLFELIRKGEHFENAVWNSISDCAKSVLKQLMKVDP AHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVE ENTTEENKPKPSTEEKLSYQPWGNVPETNYTSDEEBEEKQVGRI IAAFLEPSVKYPHHTWNIFLQICLFVVS
236	975	1	467	LSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPKQPI SGFSSPVMEGDLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYL KEEDANRKTFTVSSTLDFRVDSDDGVAVICRVDHESLNATPQ VAMQVLEMHYTPSVKIIIPSTFPFQEG
237	976	3	417	YNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPSTPKF PEDFDDGEHAKQKSVISWLLNHPAKRPTATELLKSELLPPPQ MEESELHEVLHHTLTNVDGKAYRTIDGPRSFQRISPAIA\YT YD\SDILKGN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
238	977	2	740	DQDYKYDSTSDDSNFLNPPRGWDHTAPGHRFTFETKDQPEYDST DGEGLWSLWSVCSVTCGNGNQKRTSCGYACTATESRTCDRPN CPGIEDTFRTAATEVSLLAGSEEFNATKLFVDTDSCERWMSK KSEFLKKYMHKVMNDLPSCPCSYPTVEVAYSTADIFDRIKKKDF RWKDASGPKEKLEIYKPTARYCIRSMLSLESTTLAAQHCCYGD NMQLITRGKGAGTPNLISTEFSaelHYKVDV
239	978	2	612	ESEENGESAMDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKEE DEEGEDVVTSTGRGNEIGHASTCTGLGEESEGLICESAEGDS QIGTVVEHVEAEAGAAIMNANENNVDMSGTEKGSKDITICSS AKGIVESSVTSASVSGKDEVTPVPGGCEGPMSTASDQSDS QLE KVEDTTISTGLVGGSYDVLVSgevPECEVAH
240	979	79	361	VCIICLIFSYYSFDSALQSAKSSLGGNDEL SATFLEMKGHFYM YAGSLLLKMGQHGNVQWRALSELALCYLIAFQVSLPLGAID ISRSLDVF
241	980	2	681	QHPSQEKPOVLTPSPRKQKLNRYRSHHDQMICKCLSLISYS ATIGGLTTIIGTSTSLIFLEHFNNQYPASEVNVFGTWFLFSFP ISLIMLVVSWFWMHWLFLGCNFKETCSLSKKKTKREQLSEKR IQEYEKLGDISYPEMVTGFFFFILMTVLWFTREPGFVPGWDSF FEKKGYRTDATVSVFLGFLFLIPAKKPCFGKKNDGENQEHSL GTEPIITWKDF
242	981	1	491	LEREGDKGTPVLRGFSSVSGSWSRRMPFLLLTCLFITGTSVS PVALDPCSAYISLNEPWRNTDHLQDESQGPPLCDNHVNGEWYH FTGMAGDAMPFTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQA CASFNGNCCLWNTTVEVKACPGGYVYRLTKPSV
243	982	1	983	CGR TMSDIRHSLLRDALSAKEVLYHLDIYFSSQLQSAPLPI VDKGPVELLEEFVFPKERSAQPKRLNSLQELQLEIMCNYP QEQTKDSVRQIIFSSLFSPQGNKADDSRMSLLGKLVSMAVAVC RIPVLECAASWLQRTPVVYCVRLAKALVDDYCLVPGSIQTLK QIFASAPRFCCQFITSVTALYDLSSDDLIPMDLLEMIVTWIF EDPRILITLNTPIAANLPIGFLELTPLVGLIRWCVKAPLAY KRKKKPPLSNGHVS NKVT KD PGVGM DRDSHLLYSKLHLSVLQV LMTLQLHLTEKNLYGPPGADPLRPHG
244	983	32	362	SACSTGPELPGRATRSLTRPANQKGC DGRLYYDGCAMIAMNG SVFAQGSQFSLDDVEVLTATLDLEDVRSYRAEISSRNLA VSAP VDTVCGCSSKTWKVAPFVRAWWRP
245	984	158	398	APLSRLCFPQVLVNEG GGFDRASGSFVAPVRGVYSFRFHVVKV YNRQTQVTSALAPIPGSGGWGGRRGAQLTSGWTLH
246	985	2	707	PHIIGAEDDDFGTEHEQINGQCSCFQSI ELLKSRPAHLAVFLR HVVSQFDPATLLCYLYSDLYKHTNSKETRRIFLEFHQFFLDRS AHLKVSVPDEMSADLEKRRPELIPEDLHRHYIQTMQERVHPEV QRHLEDFRQKRSMGLTLAESELTKLDAERDKDRLTLEKERTCA EQIVAKIEEVLMTAQAVEEDKSSTMQYVILMYMKHLGVKVKEP RNLEHKRGRIGFLPKIKQSM

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
247	986	18	441	SPGTGRGPGPPTS FVCLPTPQCPFIDDFILALHRKIKNEPVVFP EGPEISEELKDLILKMLDKNPETRIGVPDIKLPVWTKNGEEP LPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSP GNPFEPQARMA
248	987	3	732	HASGIKIDKTS DGP KLF L TEEDQKKLHDFEEQCVEMYFNEKDD KFHSGSEERIRVTFERVEQMCIQIKEVGDRVNYIKRSLQSLDS QIGHLQDLSALTVDTLKTLTAQKASEASKVHNEITRELSISKH LAQNLIDDGPVRPSPVWKKHGVNTLSSSLPQGDLESNNPFHCN ILMKDDKDPQCNI FGQDLPAVPQRKEFNFP EAGSSSGALFP SA VSPPELRQLHGVLELLKIFNKKQKKRA
249	988	3	468	CCRWIDCFALYDQEEELVRHIEKVHIDQRKGEDFTCFWAGCPR RYKPFNARYKLLIHMVRHSGEKPKNKCTFEGCEKAFSRLENLKI HLRSHTGEKPYLCQHPGCQKAFSNSSDRAKHQRTHLDTKPYAC QIPGCTKRYTDPSSLRKHVKAHSSK
250	989	356	553	LPLLWTLSDFGGTMDSGMEIPVTLIITKAPNQKYSQDTISCF NWTVGKCLKTHLSNVYPSKPVSV
251	990	1	895	AGTRMCVVA AAEELVCGA \ RGLWMRRTRRPRFVLMNMDDLN HYRFLNWRRIREIREVRAFRYQERFKHILVDGDTLSYHGNSG EVGCVVASRPLTKDSNYFEVSI VDSGVRGTIAVGLVPQYISLD HQPGWL PDSVAYHADDGKLYNGRAKGRQFGSKCNSGDRIGCGI EPVSFDVQTAQ IFFTNGKRVGSTIMPMSPDGLFPAVGMHSLG EEVRLHLNAELGREDDSVMMVDSYEDWGRLDVVRVCGTLLEY LGKGKSI VDVGLAQARHPLSTRSHYFEVEIVDPGEKCYIA
252	991	51	674	QQAEEHLAAYS VSDSDSGKDPSMECCRATPGTLLFLAFLLL SSRTARSEEDRDGLWDAGWPWSECSRTCGGGASYSLRRLSSK SCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYE WLPVSNPDNPNCSLKCAKGTTLVVELAPKVLDTGTRCYTESLD MCISGLCQVSADLFSFNLSRGFQCCLCVNGLHSLTL
253	992	2	554	RLLRQELVVLCHLHHPSLISLLAAGIRPRMLVMELASKGSLDR LLQQDKASLTRLQHRIALHVADGLRYLHSAMI IYRDLKPHNV LLFTLYPNAAIIAKIADYGIAQYCCRMGIKTSEGTGPFRAPEV ARGNVIYNQQADVVSFGLLLYDILTGGRIVEGLKFPNEFDEL EIQGKLDPDPVKE
254	993	3	437	KASNSTHEFRIGLPEGWESEKKAVIPLGIGPPLTLICLGVLG ILYGRKGFQTAHFYLDSPSPKVISTPPPIFPISKEVGPI IKHFPKHVANLHASRGFTEKFETLKKFYQEGQSCVTDLGITAN SSNHDPNRRHRNRLI
255	994	3	445	SFPDR TASLVLLSVVPGQAGMQQRGLAIVALAVCAALHASPAI LPIASSCCTEVSHHISRLLERVNMCR IQRADGDCDLAAVILH VKRRR ICVS PHNHTVKQWMKVQA AKKNGKGNVCHRKKHHGKRN SNRAHQGKHETYGHKTPY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine; C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
256	995	2	737	FEQPGNPGDPRVRTPPPWGPHFFALIPSSPKVEPATPSSRRDP IAPTATLLSKKTPATLAPKEALIPPAMTVPSPKKTPAIPTPKE APATPSSKEASSPPAVTPSTYKGAPSPKELLIPPAVTSPPSKE APTPPAVTPPSPEKGPATPAPKGTPTSPVTPSSLKDSPTSPA SVTCKMGATVPQASKGLPAKKGPTALKEVLVAPAPESTPIITA PTRKGPQTKKSSATSPPICPDPSAKNGSKG
257	996	79	3	FFLKIQGLGWARWLTVPVLPVWEAE
258	997	307	475	AGFGYGLPISRLYAKYFQGDNLNLYSLSGYGTDAITYLKVSLEF NSKILFLKPLLLL
259	998	26	622	WMRAPMLQKQAPRMDTPPPEERLEKQNEKLNQEEETEFKEL DGLREALANLRGLSEERSEKAMLRSRIEEQSQLICILKRRSD EALERCQILELLNAELEKMMQEAELKKAQGEYSRKL EERFMT LAANHEIMLRFKDEYKSENIKLREENEKLRL ENNSLFSQALKD EEAKVLQLTVRCEALTGELETLKERC
260	999	2	241	DPGASHASVQVQVLKEQLFAGRMPSPPFRSCALMGMCGRSADN LSCPSPLNVMEPVSFPLKSLGKGMIOHFRHIVSLV
261	1000	1	620	VTTTTHSVGRGHELQLLNEELRNIELECONIMQAHRLQKVTDQ YGDIIWTLHDGGFRNYNTSIDMQRGKLLDDIMEHPEKSDKSSSA YNTAESCRSTPLTVDRSPDSSLPRVINLTNKNLRSTMAATQS SSGQSSKESTSTKAKTTEQGCSAESKEKVLEGSKLDPQEKAVS EHIPYLSPHYSSSYRYANIPAHARHYQSYMQLIQ
262	1001	3	420	VWGCLATVSTHKKIQLPFGNCLPVSDGPFNNSTGIPFFYMTA KDPVVADLMKNPMASLMLPESEGEFCRKNIVDPEDPRCVQLTL TGQMIAVSPEEVEFAKQAMFSRHPGMRKWPROYEWFFMKMRIE HIWLQKWYG
263	1002	43	441	QAANMAVARVDAALPPGEGSVVNWSGQGLQKLGPNLPCADIH TLILDKNQIIKLENLEKCKRLIQLSVANNRLVRMMGVAKLTLL RVLNLPHNSIGCVEGLKELVHLEWLNLAGNNLIAMEQINSCTA LQHL
264	1003	3	834	FRAAVGAVPEGAWKDTAQLHKSEAKRVLRYLFGQQRVIWIE TQQAFYQVSLLDHGRSCDDVHRSRHGLSLQDQMERKAIYGNV ISIPVKSYPQLLVDEAFSIALWLADHYWYALCIFLISSISIC LSLYKTRKQSQTLRDMVKLSMRVCVCRPGGEEEWVDSSELVPG DCLVLSQEGGLMPCDAALVAGECMVNDSSLTGESI PVLKTALP EGLGPYCAETHRRHTLFCGTLILHARAYVGPHVLAVVTRTGMS REAGLERDPGSAPLKRWS
265	1004	2	670	FVGGGLHLHLCLLLCFMLPEDAAMAVLTASNHVSNTVNYNIT VERMNRMQGLRVSTVPAVLSPNATLALTAGVLVDSAVEVAFLW TFGDGEQALHQFOPPYNESFPVPDPSVAQVLVEHNVTHTYAAP GEYVLTVLASNAFENRTQQVLIRSGRVP IVSLECVSCKAQAVY EVSRSYVYLEGRCLNCSSGSKRGRWAARTFSNKTVLDETTT STGSASM

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
266	1005	2	1093	PEFLGRLFRGKAATLHVHSDQKPLHDGALGSQQNLVRMKEALR ASTMDVTTVLPSPGLEKRSVLNGSHAMMDLLVELCLQNHLNPSH HALEIRSETQQPLSFKNPTLIGTLNVHTVFLKEKVPEEKVKP GPPKVPEKSVRLVVNYLRTQKAVVRVSPEVPLQNILPVICAKC EVSPEHVLLRDNIAGEELELSKSLNELGIKELYAWDNRRETF RKSSLGNDETDKEKKKFLGFFKVNKRSNSKGCLTTPNSPSMHS RSLTLGPSLSLGSISGVSVKSEMKRRAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKRRAPAPPPPPPPPSPLIPNRTEDKEEN RKSTMVYCCASFPTQAKRF
267	1006	686	400	VQWHNLHSLQPLPAGEFK*FLCFSLPSSWDYRCAPPLP/APFFF YFLFLVELGFHHIG*AGLELTSTDLPASAS/ESAGITGMSHRA RPMDFFLKIL
268	1007	1	453	GRRFRPPSDEEREPEWEPWTQLRLSGHLKPLHYNMLTAFMENF TFSGEVNVETIACRNATRYVVLHASRVAVEKVQLAEDRAFGAVP VAGFFLYPQTQVLVVVLNRTLDAQRYNLYKIYNALINELLG FFRSSYVLHGERRFLGVTQFSP
269	1008	333	526	KELDPFFYNS*RKIKYLRITLTKEVKDLYKENYKTLLEITDDT N/KKHIPSSWTGRINTVKMTIL
270	1009	699	882	VPPLQAIHEQMNCKEYQEDLALRAQNDAAARRPSEMFKVRLA QGRGLASLSSGIQSGVG
271	1010	16	148	RWNSLTCVVLTFGLHRLKRLVLPKLRRLFKPQGHPRLLLWFK R
272	1011	1	659	YGEFVTYQGVAVTRSRKEGIAHNYKNETEWRANIDTVMWTFE EDLDLVTLYFGPEPDSTGHRYGPESPERREMVRQVDRTVGYLRE SIARNHLTDRLNLIITSDHGMTTVDKRAAGDLVEFHKFPNFTFR DIEFELLDYGPNGMLLPKEGRLEKVYDALKDAHPKLHVYKKEA FPEAFHYANNPRVTPLLMYSDLGVIHGVSRILLEAPPPGAPSP GSGS
273	1012	146	413	RIPLRLRSSTYRSKGFDTVVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF
274	1013	3	251	IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSSHSTCFQFP DIVEFCEAMANAGKTIVVAALDGTQFQKVRRLIQVSWD
275	1014	326	651	YCFCFDLLH*CIHRDVKPENILITKHSVVKLCDFGFARLLTGP SDYYTDYVATRWYRSPPELPGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK
276	1015	224	435	RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDFVRL
277	1016	2	429	GGILAMEYAPGGTLAEFIQKRCNSLLEETILHFFVQILLALH HVHTHLILHRDLKTQNILDKHRMVVKIGDFGISKILSSSKA YTVVGTPCYISPELCEGKPYNQKSDI WALGCVLYELASLKRAF EAANLPALVLKIM



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
278	1017	1	262	VQCGGIHQVSGAVVVSGLLQGMMLLGSPPGHVFPCHGPLVLAP SLVVAGLSAHREVAQFCFTHWGLALLYVSPERRGMVPSGGVWG D
279	1018	1	480	PRMTGSTHASAPSYGGSCRNNLFYREETYTPKAETDEMNEVET APIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDR CIGSTCNRYQCPAGCLNHKAKIFGSLFYESFASICRAAIHYGI LDDKGGLVDIRNGKVPFFVKSERHGVQSLR
280	1019	271	792	VPQNIICAFFCVPCRFASITPFWGLTLHLQHLGNNVFLLOTLF GAVTLLANCVPWALNHSRRLSQMLLMFLLATCLLAIIFVPQ EMQTLRVVLATLGVGAASLGITCSTAQENELIPSIIRGRATGI TGNFANIGGALASLVMILSIYSRPLPWIIYGVFAILSGLVLVLL LP
281	1020	2	679	VLVSRDHMKSAQQFFQLVGGSSASECDTIPGRQCMASCFLLKQ FDDVLIYLNFSKSHFYNDIFNFNYAQAATGNTSEGEAFL LIQSEKMKNDYIYLSWLARGYIMNKKPRLAWELYLKMETSSES FSLQLLIANDCYKMGQFYSAKAFDVLRLDPNPEYWEGKRG CVGIFQMIITAGREPKETLREVLHLLRSTGNTQVEYMRIMKKW AKENRVSILK
282	1021	3	359	LKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVREITVHQRVTVDFVALHIVTLL LPQLSHFFCLRIERVIIYLEKPIFARLRWLMP
283	1022	3	538	GVPRNLPSLSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNC RRCDHAPNPMCPCPRHFPQLHPDTFSLHSLRLEGLVLKDSLSW LNASWFRGLGNLRVLDLSENFYKCIKTKAFQGLTQLRKLNL SFNYQKRVSFAHLVSGPPFLRGSGLGRPLKGAGTWHGNLSFPLH FEWGKT
284	1023	3	442	ILFAALIWSSFDENIEASAGGGGGSSSIDAVMVDGAVVEQYKR MQSQESSAKRSDEQRKMKEQQAEEELREKQAAEQERLKQLEKE RLAAQEQKKQAEAAKQAEELKQKQAEAAKAAADAKAKAEAD AKAAEEAAKAAADAKK
285	1024	1	119	AMEIVHEPRDLERYMREAVKVSNDSPVLLDRFLNDAIEC
286	1025	67	227	MLSPGYDYGVCVEFSLEDAIGCMEANQVALYFGQMMLEGYI FLYMGREGFK
287	1026	2	1101	PRVRSQGGQEDPASQQWARPRFTQPSKMRRRVIRPVGSSVRL KCVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRP EDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLTGTHPVNT TVDFGGTTSFQCKVRSVDKPVIQWLKRVEYGAEGRHNSTIDVG GQKFVVLPTGDVWSRPGDGYLNLKLITRARQDDAGMYICLGAN TMGYSFRSAFLTVPDPKPPGPPVASSSSATSLPWPVVIGIPA GAVFILGTLLLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSG DKDLPSLAALSAGPGVGLCEEHGSAPAPQHLLGPGVPAGPKLY PKLYT\DI PHHTHTHTPHPPAN
288	1027	3	96	NFHFTGKCLFMSGLSEVQLTHMDHTLPGY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
289	1028	95	407	SPRKRRKTRHSTNPPLECHVGWVMDSRDHGPGTSSVSTSNASPS EGAPLAGSYGCTPHSFPKFQHPSHELLKENGFTQQVYHKYRRR CLSERKRLGIGQSQEMNT
290	1029	1	359	PGSGGSAGGRDGSAYQGALLPREQFAAPLGRPVGTSYSATYPA YVSPDVAQSWTAGPFDGSVLHGLPGRRPFTFVSDFLEEFPGEGR ECVNCGALSTPLWRRDGTGHYLCNACGLYHKMN
291	1030	2	513	PDHRHGALWVWYSCGVLPVTVSRNEGDERNQVLTLYLWIRQEW TDAYLRWDPNAYGGLDAIRIPSSLVWRPDIIVLYNKYCLS/AAP PLSYPSLDLPLAVGV**SPLPTT*PGCHAALEAFPQDPSKLPS TQPLHGTPTLGYPRPAQAERLLGTYCVVQGRCLNHKGLSRAHF
292	1031	1	595	YALTGALVIVTGMVMGNIADYFNLVSSMSNTFTFLNAGILIS IFLNAWLMEIVPLKTQLRFGFLMVLAVAGLMFSSHLSALFSAA MIFILGVVSGITMSIGTFLVTQMYEGRQGRSRLFTDSFFSMAG MIFPMIAAFLARSIEWYVWYACIGLVYVAIFILTFGCEFPAL CSHATKLGTAASSYPSLDVVQLRTLNA
293	1032	71	479	MAKVGLKTEHYDRYPHMFSGGQQRQRIAIARGLMLDPDVVIAD PVSALDVSRAQVLNLMDLQQLGLSYVFIHDLVSVEHIAD EVMVMYLGRVCVEKGTQDI FNNPRHPYTQALLSATPRLNPPDR RERIKLSX*
294	1033	2	427	SATLERVLNHPDETQARRLMTLEDIVSGYSNVLISLADSQGKT VYHSPGAPDIREFTDAIPDKDAQGGEVYLLSGPTMMMPGHGH GHMEHSNWRMINLPVGPLVDGKPIYTLTYALSIDFHLHYINDL MNKLIMTASVII
295	1034	3	342	VLAYPGIKVSTAEARAILPAQYRRQDCIAHGRHLAGFIHACYS RQPELAAKLMKDVIAPYRERLLPGFRQARQAVAEIGAVASGI SGSGPTLFALCDKPETAQRVADWLK
296	1035	2	279	GQQQRVALARALIILKPKVLLFDEPLSNLDANLRRSMRDKIREL QKQFDITSLYVTHDQSEAFVSDTVLVMNKGHIMQIGSPQDLR VRRLNW
297	1036	3	157	AVHYLERVRIAEHAHKFPQGQISGGQQQRVAIARSLCMKPKIML FDEPTSAL
298	1037	1	217	APYDAENYFDYDNLNNGPSLQHWFGVDSIGRDI FSRVLVGAQI SLAAGVFAVFIGAAIGTLLGLLAGYYEGW
299	1038	3	570	VFCLIALDLPIDELVDFPIVYASALNGIAGLDHEDMAEDMTPL YQAIVDHVPAPDVLDLGGPFQMQISQLDYNYSYVGVIGIGRIKRG KVKPNQQVTIIDSEGKTRNAKVGKVLGHLGLERIEITDLAAGD IVAITGLGELNISDTVCDTQNVLEALPALSVDDEPTVSMFFCVNT SPFCGKEGKFVTSRQI
300	1039	1	366	QGTRAESQGSSKDKTRIAFAGLKFGDYGSIDYGRNYGVAYDIG AWTDVLPFEGGDTWTQTDVFMTRATGVATYRNNDFFGLVDGL NFAAQYQGNDRSDFDNYTEGNHGHGFSATYEYEG
301	1040	3	201	DTYSVSIPLGATINMAGAAITITVLTAAVNTLGIPVDLPAL LLSVVASLACAGSGVAGGSLL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
302	1041	1	140	ANAQQGLPSGITLKLNNLVDKGLVDRLYAASSSGVPVNNLLVRG TCS
303	1042	2	442	ARMTLIPGTHLLENIHNIWVNGVGTNSAPFWRMLLNSFVMAFS ITLGKITVSMLSAFAIVWFRFPLRNLFWMIFITMLPVEVRI FPTVEVIANLQMLDSYAGLTLPMLASATATFLFRKLNMSPDK VVPAARISGYGPRVRKQ
304	1043	2	403	CAKCLRDADCEPSGAFERIGRDISLDALEREVMKDDIFFRTSG GGVTLSSGGEVLMQAEFATRFLORLRLWGVSCAETAGDAPASK LLPLAKLCDEVLFDLKIMDATQARDVVKMNLPRVLENLRLLS EGVN
305	1044	1	346	YLLLFVCFVLVMSLLVGLVYKFTAERAGKQSLDDLMNSSLYLMR SELREIPPHDWGKTLKEMDLNLSFDLRVEPLSKYHLDDISMHR LRGGEIVALDDQYTFLORI PRSHVLA VG
306	1045	1	207	VELFLSDEGDDVVEVADQCGVPESLRDKIFEQGVSTRADEP GEHGIGLYLIASVYTRCGGVITLEDN
307	1046	3	213	DAITAPDANALPAAQAENLKNKVAIVGFSTPNVMPYVER GTVKEFGLWDVVQGGKISVYVADALQ
308	1047	1	129	YIVVTGKTHCGTPLTTVTGDATQSGYLTNLNPEMWEVSGYNRV
309	1048	271	46	XEGVEPDINASKTRQQLNDVAGKMKIIEARLSALTNQTKSLK LNPVALPKVASQLLDELGYSLARRADLQSAHX*
310	1049	16	253	ENIAEEYATKRYRSNVINWGMLPLQMAEVPTFEVGDYIYIPGI KAALDNP GTTFKGYVIHEDAPVTEITLYMESQEART
311	1050	2	299	LQTEIGSMVYAVKPGDGSAREQAASCQRVIGGLANIAEEYATK RYRSNVINWGMLPLQMAEVPTFEVGDYIYILGFKAAYSPGTA FTVYAISGYGPRI
312	1051	1	344	TLEDLLMALDGEQHLQQQVSEKVLADNVLIAPGSVKPDATFWS ALIQDRYNVMTICIEKDACVLVEQDLNSDGQAERILFAFNDDR IVYGFDSDRKEWDALDMSLLPNEITKEK
313	1052	2	630	ESNSRCRKMPGERCRGGPARLSLLDLPTPLPHPRQVIDFGS ASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCV MDELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHH FFKRNPHPDAA NPWLKSSADYLAETKVRPLERRKYMLKSLDQ IETVNGGSAVSRITFPDREALAEHADLKS MVEL/MKRL
314	1053	1	302	RLVKKRVECRQCGKAGRNQSTLKTMRSHGTGEKPYECDHCGKA FSIGSNLNVHRRHTGEKPYECLVCGEAFSDHSSLSRSHVKTHR GEKLFVSSVWKRLQ
315	1054	1318	730	CGPGFSLSFFFLRWSF\ALVAQAGVQWHDLGSLQPPAPGFKRF SLSLSLRWDYRHAHARLIFVFLVEMGFLHVGQAGLELPTSGD PPTSASQSARITGVTTPLGTFFFFL RWSFALVAQAGGQCLDLG SLQLPPP GFKRLVCHFQTPQKHRCSCQAPGDCLQESFVMTGCV LRTVSESQVRANAGAGAETVQGL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
316	1055	2486	1429	MGNAAAARKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHL DQ FERIKTLGTGSFGRVMLVKHKETGNHYAMKILD*QKVGKLGQI EHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVPGGEM FSHLRRIGRFSEPHARFYAAQIVLTFEYLHSLDLIYRDLKPEN LLIDQQGYIQVTDGFAKRVKGRWTWLCGTPEYLAPEIILSKG YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRF PSHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATT DWIAIYQRKVEAPFIPKFKGPGDTS\NFDDYEEEEIRV\SINE KFG\KEFSEF
317	1056	867	461	SSSRSSHGDSPPHSQTPCDTNRGLDTKH*/DSQSIEEKDSSQS E*NRIERRKEVERILQTNSDYM*HWSN*PENILPKKFFSKHQK CTATLSMRNTSIM/KKEGLF*AQFPSLLLSHLPAVGLGIYTG HLTTSTSTF
318	1057	544	784	TFHSSLEKNILQPCR*RR*\ICLPLL*PSVPLLAPQYFSDLR NSIVNSQPPEKQAMHL CFENLMEGIERNLLTKNRDR
319	1058	1606	228	GTSGVQQEISRLTNENLDLKELEKLEKNERKLKKQLKIYMKK AQDLEAAQALAQSERKRHELNQVTVQRKEKDFQGMLEYHKED EALLIRNLVTDLPQMLSGTVPCLPAYILYMCIRHA\DYTNDD LKVHSLLTSTINGIKKVLKKNDDFEMTSFWLSNTC\RLHLCL KQYSGDEGFMQTAKQN\EHCLKNFDLTEYRQV\L\SDL SIQ IYQQLIKIAEGLVQPMIVSAMLEN*SIQGLSGVKPTGSQKHSS SMADEDNSYRLEAIIRQMNAFHTVMCDQGLDPEIILQVFKQLF YMINAVTLNDLLLRKDVCWSWSTGMQLRYNISQLEEWLRGRNLH QSGAVQTMEPLIQAAQLLQLKKKTQEDAEAI CSLCTSLSSTQOI VKILNLYTPLNEFEERVTVAFIRTIQAQLQERNDPQQLLLDAK HMFVPLFPFNPSSLTMDSIHIPACLNLEFLNEV
320	1059	3	250	HEENTILKAAEVQVPPK*VVTPEAKAFI*RCLAYQKEDCIDAQ QLACDP\YLLHYIQKL V FVSSPAGAAI ASTFGVSNSSSN
321	1060	1332	500	GTTDEIMTRWARVSTTYNKRPLPATSWEDMKKGSFEGTSQNL P KRKQLEANRLSLKNDAPQAKHKKNKKKEYLNEDVNGFMEYLR QNSQM VHNQIIATDSEEVREEIAVALKKDSRREGRR LKRQAA KKNAMVCFHCRKPGHGIADCPAALENQDMGTGICYRCGSTEHE ITCKAKVDPALGEFFFAKCFVCGEMGHL SRSCPDPNPKGLYAD GGGCKLCGSVEHLKKDCPESQNSERMVTVGRWAKGMSADYEEI LDVFPKPKPKTKIPKVVNF
322	1061	384	102	DHVRKSLKRNRAENIVNIFKCNVVS L PNLPAFGQAQWLTVPVIP ALWEAEVGG*GQEIETILANAVK/SPFLKIQKKKISRWWR AP/VSPRYSGG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
323	1062	1	777	SDAWADAWARSLSVSPSSYPELHTEVPLSVLILGLLVVFILSV CFGAGLFVFLKRRKGVPSVERNTNNLDVSSFQQLQYGSYNTET HDKTDGHVYNYI PPPVVMQCNPIYMAGREGRESSLLPKPGKE FQLLGNLEEKKEEPATPAYTISATELLEKQATPREPELLYQNI AE/PSQGTS/TAQA*STITFVPYLLKGQFAPSYESRRQNQDRIN KTVLYGTPRKCFVGQSKPNHPLLQAKPQSEPDYLEVLEKQTAI SQL
324	1063	1	1496	ALCHIAVGQQMNLHLHLKIGLVVILASTVVAMSAVAQLWEDEW EVLLISLQGTAPFLHVGAAVMTLSWIVAGQFARAERTSSQV TILCTFTTVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGA PMLAPEHTLMSFRKALEQKLYGLQADITISLDGVPFLMHD'TTL RRTTNVEEEFPELARRPASMLNWTTLQRLNAGQWFLKTDPFWT ASSLSPSDHREAQNSICSLAEELLEAKGNATLLNLRDPPRE HPYRSSFINVTLEAVLHSGFPQHQMVLPSRQRPPLVRKVAPGF QQTSGSKEAVASLRRGHIQRLNLRYTQVSRQELRDYASWNLSV NLYTVNAPWLFSLWCAGVPSVTSDNSHTLSQVPSPLWIMPPD EYCLMWVTADLVSFLLIVGLFVLQKWRLGGIRSYNPEQIMLSA AVRRTSRDVSIMKEKLI FSEISDGVESDVLVSCDNSYDTYA NSTATPVGPRGGGSHTKTLIERSGR
325	1064	1899	776	NSADYGDGPDSSDADPDSGTEEGVLDFSDPFSTEVKPRILLMG LRRSGKSSI QKVVFHKMSPNETLFLESTNKICREDVSNSSFN FQIWDFFGQIDFFDPTFDYEMIFRGTGALIFVIDSQDDYMEAL ARLHLTVTRAYKVNTDINFEVFIHKVDGLSDDHKIETQRDIHQ RANDDLADAGLEKIHLSFYLTSIYDHSIFEAFSKVVQKLI PQ PTLENLLNIFISNSGIEKAFLEFDVVSKIYIATDSTPVDMQTYE LCCDMIDVVIDISCIYGLKEDGAGTPYDKESTAI IKLNNTTVL YLKEVTKFLALVCFVREESFERKGLIDYNFHCFRKAIHEVFEV RMKVVKSRKVQNRLLQKKRATPNGTPRVLL
326	1065	1181	346	RTRGRDPGAGFRRTANKRCCRRRFLIGCGWLPLRSDWPLVSKM LSKGLKRRKEEEEEKEPLAVDSWWLDPGHAAVAQAPPVASSS LFDLSVLKLHHSLLQSEPDRLHLVVLVNTLRRIQASMAPAAAL PPVPSPPAAPSVADNLLASSDAALSASMASLLEDLSHIEGLSQ APQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDGGLGL FEDIDTSMYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELD YLMVDVLVGTQALERPPGPGR

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
327	1066	1844	337	LQEVKARRNTLHKEKDHLVNDYEQNMKLLQTKYDADINLLKQEHALSASKASSMIEELEQNVCQLKQQLQESSELQRKQQLRDQENK FQMEKSHLKHIEYKKAHDLQSELDKGKEDTQKKIHKFEEALKW KKWRQI*LDPN/LLREKQSKEFLWQLEDIRQRYEQQIVELKLE HEQEKTHLLQQHNAEKDSLVRDHEREIENLEKQLRAANMEHEN QIQEFKKRDAQVIADMEAQVHKLREELINVNSQRKQQLVELGL LREEEKQRATREHEIVVNKLKAESEKMKIELKTHAAETEMTL EKANSKLQIEKEYTQKLAKSSQI LAELQTTISSLKEENSQQO LAAERRLQDVRQKFEDEKKQLIRDNDQAIKVLQDELENRSNQV RCAEKKLQHKELESQEQITYIRQYETKLKGLMPASLRQELD TISSLSQVNFLQKRASILQEE/RDYISRQKVQPIR*LHERM QMRISRLCCGTSSSRFEDLDIVNCEISGIF
328	1067	1149	238	VINLVYLISSPRPELKPVDKESVVMKFPDGFKEKFSPPILQLD EVDFYYDPKHVIFSRLSVSADLESRICVVGENGAGKSTMLKLL LGDLAPVVRGIRHAHRNLKIGYFSQHHV\EQL/DLNVQCLWELA GHASFPG\RPEEEY\RHQLGFGMGISGEL\AMRPLCQPVLGAR KKPWPFAQMDYCPAPTFYIL\DEPTN\HLGHGRAIEALGPCL QTISGVGVILVSHE*SALSRLVCRE\LWVC*G\GGVTRVERKD FDQYRALLQGTVSAREGFPLGPPRLKDSPRDMGLVSQTPWGHV VGYPLPGRG
329	1068	26	674	CSAVEVKMAARTAFGAVCRRLWQGLGNFSVNTSKGNTAKNGGL LLSTNMKWVQFSNLHVDVDPKDLTKPVVTISDEPDILYKRLSVL VKGHDKAVLDSYEFYFAVLA AKELGISIKVHEPPRKIERFTLLQ SVHIYKKHRVQYEMRTLYRCLELEHLLTGSTADVLEYIQRLNP EGVAMEVTKFCFFIFL\TQLEQLPEHIKEPIWETLSEEKEESK S
330	1069	2105	1283	DFWDTAGQERFQSMHASYYHKTHACIMVFDVQRKVTHRNLSW YTELREFRPEIPCI VVANKIDGGAIPAPGC*QFTGDLPSYISS SIPRAGNLQ*LVLPPITIRYNPWL VACILPTL*RSQLSRPALFP RHRSLLTFLGFPVSQSSLP IPLSGMKASSGPPLQTFPSPDR QTNVLPSTLY\ADINVTQKSFNFAKKFSLPLYFVSAADGTNVVK LFNDAIRLAVSYKQNSQDFMDEIFQELENFSLQEEDVDPDQE QSSSIETPSEEVASPHS
331	1070	1	1109	GATPLGSVGGRTGKMDAATLT YDTLRF AEFEDFPETSEP VWIL GRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGW GCMLRCGQMIFAQALVCRHLGRDWRWTQKRQPD SYFSVLNAF IDRKDSYYSIHQIAQMGVGEKSGIQWYGPNVTVAQVLKLA VF DTWSSLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDR HCNGFPAGAEVTNRPS PWRPLVLLIPLRLGLTDINEAYVETLK HCFM\MPQSLGVIGGKPNSAH\YFIG*VG\EELIYLDPHTTQP AVEPTDGC FIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLST QAFGAECCLGMTRKT FGFLRFFFSMLG
332	1071	39	284	ALCVVPFNTFHN\DFLLLDKEGTLDPVMSFSTHWTITIGPADM FFS\FRQHYKNFKSHGTNPSKSVWAHATCQSCAFPNLLGW

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
333	1072	2	1484	<p>TRLAEFGTRDPCAQAPCEQQCEPGGPQGYSCHCRLGFRPAEDD  PHRCVDTDECQIAGVCQQMCVNYVGGFECYCSEGHLEADGIS  CSPAGAMGAQASQDLGDELLDDGEDEDEDEAWKAFNGGWTEM  PGILWMEPTQPPDFALAYRPSFPEDREPQIPYPEPTWPPPLSA  PRVPYHSSVLSVTRPVVVSATHPTLPSAHQPPVI PATHPALSR  DHQIPVIAANYPDLPSAYQPGILSVSHSAQPPAHQPPMISTKY  PELFPAHQSPMFPDTRVAGTQTTTHLPGIPPNHAPLVTTLGAQ  LPPQAPDALVLRTOATQLPIIPTAQPSLTTSRSPVSPAHOIS  VPAATQPAALPTLLPSQSPTNQTSPISPTHPSKAPQIPREDG  PSPKLALWLPSAPATAAPTALGEAGLAHESQRDDRWLLVALLV  PTCVFLVLLALGIVYCTRCGPHAPNKRTDCYRWVIHAGSKS  PTEPMPPRGSLTGVQTCRTSV</p>
334	1073	1	1406	<p>LRVRRRPHLPAPPALRARRSDRRSSRAPAAFPPRPPHASPAPG  PAMAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTDSPA  TTGAVVTISASLVAKDNGSLALPADAHLYRFHWIHTPLVLTGK  MEKGLSSTIRVVGHVPGEFPVSVVVTAADCWMCQPVARGFVVL  PITEFLVGDLLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNSFL  KTALFLYSWDFGDGTQMVTEDSVVYYNYSIIGTFTVKLKVVAE  WEEVEPDATRAVKQKTGDFASLKLQETLRGIQVLGPTLIQTF  QKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAY  NLTHTRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVF  AFPCATLITVMLAFIMYMTLRNATQQKDMVENPEPPSGVRCCC  QMCCGPFLLETSPSEYLEIVRENHGLLPPLYKSVKTYTV</p>
335	1074	1	866	<p>VVEFAFQLSSSVSVCLTVSFGWQLGTVSSCLSRDWFLKGNLLII  IVSVLIILPLALMKHLGYLGYSGLSLTCMLFFLVSVIYKKFQ  LGCAIGHNETAMESEALVGLPSQGLNSSCEAQMFTVDSQMSYT  VPIMAFVCHPEVLPITYELCRPSKRRMQAVANVSIGAMFCM  YGLTATFGYLTIFYSSVKAEMLMYSQKDPLILCVRLAVLLA\V  TLTVPVVLFPIRRALQQLLFPGKAFSWPRHVAIALILLVLVNV  LVICVPTIRDIFGVIGSTSAPSLIFILPSCI</p>
336	1075	3	825	<p>GAGSKSSMMQLMHLESFYEK\PPPGLIKEDDTKPEDCIPDVPG  NEHAREFLAHTPTKGLWMPLEKEVKVKH/CTFHWIAS*FLGDG  KFIPKATRLKDVVWSN*FTCLFWDLTRFIHDCIFF*NWSLMNK  NFNIYY*FFISLR*NTLILQKYFPFSLLLGWCHCKWYGHRTGYK  ECPFFIKDNQKLQQFRVAHEDFMYDIIIRDNKQHEKNVRIQQLK  QLLEDSTSGEDRSSSSSSSEGKEKHKKKKKKKEKHKKKKKK  KKRKHKSSKSNEGSDSE</p>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
337	1076	3	2451	<p>EIAGAAENMLGSLCLPGSGSVLLDPCTGSTISETTSEAWSV  EVLPSDSEAPDLKQEERLQELESCSGLGSTDDTDVREVSSRP  STPGLSVVSGISATSEDI PNKIEDLRSECSSDFGKDSVTS PD  MDEITHDFLYILQPKQHFQHI EAEADMRIQLSSSAHQLTSPPS  QSESLAMFDPLSSHEGASAVVRPKVHYARPSHPPDPPILEG  AVGGNEARLPNFGSPMF* LPAEM EAFKQRHS /YTPERLVRSSRS  S \DIVSSVRPMSDPSWNR RP \GNEERELPPAAIGATSLVAA  PHSSSSSPSKDSSRGETEERKSDDEKSDRNPWRKRFVSAM  PKAPIPFRKKEKQEKDKDDLGPDRFSTLTDDPSRLSAQAQVA  EDILDKYRNAIKRTSPSDGAMANYESTEVMGDGE SAHDSPRDE  ALQNISADDLPDSASQAHPQDSAFSYRDAKKKLRLALCSADS  VAFPVLT \HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQDK  NLMAQLQETMRCVCRFDNRTCRKLLASIAEDYRK RAPIYAYLT  RCRQGLQTTQAHLE RLLQRVLRDKEVANRYFTTV CVRLLESK  EKKIREFIQDFQKLTAADDKTAQVEDFLQFLYGAMAQDVIWQN  ASEEQ LQDAQLAIERSVMNRIFKLAFYPNQDGDILRDQVLHEH  IQRLSKVVTANHRALQIPEVYLREAPWPSPAQSEIRTISAYKTP  RDKVQCILRMCSTIMNLLSLANEDSVPGADDFVPVLVFLIKA  NPPCLLSTVQYISSFYASCLSGEESYWWMQFTA AVEFIKTIDD  RK</p>
338	1077	536	1305	<p>WPM SLARGHGDTAASTAAPLSEEGEVTSG LQALAVEDTGGP SA  SAGKA EDEGE GREGRETEREGSGGEEAQGEVPSAGGEP AEEDS  EDWCVP CSDEEVELPADGQPWMP PPSEIQRLYELLAHGTLEL  QAEILPRRPPTPEAQSEEERSDEEPEAKEEEEEKPHMPTEFDF  DDEPVT PKDSLIDRRRTPGSSARSQKREARLDKVLSDMKRHKK  LEEQILRTGRDLFSLDSEDPSPASPLRSSGSSSLFPQRKY</p>
339	1078	2	1771	<p>LGRGTFGQVV*CWKRG TNEIVA I KILKNHPSYARQQIEVSIL  ARLSTESADDYNFVRAYECFQHK NHTCLVFEMLEQNLYDFLKQ  NKFSPLPLKYIRPVLQQVATALMKLKS LGLIHADLKPENIMLV  DPSRQPYRVKVIDFGSASHVSKAVCSTYLQSRYYRAPI I LGL  PFCEAIDMWSLGCVIAELFLGWPLYPGASEYDQI /RYSISQTQG  LPAEYLLSAGTKTTRFFNRD TDSPYPLWRLKTPDDHEAETGIK  SKEARKYIFNCLDDMAQVNMTTDL EGS DMLVEKAVRREFIDLL  KKMLSIDSVKRFS PVGSLNHPFVTMSLFLDFPHSTHVKSCFQ N  MEICKRRVNM YD TVNQSKTPFITHVAPSTSTNLTMTFNNQLTT  VHNQPSAASMAAVAQRSMPLQTGTAQICARPD PFQQALIVCPP  GFQGLQASPSKHAGYSVRMENAVPIVTQAPGAQPLQIQPGLLA  QQAWPSGTQQILLPPAWQQLTG VATHTSVQHA AVI PETMAGTQ  QLADWRNTHAGSHYNPIMQQPALLTGHVTLPA AQPLNVGVAH  VMRQQPTSTTSSRKSQHL YCGRARVSKIASR</p>



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
340	1079	2	2721	EFAICRYPLGMSGGQIPDEDITASSQWSESTAACYGRDLSEEG DGAWCPEIPVEPDDLKEFLQIDLHTLHFITLVGTQGRHAGGHG IEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDIFLKD LEPPIVARFVRFIPTDHSNMVCMRVELYGCWLDGLVSYNAP AGQQFVLPGGSI IYLNDSVYDGAVGYSMTEGLGQLTDGVSGLD DFTQTHEYHVWPGYDYVGWRNESATNGYIEIMFEFDRIRNFTT MKVHCNNMFAKGVKIFKEVQCYFRSEASEWEPNAISFPLVLDL VNPSARFVTVP LHRMASAIKCQYHFADTWMMFSEITFQSDAA MYNNSEALPTS PMAPTTYDPMLKVDDSNTRILIGCLVAIIFIL LAIIVII LRQFWQKMLEKASRRMLDDEMTVSLSLPSDSSMFN NNRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGE EESGCSGVVKPVQPSGPEGVPHYAEADIVNLQGVGTGGNTYSVP AVTMDLLSGKRCGCGREFPPGKLLTFKEKLGEQFGEVHLCEV EGMEKFKDKDFALDVSANQPVLVAVKMLRADANKNARNDLKE IKIMSRLKDPNIIHLLSVCITDDPLCMITEYMENGDLNQFLSR HEPPNSSSSSDVRTVSYTNLKFMATQIASGMKYLSSLNFVHRDL ATRNCVLGKNYTIKIADFGMSRNLYSGDYRIQGRAVLPIRWM SWESILLGKFTTASDVWAFG\VTLWE\TFTFCQRKGPYS\QLS \DETGY*RNTGEFFPRPKGGQTYLPSTSPFVPDSCVIKMLMSC WRDRTKNRPSFQEIHL LLLQQGDERCCQCLAMFLRLRSSLQDL PLTHAYATPSGHLMKLRDRGLFALPSFPGHPHSLPLTHIYFFF FTLKN
341	1080	916	3	CSASPLRPGLLAPDLLYLPAGAGQPRRPEAEFGQKPVVPTLYVT EABAHSPALPGLSGPQPKWVEVEETIEVRVKMGPGQVSPTE VPRSSSGHLFTLPGATPGGDPNSNNSNNKLLAQEAWAQGTAMV GVREPLVFRVDARGSVDAASGMGSLEEEGTMEEEAGEEEGEDG DAFVTEESQDTHSLGDRDPKILTHNGRMLTLADLEDYVPGEGE TFHCGGPGPGAPDDPPCEVSVIQREIGEPTVG\SLCCSAWGMH WVPEALSASGLSPMGR\HHRDPRSVALRAPPSGGRPLGLW AVLPG
342	1081	862	444	QGLAAEFLOQPAVTRAYTAACVLTTAAVQLELLSPFQLYFNPH LVFRKFQAPFLPWALMGFSLLLGNSILVDLLGIAGVHIYYFLE DVFFNQPGGKRLQLTPGFLGLQSSKAPAGSSLTITWTQQSQGGP GTAGELAAPS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
343	1082	3658	337	EKNALEPTVYFGMGV*APQVPRFQQRITGYQYYLQLRKDIWEE GIPCTLEQPIHLAAGLAVQAI FGDFDQYESQDFLQKFALFPVWG LQDEKVL EEATQKVALLHQKYRGLTAPDAEMLYMQEVERMDGY GEESYPAKDSQGS DISIGACLEGIFVKHKNRHPVVFWRWDIA NMSHNKSFFALELANKEETIQFQTEDMETAKYIWRLCVARHKF YRLNQCNLQTQTVTVNPIRRRSSRMSLPKPQPYVMPPPP\QL HYNGHYTEPYASSQDNLFVPNQEG\YQGQFQTSLNRAQIDFNG RIR\NASVYSAHSTNSLNNPQPYLQSPMSSNPSITGSDVMRP DYLPSHRHSAVIPPSYRPTPDYETVMKQLNRGLVHAERQSHSL RNLNIGSSYAYSRAALVYSQPEIREHAQLPSPAAAHCPFSL YSFHSPSPYPYPAERRPVVGAVSVPELTNAQLQAQDYPSPNIM RTQVYRPPPPYPYPPRANSTPDLSRHLIYSSNPDITRRVHH SVQTFQEDSLPVAHSLQEVSEPLTAARHAQLHKRNSIEVAGLS HGLEGLRLKERTLSASAAEV\APRAVS VGSQF\SVFTERTQRE GP EEAEGLRYGHKKSLS DATMLIHSSEEEDEDFEEESGARAP PARAREPRPGLAQDPPGCPRVLLAGPLHILEPKAHVPDAEKRM MDS SPVRTTAEAQRPWRDGLLMPSMS ESDLTSGRYRARRDSL KKRPVSDLLSGKKNIVEGLPPLGGMKKTRVDAKKIGPLKLAAL NGLSLSRVPLPDEGKEVATRATNDERCKILEQRLEQGMVFTEY ERILKKRLVDGECSTARLPENAERNRFQDVL PYDDVRVELVPT KENNTGYINASHIKVSVSGIEWDYIATQG PLQNTCQDFWQMVW EQGIAI IAMVTAE EGGREKSFRYWPRLGSRHNTVTYGRFKIT TRFR TDSGCYATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPE DLKGFLSYLEEIQSVRRHTNSTSDPQSPNPPLLVHCSAGVGRT GVVILSEIMIACLEHNEVLDIPRVLDMLR\QQRMMLVQTLQCY TFVYRVLIQVPEKAPRLILSSPQFPYGAQSCEAFTA
344	1083	6	304	RKKQKLAEE*VELSKLADLKDAEAVQKFFLEET*L\GEETLAK GVDHLTNPSAVCGQPQWLLQVLQQTLPVQMLLT KPLPVNQ RLVSAG/SLAKDDVE
345	1084	1255	635	SFCLHEFGWLGS SPQSDHPVPALLGLGAFVHHSLLQVHSSPGA GPVSFLFLGESCPVDEPRCVPSCAFGLSCFPLLN SAALERG LFFFVVFVFFLES GSCQVARAGVRD/RDRGSLQPPPPGLKQFCL SLPSRWDHRHPPPLRVP*FVFVFLVELGFHHVAQAGLKLTL DPPAPASHSAGITGVSQRDQPVFLRWASCSSELVG
346	1085	116	415	EGFPGRSLSGGLCCRLRRRFPIDGYRPRRRRRWSCCPSGVRPV RRMSQKSWIESTLT KRECVYIIPSSKDPHRCLPGCQICQQLVR RGFTVLARMVSI
347	1086	918	760	QNSTCLTAQTHSLLQHQPQLTLLDQYIREQREKDSVMSANG KPD PDTV PDS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
348	1087	1	750	LNPWKNALQDFCLPFLRITSLLQHHLFGEGLPSCQEEEEFSVL ASCLGLLPTFYQTEHPFISASCLDWPVPAFDIITHWCFEIKSF TERHAEQKGALLIQESKWKLPHLLQLPENYNTIFQYYHRKTCS VCTKVPKDPVCLVCGTFVCLKGLCKQSQSYCECVLHSQNCGA GTGIFLLINASVIIIRGHRFCLWGSVYLDAGHEEDRDLRRGK PLYICKERYKVKLEQQWISHTFDHINKRWGPHYNGL
349	1088	3	1374	KGQLVNLPPENFPWCQGSQGPRLRRTCYVLCQAGPRSRGWQ SLSFDDGAFHLKGTGELTRALLVLRCAWPPLVTHGLLLQAWS RRLGSRSLSGAFLRASVYQGFVAGETAEEVKGCVQQLRTLRLR PLLAVPTEEEPDSAAKSGEAWYEGNLGAMLRCDLSRGLLEPP SLAEASLMQLKVLTALTSTRICKELASWVRPGLASLELSPERLA EAMDQGNLQVSCNLAEQNQHRLRASLSRLHRVAQYARAQHVRL LVDAEYTSNLPALSLVAALAVRWNSPGEQGPWWNTYQACLK DTFERLGRDAEAAHRAGLAFGVKLVRGAYLDKERAVAQL\HG\ MEDPPTQADYEATS\QSYS\RCELEMLTHVARHGPMCHLMVAS HNEESVRQATK\GQAGYVVKSIPIYGSLEEVIPIYLRRAQENR SVLQGARREQELLSQKLWRLLPGCRRIPH
350	1089	1036	306	VVEFGEMSTARAPEGLRWFLYVHPDLQLNKQLIQRVESLGFK ALVITLDTVPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYF QMTPISTSLCWNDSLWFQSI TRLP IILKGILTKEDAELAVKHN VQGIIVSNHGGRLDEVLAS IDALTEVGAAE*GNMKYYLDAGV RTGNDVQKALALGAKCIFLGRPIILWGLACKGEHGVKEVLNILT NEFHTSMA\LTGCRSVAEINRNLVQFSRL
351	1090	1229	957	FFLRWSFTL\LPRLE/CQWNLGSLQPPPPGFK*SSCLRLSS WGLQVPTSMLG*FFCIFSREGISPCWPGWSQTPKVIHLRPPR VLRLQA
352	1091	1145	365	LLCFVHTALQSFQGELEPHVVIIVVFLVKLGICK*RASWRK KVTLVVK*S/LKICFTKYGSCYHPGEKSSSWLFN*RMVNDCLA TSCSNRSFVIQIIPSSNLFMVVDSSCLCESVAPITMAPIEIR YILLCAGPLTTTETSKGYQW*GNLGEKY*RRKITSFPLLERES S*ESCHQILTSEMQRKKQSLETCLNYSQHNSLKCERLKAQ KIRRRPESCHGFHPEENARECGGAPSLQAQTVLLLLPLLLMLF SR
353	1092	1140	790	VPSPTHDPKPAEAPMPA*PAPPGPASPGGALEPPAAARAGGSP TAVRSILTKERRPEGGYKAVWFGEDIGTEADVVLNAPTLDVD GASDSGSGDEGEGAGRGGGPYDAPGGDDSYI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
354	1093	3	2293	LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPYVAD GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDEHSK TNRMTGREFFSRPELYPFLKQLETVANVDSMDGEPNHRPS MFLLLLVLERLYASPM DGTSSALSMGPFVPFIMRCGHSPVYHS REMAARALVPFVMDHIPNTIRTLLSTLPSCDQCFRQNHIG TLLQVFHLVQAYSDSKHGTNSDFQHELTDTVCTKAKLWLAKR QNPCLVTRAVYIDILFLLTCCLNRSKDNQPVLES LGFWEEVR GIISGSELITGFPWAFKVPGLPQYLQSLTRLAIAAVWAAAAS GERETNPVIFSQLLSAFPEVRS LTLEALLEKFLAAASGLGE KGVPELLCNMGEKFLLLAMKENHPECFCCKILKILHCDPGEWL PQTEHCVHLTPKEFLIWTMDIASNERSEIQSVALRLASKVISH HMQTCVENRELIAELKQWVQLVILSCEDHLP TESRLAVEVL TSTTPLFLTNPHPILELQDTLALWKCVLTLLQSEEQAVRDAAT ETVTAMSQENTCQSTEFQAFQVDASIALALALAVLCDLLQW DQLAPGLPILLGWLLGESDDL VACVESMHQVEEDYLF EKA EVN FWAETLIFVKYLCKHLFCLLSKSGWRPPSP EMLCHLQRMVSEQ C\HLLSQFFRELPPAEFVKTVETRLRIQEERTLACLRL LAF LEGKEGEDTLVLVSVD SYAESRQLTLPRTEAAC
355	1094	25	1265	HAFRPIALQRGVSFRGCSNQYAESRR LQGESGSRFAHLMESL LQHLDRFSELLAVSSTTYVSTWDPATVRRALQWARYLRHIHR FGRHGPIRTALERRLNQWRQEGGFGRGPVPGLANALGHCD VLLSLRLLENRALGDAARYHLVQQLFPGPGVRDADEETLQESL ARLARRRS AVHMLRFNGYRENPNLQEDSLMKTQAE LLLERLQE VGKAEAE RPARFLSSLWERLPQNNFLKVIAVALLQPPLSRRPQ EELEPGIHKSPGEGSQVLVHWLLGNSEVF AAFCRALPAGLLTL VTSRHPALSPVYLGLLTDWGQRLHYDLQKGIWVGTESQDVPWE ELHNRFSQSLCQAPPPLKDKVLTALETCKAQDGFEEPGLSIWT DLLLALRSGAFRKRQVLGLSAGLSSV
356	1095	3	1027	SHLIQHQR IHT*E*AHECNECGKAFSQTSLIQH HKMHRKEKS YECNEYEGSFSSHSD LILQQEVLTROKAFDCDVWEKNSSQRAH LVQHQS IHTKE/K/PHECNEDGKIF/NQIQ A/LIQHLRVHTRE K\YVCTACGKAFSHSSAIAHQHIHTREK PSECDE*RGKISVK LLIDSC/RIYTSEKSYKCI ECGKFFMLLVFSYLSHIWRIHMG I KFHCCNECEKAISQRNYLV*YQIHAMQKDYKCN/EACMCVRRF SHNPTLIQHQR IYT*ENLFGCSK/C/GRSFNRS LSTSLCHIRIS I/RRQEFDV TQMEKLD TTFQA/STQHRNNGEKIVDYL FMKLLI HSPNLFHCTKI
357	1096	2638	2867	AVTLTAKICSFTPEPSETMSPAGTNN SRHAALRAVTL PVKVC SFTPEPARSRTHQKEETPNTSEHQKEQTPEAPP

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
358	1097	4747	4550	MAYSWQTDPNPNESHEKQYEHQEFLLFVNQPHSSSQVSLGFDQI VDEISGKIPHYESEIDENTFFVPTAPKWDSTGHSLNEAHQISL NEFTSKSRELSWHQVSKAPAGFSPSVLPKPQNTNKECSWGS IGKHHGADDSRFSILAPSFSLDKINLEKELENENHNYHIGFE SSIPPTNSSFSDFMPKEENKRSGHVNI VEPSLMLLKGSLOPG MWESTWQKNIESIGCSIQLVEVPQSSNTSLASFCKNVKKIRER YHAADVNFNSGKIWSTTTAFPPYQLFSKTKFNIHIFIDNSTQPL HFMPCANLVLKDLIAEILHFCTNDQLLPKDHILSVWGSEEFLLQ NDHCLGSHKMFQKDKSVIQLHLQKSREAPGKLSRKHEEDHSQF YLNQLEEFMHIVKVSRCQLLTLIRKYDFHLKYLLKTQENVYNI IEEVKKICSVLGCVETKQITDAVNELSLILQRKGENFYQSSET SAKGLIEKVTTTELSTSIYQLINVYCNSFYADQPVNVPRCTSY LNPGLPSHLSFTVYAAHNIPETWVHRINFPLEIKSLPRESMLT VKLFGIACATNNANLLAWTCLPLFPKEKSILGSMFLSMTLQSE PPVEMITPGVWDVSPSPVTLQIDFPATGWEYMKPDSEENRSN LEEPLKECIKHIALRSQKQTPLLLSEEKKRYLWFYRFYCNNEN CSLPLVLGSAPGWDERTVSEMHTILRRWTFSPLEALGLLTSS FPDQEIIRKVAVQQLDNLNDELLEYLPQLVQAVKFEWNLESPL VQLLLHRSLSQSIQVAHRLYWLLKNAENEAFFKSWYQKLLAALQ FCAGKALNDEFSEKQKLIKILGDIGERVKSASDHQREQEVLKKE IGRLEEFFQDVNTCHLPLNPALCIKGIDHDACSFTSNALPLK ITFINANLMGKNISIIIFKAGDDLQDMLVLQLIQVMDNIWLQ GLDMQMIIRCLSTGKDQRLVQMVPDAVTLAKIHRHSGLIGPL KENTIKKWFSSQHNLKADYEKALRNFFYSAGWCVVTFILGVC DRHNDNIMLTKSGHMFHIDFGKFLGHAQTFGGIKRDRAPFI FT SEM\EYFITEGG\KNPQHFDQFV\ELCCRAYNIIRKHSQLLL\ NLL\EMMLYAG\LPELSGI\QDLKYVYNNLRPQDQTDLEATSHF TKKIKESLECFPVKLNLIHTLAQMSAISPAKSTSQTFFPQESC LLSTTRSIERATILGFSKKSSNLYLIQVTHSNNETSLTEKSFE QFSKLHSQLOKQFASLTLPEFPWWHLPTNSDHRFRDLNHY MEQILNVSHEVTNSDCVLSFFLSEAGQQTVEESSPVYLGEKFP DKKPKVQLVISYEDVKLTILVKHMKNIHLPDGSAPSAHVEFY LPYPSEVRRRKTKSVPKCTDPTYNEIVVYDEVTELQGHVLM VKSKTIVFGAINIRLCSVPLDKEKWYPLGNSII*PLLLFYTSN FMQSVLH
359	1098	679	346	FFLRWSLDSVTQAGVQSHDLSSLQPPPPGFKQSSSLFGLPSSWE *RWVPPCPANFFVFLVETGFRHVGQAGLELLTSNDLPVSACQS AGITGVTTVPQRKSMILYEVTICY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
360	1099	2	1601	FVREIRGPAVPRLTSAEDRHRHGPHAHSPQLQRTGRDYSLDYL PFRLWVGIVVATFCLVLVATEASVLVRYFTRFTEEGFCALISL IFIYDAVGKMLNLTHTYPIQKPGSSAYGCLCQYPGPGGNESQW IRTRPKDRDDIVSMDLGLINASLLPPPECTRQGGHPRGPGCHT VPDIAFFSLLLFLTSFFFAMALKCVKTSRFFPSVVRKGLSDFS SVLAAILLGCGLDAFLGLATPKLMVPREFKPTLPGRGWLVSDFG ANPWWWSVAAALPALLLSILIFMDQQITAVILNRMEYRLQKGA GFHLDLFWVAVLMLLTSALGLPWVVSATVISLAHMSLRRESR ACAPGERPNFLGIREQRLTGLVVILTGLSIFLAPVLKFIPMP VLYGIFLYMGVAALSSIQFTNRVKLL\MPAKHQPDLLLRHV PLTRVHLFTAISFA\CLGLLW\IIKSTPAAIIFPLMLLGLVGV RKALERVFSPOELLWLDELMPPEERSIPEKGLEPEHSFSGSDS EDSELMYQKAPENISVN*LE*EFVREIRGPAVPRLTSAEDR HRHGPHAHSPQLQRTGRDYSLDYLPFRLWVGIVVATFCLVLVA TEASVLVRYFTRFTEEGFCALISLIFIYDAVGKMLNLTHTYPI QKPGSSAYGCLCQYPGPGGNESQWIRTRPKDRDDIVSMDLGLI NASLLPPPECTRQGGHPRGPGCHTVPDIAFFSLLLFLTSFFFA MALKCVKTSRFFPSVVRKGLSDFS SVLAAILLGCGLDAFLGLAT PKLMVPREFKPTLPGRGWLVSDFGANPWWWSVAAALPALLLSI LIFMDQQITAVILNRMEYRLQKGA GFHLDLFCVAVLMLLTSAL GLPWVVSATVISLAHMSLRRESRACAPGERPNFLGIREQRLT GLVVILTGLSIFLAPVLKFIPMPVLYGIFLYMGVAALSSIQF TNRVKLLLDASKTPARPATLAACASDQGPPLHSHQLCPVWGCF GIKSTPAAIIFPLMLLGLVGV RKALERVFSPOELLWLDELMP PEERSIPEKGLEPEHSFSGSDSEDSSELMYQKAPENISVN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
361	1100	1	2636	MGLKARRAAGAAGGGGDDGGGGGGAANPAGDAAAAGDEERKV GLAPGDVEQVTLALGAGADKDGTLTLLLEGGGRDEGQRRTPOGIG LLAKTPLSRPVKRNNAKYRRIQTLYDALERPRGWALLYH\AL VFLIVLG\CLILAVL\TTFKEYETVSGDWLLLLLETFAIFIFGA EFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV VAVGNQGNVLATSLRSLRFLQILRMLRDGPGEGGTWKL LG\SA ICAH\$KELITAWYIGFLTLILSSFLVYLVEKDVPEVDAQGEEM KEEFETYADALWWGLITLATIGYGDKTPKTWEGRLIAATFSLI GVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAA WRYATNPNRIDL VATWRFYESVVSFPFRKEQLEAASSQKLG LLDRVRLSNPRGSNTKGKLF TPLNVD AIEESPSKEPKPVGLNN KERFRTAFRMKAYAFWQSSDAGTGDPMAEDRGYGNDFPIEDM IPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKD VIEQYSAGH LDMLSRIKYLQTRIDMIFTGPPSTPKHKKSQKGS AFTFPSQQ SPRNEPYV\ARPST\SEI\EDQRH*WGKFVKS LKGQV\QGLGR KLDFLVDMMQHMERLQVQVTEYYPTKGTSSPAEAEKKEDNRY SDLKTIICNYSETGPPEPPYSFHQVTIDKVS PYGFFAHDPVNL PRGGPSSGKVQATPPSSATTYVERPTVLPILTLLDSRVSCHSQ ADLQGPYSDRISPRQRRSITRSDTPLSLMSVNHEELERSPSG FSISQDRDDYVFGPNGGSSWMREKRYLAEGETD TDTDPFTPSG SMP\LSSTGDGISDSVWTPSNKPI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide(A = Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
362	1101	1	5433	<p>RTRGIIIEFDPKYTAFEVEEDVGLIMIPVVRHLGTYGYVTADFTSQSSASAPGG VDYILHGSTVTFQHGQNLSPFINISIDNESEFEPIEILLTGATGGAVLGRH LVSRIIIAKSDSPFGVIRFLNQSISIANPNSTMILSLVLERTGGLGGEIQVN WETVGPNSQEALLPQNRDIADPVSGLFYFGEQGGVRTIILTIYPHEEIEVEE TFIIKLHLVKGEAKLDSRAKDVTLTIQEFQDPNGVVOFAPETLSKKTYSPLA LEGPLLIITFFVRRVKGTGFEIMVYELSSFPDITEDFLSTSGFPTIADGESEA SFDVHLLPDEVPEIEEDYVQLVSVGGAELEKESITWFSVYANDDPHGVA LYSDRQSLIGQNLIRSIQINITRLAGTFGDVAVGLRISSDHKEQRTVTENAE RQLVVKDGATYKVDVVPKIQVFLSLGSNFTLQLVTVMVGGREFYGMPTILQE AKSAVLPVSEKAANSQVGFESTAFQLMNITAGTSHVMSRRGTYGALSVAWTT GYAPGLEIPEFIVVGNMPTLGSLSFSHGEQKGVFLWTFPSPGWPEAFVLHL SGVQSSAPGGAQLRSGFIVAEIPEMGVFOFSTSSRNIIVSEDQMIRLHVQRL FGFHSDLIKVSYQTAGSAKPLEDFEPVQNGELFFQKFQTEVDFEITINDQL SEIEEFFYINLTSVEIRGLQKFDVNWSPRLNLDVSAVITILDNDLAGMDIS FPETTAVAVDVTLLIPVETESTYLTSTKTTTILQPTNVVAIVTEATGVSAP EKLVTLHGTTPAVSEKPDVATVTANVSIHGTFSLGPSIVYIEEMKNGTFNTAE VLIRRTGGFTGNVSIIVKTFGERCAQMEPNALPFRGIYGINLTWAVEEEDFE EQTLTLIFLDGERERKVSQVILDDDEPEGQEFYVFLTNPQGAQIVGKDDT GFAAFAMVIITGSDLHNGIIGFSEESQSGLELREGAVMRRLHLIVTRQPNRAF EDVKVFWRVTLNKTIVVVLQKDGVNLMEEQLQSVSGTTCTMGQTKCFISIELKP EKVPQVEVYFFVELYEATAGAAINNSARFAQIKILESDESQSLVYFVSGSRLA VAHKKATLISLQVARDSGTGLMMSVNFSTQELRSAETIGRTIISPAISGKDFV ITEGTLVFEPGQRSTVLDVILTPETGSLNSFPKRFQIVLDFPKGGARIDKVG TANITLVSDADSAIINGLADQLHQPVNDDILNRVLHTISMKVATENTDEQLSA MMHLIEKITTEGKIQAQSVASRTLFYEILCSLINPKRKDTRGFSHFAELTENF AFSLLTNVTCGSPGEKSKTILDSCTPYLSIALHWPQQINGHKFEGKEGDYIR IPERLLDVQDAEIMAGKSTCKLVQFTEYSQQWFISGNNLPTLKNKVLVLSVK QSSQLLTNDNEVLRYIAAEPRIIPTSLCLLWNQAAASWLSDSQFCVKVIEE TADYVEACALHMSVYAVYARTDNLSYNEAFTSGFICISGLCLAVLSHFCA RYSMFAAKLLTHMMAASLGTOILFLASAYASPLAEESCSAMAAVTHYLCL FSWMLIQSVNFWYVLMNDEHTERRVLLFFLLSWGLPAFVVILLIVILKGIYH QSMSQIYGLIHGDLCFIPNVYALFTAALVPLTCLVVFVVFVTHAYQVKPQWK AYDDVFRGRTNAAEIPILILYLFALISVTLWGLHLMAYRHFVWLVLVFI QLL\YPLFYFLLL*QSSASAPGGVDYILHGSTVTFQHGQNLSPFINISIDN ESEFEPIEILLTGATGGAVLGRHLVSRIIIAKSDSPFGVIRFLNQSISIAN PNSTMILSLVLERTGGLGGEIQVNWETVGPNSQEALLPQNRDIADPVSGLFYF GEGEGGVRTIILTIYPHEEIEVEETFIKLHLVKGEAKLDSRAKDVTLTIQEF GDPNGVVOFAPETLSKKTYSPLALEGPLLIITFFVRRVKGTGFEIMVYELSS EPDITEDFLSTSGFPTIADGESEASFDVHLLPDEVPEIEEDYVQLVSVGGAE ELDEKESITWFSVYANDDPHGVAFLYSDRQSLIGQNLIRSIQINITRLAGTF GDVAVGLRISSDHKEQPIVTENAEQRLVVKDGATYKVDVVPKIQVFLSLGSN FTLQLVTVMVGGREFYGMPTILQEAKSAVLPVSEKAANSQVGFESTAFQLMNI TAGTSHVMSRRGTYGALSVAWTTGYAPGLEIPEFIVVGNMPTLGSLSFSHG EQKGVFLWTFPSPGWPEAFVLHLSGVQSSAPGGAQLRSGFIVAEIPEMGVFO FSTSSRNIIVSEDQMIRLHVQRLFGFHSDLIKVSYQTAGSAKPLEDFEPVQ NGELFFQKFQTEVDFEITINDQLSEIEEFFYINLTSVEIRGLQKFDVNWSPR LNLDVSAVITILDNDLAGMDISFPETTAVAVDVTLLIPVETESTYLTSTSK TTTTLQPTNVVAIVTEATGVSAPKELVTLHGTTPAVSEKPDVATVTANVSIH TFSLGPSIVYIEEMKNGTFNTAEVLIRRTGGFTGNVSIIVKTFGERCAQMEP NALPFRGIYGINLTWAVEEEDFEEQTLTLIFLDGERERKVSQVILDDDEPEG QEFFYVFLTNPQGAQIVGKDDTGFAAFAMVIITGSDLHNGIIGFSEESQSG LELREGAVMRRLHLIVTRQPNRAFEDVKVFWRVTLNKTIVVVLQKDGVNLMEE QSVSGTTCTMGQTKCFISIELKPEKVPQVEVYFFVELYEATAGAAINNSARF AQIKILESDESQSLVYFVSGSRLAVAHKKATLISLQVARDSGTGLMMSVNFST QELRSAETIGRTIISPAISGKDFVITEGTLVFEPGQRSTVLDVILTPETGSLN SFPKRFQIVLDFPKGGARIDKVGTTANITLVSDADSAIINGLADQLHQPVNDD ILNRVLHTISMKVATENTDEQLSAMMHLIEKITTEGKIQAQSVASRTLFYEIL CSLINPKRKDTRGFSHFAELTENFAFSLLTNVTCGSPGEKSKTILDSCTPYLSI IALHWPQQINGHKFEGKEGDYIRIPERLLDVQDAEIMAGKSTCKLVQFTEYS SQQWFISGNNLPTLKNKVLVLSVKQSSQLLTNDNEVLRYIAAEPRIIPTSL LCLLWNQAAASWLSDSQCKVIEETADYVEACALHMSVYAVYARTDNLSYNE AFTSGFICISGLCLAVLSHFCA RYSMFAAKLLTHMMAASLGTOILFLASAY ASPQLAEESCSAMAAVTHYLCLQFSWMLIQSVNFWYVLMNDEHTERRVLLF FLLSWGLPAFVVILLIVILKGIYH QSMSQIYGLIHGDLCFIPNVYALFTAAL VPLTCLVVFVVFVTHAYQVKPQWKAYDDVFRGRTNAAEIPILILYLFALISV TLWGLHLMAYRHFVWLVLVFI NSLQLLVPSVLLFTSMRSTFFSFHTGTLTSRE KKSTFVLTCLLSPDSKGLGVLCFLNTEWAFQVH</p>



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
363	1102	2	2855	AAGATMERDGCAGGSGRGEGGRAPREGPAGNGRDRGRSHAAE APGDPQAAAALLAPMDVGEEPLEKAAARTAKDPNTYKVLVSLV LSVCVLTTILGCIFGLKPSCAKEVKSKGRCFERTFG\NCRCD AACVELG\NCCLGLPGGTCT\EP\EHIW\TCNKFRCG\EKRLT RSLCACDDCKD\RGDCLPSNLQFLCVQGE\KSWGRKNPCESH LMEP\QCP\AGFETPSLPLLIIF/SLDGFRAEYLHTWGGLLPVI SKLKKCGTYTKMNPVYPTKTTPNHYSIVTGLYPESHGIINN MYDPKMNASFSLKSKEKFNPEWYKGEPWVTAKYQGLKSGTFF WPGSDVEINGIFPDYKMYNGSVPFERILAVLQWLQPKDER PHFYTTYLEEDSSGHSYGPVSSEVIKALQRVDGMVGMMDGL KEINLHRCNLILISDHGMEQGSCKKIYLNKYLGDVKNIKVI YGPAARLRPSDVPDKYYSFNYEGIARNLSCREPNQHFYPYLKH FLPKRLHFAKSDRIEPLTFYLDPOWQLALNPSEKCYGSGFHG SDNVFSNMQALFVGYGPGFKHGIEADTFENIEVYNLMCDLLNL TPAPNNGTHGSLNHLKKNPVYTPKHPKEVHPLVQCPFTRNPRD NLGCSCNPSILPIEDFQTQFNLTVAEEKIKHETLPYGRPRVL QKENTICLLSQHFMSGYSQDILMPLWTSYTVDRNDSFSTEDF SNCLYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPPQLNKNSSG IYSEALLTINIVPMYQSFOVIWRYFHDTLRKYAERNGVNVV SGPVDFDYDG\RCDL\ENLRQKRRVHPVTQENFWIPNSTSF Y/VVLTSC\KDTSTPLHC\ENL\DTLGFPPCLHRDWINSETC \VHG\KHDSSW\VEEFVKCLHRA\RITGC*GTSGLSFYQQRK EPVSDILKLKTHLPTFSQED
364	1103	657	1	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERLPGRKASCSTA GSGSRGLPPL\SPMVSSAHNPNAEIPERRKDSTSTPNLPPS MMTRNTYVCTERPGAERPSSLNPKENSSGTPRVPPASPSSH SLAPPSGERSRLARGSTIRSTFHGGQVRDRAGGWGFFNKHA LQRAPRNAGAPSLMPGHRTVLINYGQDLKNWETCLAAPPNK HRR
365	1104	1	1313	HTLHSSPTSEAEFVSRSLSTQNYFRSLPRGTSNMITYGTNFI GGRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLA GCQTLLSPIVSCGPPG\VLLTRPVILG\MDHCG\EPSPDSW\S LRLKKQSCGSEWEDVLHLGEEAPSHLYCQLEASACYVFTEQL SRVALVGEALSVAARLKLKLLFAPVACTSLEYNIVLYCLHDT HDALNVVVQLEKQLQGLIQEPLVLHFKDSYHNLRSLIHDVPS SLWKSLLVSYQEIIPFYHIWNGTQRYLHCTFTLERVSPSTSD ACKLWVWQVEGDGQSFSINFNITKDTRFAELLALAESEAGVPAL VGPSAFKIPFLIRQKTISSLDPPCRRGADWRTLAQKLHLDLH SFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGTGPAWR LLSQCEAEC
366	1105	1	343	GSAAGQVQQQQRRHQQKVTVKYDRKELRKRLVLEEWIVEQL GQLYGCEEEEMPEVEIDIDDLFDAYSDEQRASKLQEALVDCYK PTEEFIKELLSRIRGMRKLSP\PQKKS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
367	1106	2	1398	IMLDGRVRWLTPTVISALWEAEMEDVIARMQDEKNGIPIRTVKS FLSKIPSVFSGSDIVQWLIKNTLIEDPVEALHLGLTMAAHGYF FPISDHVLTLKDDGTFYRFQTPYFWPSNCWEPENTDYAVYLCK RTMQNKARLELADYEAESLARLQRAFARKWEFI FMOAEAQAKV DKKRDKIERKILDSQERAFWDVHRPVPVGCVNTTEVDIKSSRM RNPBKTRKSVYGLQNDIRSHSPHTPTPETKPPTEDELQQIK YWQIQLDHRHLKMSKVADSLLSYTEQYLEYDPFLLPPDPSPNW LSDDTTFWEELEASKEPSQQRVKRWGFGMDEALKDPVGREQFLK FLESEFSSSENLRFWLAVEDLKKRPIKEVPSRVQEIWQEFAPG APSAINLDSKSYDKTTQNVKEPGRYTFEDAQEHYKLMKSDSY PRFIRSSAYQELLQAKK\KGKSLTSKRLTSLAQSY
368	1107	1	461	GTRDYPRIVNHLDHTYVTAPQAFMMFQYFVKVPTVYMKVDGE VLTNNTQIYVTRHEKAAVYLMGDQGLPGVFILYELSPMMVNLT IHTFFSLFLTIVGA\TIGGMFFEHFVINYLTHKWGLGFYFKNE NSLQGGHRTLYGVNFFMYWSLRGGS
369	1108	2	1522	SVWWSQRQFVVRWAGCAGPCGRAVFLAFGLGLGLIEEKQAES RRAVSACQEIQAIFTQKSKPGPDPLDTRRLQGRFLEEYLIQGS IGKGCSSAAVYEATMPTLPQNLEVTKSTGLLPGRGPGTSAPGEG QERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQELVPASRV ALAGEYGAVTYRKS KRGPQLAPHPNIIIRVLRAFTSSVPLLP ALVDYDPDVLPSRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNT PSPRLAAMMLLQLLEGVDHLVQQGIAHRDLKSDNILELDPDG CPWLVIADFGCCLADESIGLQLPFSSWYVDRGNGCLMAPEVS TARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFFYGGKAHLE SRSYQEAQLPALPESVPPDVRQLVRALLQREASKRPSARVAAN VLHLSLWGEHILALKNLKLDKMGVWLLQQSAATLLANRLTEKC CVETKMKMLFLANLECE TLCQAALLCSWRAAL
370	1109	105	1252	RPLLRLAELPDHCYRMNSSPAGTSPSPQPSRANGNINLGPSANP NAQPTDFDFLKVIGKNGYGVLLAKRKSDGAFYAVKVLQKKS LKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLD YVNGGELFFHLQRERRFLEPRARFYAAEVASAI GYLHSLNIY RDLKPENILLDCQGHVVLTD FGLCKEGVEPEDTTSTFCGTPEY LAPEVL\RKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVSQM YENILHQPLQIPGGRTVAACDLLQSL LHKDQORLGSKADFLE IKNHVFFSPINWDDLYHKRLTPPFNPNTG PADLKHDFPEFTQ EAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILD

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
371	1110	3	1608	RPQTLKGHQEKIRQQRQSILPPQGPAPIPFQHRGGDSPEAKNR VGPQVPLSEPGFRRRESQEEPRAVLAQKIEKETQIILNCALDDI EWFVARLQKAAEAFKQLNQRKKGKKKKKAPAEGLVTLRARPP \SEGEFIDCFQKIKLAINLLAKLQKHIONPSAAELVHFLFGPL DLIVNTCSGPDIAISVSCPLLSRDAVDLFRGHLVPKEMSLWES LGESWMRPRSEWPREPQVPLYVPKFHSGWEPPVDVLQEAPEWEV EGLASAPIEEVSPVSRQSIIRNSQKHSPTSEPTPPGDALPPVSS PHTHRGYQPTPAMAKYVKILYDFTARNANELSVLKDEVLEVLE DGRQWWKLRSRSGQAGYVPCNILGEARPEADAGAPFEQAGQKYW GPASPTHKLPPSPFGNKDELMQHMDENVDELIRKISNIRAQPP RHFRVERSOPVSQPLTYESGPDEVRWLEAKAFSPRIVENLGI LTGPQLFSLNKEELKKVCGEEGVRVYSQLTMQKAFLEKQQSGS ELEELMNKFFHSMNQRRGDS
372	1111	3	1046	AWHEGLVSSPAIGAYLSASYGDSLVLVATVVALLDICFILVA VPESLPEKMRPVSWGAQISWKQADPFASLKKVGKDSTVLL\IC ITVCLSYLPEAG\QYSSFF\LYLR\QVIGFG\SVKIAAFIAMV GILSIVAQTAFLSILMRSLGNKNTVLLGLGFQMLQLAWYGFSGS QAWMMWAAGTVAAMSSITFPAISALVSRNAESDQQGVAQGIIT GIRGLCNGLPALYGFIFYMFHVELTELGPKLNSNNVPLQGA V IPGPPFLFGACIVLMSFLAALFIPEYSKASGVQKHSNSSSGSL TNTPERGSDIEDIEPLLQDSSIWELSSFEEPGNQCTEL*TRQKV GFCIRHL
373	1112	1	1950	MAAGLATWLPFARAAAVGWLPLAQQLPPAPGVKASRGDEVLV VNVSGRRFETWKNTLDYPTDLLGSSEKEFFYDADSGEYFFDR DPDMFRHVLNFYRTGRHLHCPQECIQAFDEELAFYGLVPELVG DCCLEEYRDRKKENAERLAEDDEAEQAGDGPALPAGSSLRQL WRAFENPHTSTAALVFYVVTGFFIAVSVIANVETIPCRGSAR RSSREQPCGERFPQAFECMDTACVLIFTGEYLLRLFAAPSRGR FLRSVMSLIDVVAILPYYIGLLVPKNDDVSGAFVTLRVFRVFR IFKFSRHSQGLRILGYTLKSCASELGFLFLSLTMAIIIFATVM FYAEKGTNKTNFTSIPAAFWYTIIVTMTTLGYGDMVPSTIAGKI FGSICSLSGVLVIALPVPVIVSNFSRIYHQNRADKRRRAQQKV RLARIRLAKSGTTNAFLQYKQNGGLEDSSGSGEEQAVCVNRNSA FEQQHHHLHCLEKTTCHFTDELTFSEALGAVSPGGRTSRST SVSSQPVGPGSLLSSCCPRRAKRRAIRLANSTASVSRG\SMQE LDMLAGL\RRSHAP\QSRSSL\NAKPHDSLNLNCDSG\DFVAA IISIPTPANTPDESQPSSPGGGGRAGSTLRNSSLGTPCLFPE TVKISSL
374	1113	4	664	GWGKPKFDWTTGGQDTGGEPALLVGAGEGRAPRLNCPSGQIRS PGPGLDSIYDNWIRYFNRS SPVYGLVP/RSKTSARIYPTYHTA FDTFDYVDKFLDPGEEGDKGHPETRTGEAED*ALALSPCRR\F SSHQAVARTAGSVILRLSDSFFLPLKVSDYSETLRSFLQAAQQ DLGALLEQHSISLGPLVTAVEKFEAEAAALGQRISTLQKGSPLQVRML

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
375	1114	1	1147	GIRGGGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCF LLGVGCRLTPGLYHLGRTVLCIDFMVFTVRLLIHIFTVNKQLGP KIVIVSKMMKDVFFFLFFLGVWLVAVGVAEGLLRPRSDFPS ILRRVFYRPLYQIFGQIPQEDMDVALMEHSNCSSEPGFWAHP GAQAGTCVSYANWLVLVLLVIFLLVANILLVNLIIAMFSYTF GKVQGNSDLYWKAQRYRLIREFHRSRPAAPPFIVISHRLRLLR QLCRPRSPQPSSPALEHFRVYLSKEARKLLTWESVHKENFL LARARDKRESDSERLKRTSQKVDLALKQLGHIREYEQRLKYLE REVQQCSRVLGWVAEALSRSALLPPGGPPPPDLPGSKD
376	1115	3	329	LIKLCCKSAKSCENDLEMGLNSKFKKTRYQAGMRNSENLTAN NTLSKPTRY/QGELKEIKQDISSLRYLEEKSQATGELADLI QQLSEKFGKNLNKDHLRVNKGKDI
377	1116	1	2043	LPLLHAGFNRRFMENSSIIACYNELIQIEHGEVRSQFKLRACN SVFTALDHCEAIEITSDDHVIQYVNPFAFERMMGYHKGELGK ELADLPKSDKNRADLLDTINTCIKKGKEWQGVYARRKSGDSI QQHVKITPVIGQGGKIRHFVSLKKLCCTTDNNKQIHKIHRDSG DNSQTEPHSFRYKNRRKESIDVKSISSRGS DAPSLQNRYP SMARIHSMTIEAPITKVINIINAAQENSPVTVAEALDRVLEILRT TELYSPQLGTDKEDPHTSDLVGGLMTDGLRRLSGNEYVFTKNV HQSHSHLAMPITINDVPPCISQLLDNEESWDFNIFELEATHK RPLVYLGLKVFSRFGVCEFLNCSETTLRAWFQVIEANYHSSNA YHNSTHAADV LHATAFFLGKERVKGS LDQLDEVAALIAATVHD VDHPGRTNSFL/CNAGSELAVLYNDT\AV\LESHHTALAFQ\L TVKDTK\CNIFKNID/RGNHYRTLROAIIDMVLATEMTKHFEH VNKFVNSINKPMAAEIEGSDCECNPAGKNFPENQILIKRMMIK CADVANPCRPLDLCIEWAGRIS EEFYFAQTDEEKRQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFAHLPALMQHLADN YKHWKTLDDLCKSLRLPSDRLKPSHRGGLLTDKGHCESQ

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
378	1117	1	3585	<p>AFLSKVEEDDYPSEELLEDEDENAINAKRSKEKNPGNQGRQFDVN</p> <p>LQVPDRAVLGTIHPDPEIEESKQETSMILDSEKTSETAAGVNV</p> <p>TGGREPNTMVEKERPLADKKAQRPFERSDFSISIKIQTPELGE</p> <p>VFQNKDSDYLKNDNP EEHLKTSGLAGEPEGELSKEHDHENTEKY</p> <p>MGTESQGSAAEPEDDSFHWTPHTSVPEPGHSDKREDLLIISSE</p> <p>FKEQQSLQRFQKYFNVHELEALLQEMSSKLKSAQVESLPYNME</p> <p>KVLDDKVFRASESQILSIAEKMLDTRVAENRDLGMNENNI FEEA</p> <p>AVLDDIQDLIYFVRYKHSTAEETATLVMA PPLEEGLGGAMEEM</p> <p>QPLHEDNFSREKTAELNVQVPEEPHTLDQRVIGDTHASEVSQK</p> <p>PNTEKDLDPGPVTTEDTPMDAIDANKQPETA AEEPASVTPLEN</p> <p>AILLIYSFMFYLT KSLVATLPDDVQPGPDFYGLPWKPVFITAF</p> <p>LGIASF AIFLWRTVLVVKDRVYQVTEQQISEKLKTIMKENTEL</p> <p>VQKLSNYEQKIKESKKHVQETRKQNMILSDEAIKYKDKIKTLE</p> <p>KNQEILDDTAKNLRVMLESEREQNVKNQDLISENKKSEIKLKD</p> <p>VISMNASEFSEVQIALNEAKLSEEKVKSECHRVQEENARLKKK</p> <p>KEQLQQEIEDWSKLHAE LSEQIKSF EKSKQDLEVALTHKDDNI</p> <p>NALTNCITQLNLLECESESEGNKGGNDSDELANGEVGGDRNE</p> <p>KMKNQIKQMDVSRQTATISVVEEDLKLQLKL\RASVSTKC\</p> <p>NLEDQVKKLEDDRNSLQAAKAGLEDECKTLRQKVEILNELYQQ</p> <p>KEMALQKKLSQEEYERQERHRLSAADEKAVSAAEEVKTYKRR</p> <p>IEEMEDELQKTERS FKNQIATHEKKAHENWLKARAAERAIAEE</p> <p>KREAAANLRHKLLDLTQKMAMLQEEPVI VKPMPGKPNTQNPPRR</p> <p>GPLSQNGSFGSPVSGECSPLTVEPPVRPLSATLNRRDMPR</p> <p>SEFGSLDGPLPHPRWSAEASGKPSPSDPGSGTATMMNSSSRGS</p> <p>SPTRVLDEGKVNMAPKGPPFPFPGVPLMSTPMGGVPVPPPIRYGP</p> <p>PPQLCGPFGPRPLPPFPGPMRPPLGLREFAPGVPPGRRDLPL</p> <p>HPRGFLPGHAPFRPLGSLGPREFYFIPGTRLPPTHTGPPQEYPPP</p> <p>PAVRDLLPSGSRDEPPPASQSTSQDCSQALKQSP</p>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
379	1118	3	2946	MAADSEPESEVFETDFTTASEWERFISKVEEVLNDWKLGINS LGKPLEKGIFTSGTWEEKSDEISFADFKFSVTHHYLVQESTDK EGKDELLEDVVPQSMQDLLGMNDFPPRAHCLVRWYGLREFVV IAPAAHSDAVLSESKCNLLSSVSIALGNTGCQVPLFVQIHKK WRRMYVGECQGPVRTDFEMVHLRKVPNQYTHLSGLLDIFKSK IGCPLTPLPPVSIARFTYVLQDWQQYFWPQQPPDIDALVGGE VGGLEFGKLPFGACEDPISELHLATTW\PHLTEGIIVDNDVYS DLDPIQAPHWSVRVRKAENPQCLLGDFVTEFFKICRRKESTDE ILGRSAFEEEGKETADITHALSKLTEPASVPIHKLSVSNMVHT AKKKIRKHRGVEESPLNNDVLNTILLFLFPDAVSEKPLDGTTS TDNNNPPSESEDYNLYNQFKSAPSDSLTYKLALCLCMINFYHG GLKGVHLWQEFVLEMRFRWENNFLIPGLASGPPDLRCCLLHQ KLQMLNCCIERKKARDEGKKTASDVNTNIYPGDAGKAGQQLVP DNLKETDKEKGEVGSWDSWSDSEEEFFECLESDTEELKGNQGE SGKKGGPKEMANLRPEGRLYQHGLTLLHNGEPLYIPVTQEPAPMTEDLLEEQSEVLAKLGTSAEGAHLRARMQSACLLSDMESFK AANPGCSLEDFVRWYSPRDYIEEEVIDEKGNVVLKGELSARMK IPSNMWVEAWETAKPIPARQRRLFDDTREAEKVLHYLAIQKP ADLARHLLPCVIHAAVLKVKEESLENISSVKKI IKQII SHSS KVLHFPNPEDKKLEEI IHQITNVEAL IARARSLKAKFGTEKCE QEEEEKEDLERFVSCLEQPEVLVTGAGRGHAGRI IHKL FVNAQ RAAAMTPPEELKRMGSPERRQNSVSDFPFPAGREFILRTTV PRPAPYSKALPQRMYSVLTKEDFRLAGAFSSDTSFF
380	1119	2333	670	SPTRTGDRSVSLIVFLTEGKPTVGETHTLKLNNNTREAAAGQV CIFTIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGF YDEIRTPLLSDIRIDYPPSSVVQATKTLFPNYFNGSEII IAGK LVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTSR RPPGGDGEDTNHIERLWSYLTTKELLSWLQSDDEPEKERLRQ RAQALAVSYRFLTPFTSMKLRGPVPRMDGLEEAHGMSAAMGPE PVVQSVRGAGTQPGPLLKKPYQPRIKISKTSVDGDPHFVVDFF LSRLTVCFNIDGQPGDILRLVSDHRDSGVTVNGELIGAPAPPN GHKKQRTYLRITITILINKPERSYLEITPSRVILDGGDRLLVPC NQSVVVGSGLEVSANANVTVTIQGSIAFVILIHLYKKPAP FQRHHLGFYIANSEGLSSNCHGLLGQFLNQDARLTEDPAGPSQ NLTHPLLLQVGEGPEAVLTVKGHQVPVWVKQRKIYNGEEQIDC WFARNNAAKLIDGEYKDYLAHPFDTGMTLGQGMREL
381	1120	102	426	VPLESLSCHADNWKQELTKFISPDQLPVEFGGTMTDPDGNPK CLTKINYGGEVPKSYLCKQVRLQYEHTRSVGRGSSSLQVENEI LFPGCVLRCPVLQHLQPGSF

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
382	1121	3	3726	<p>PAAPEHTDPSEPRGSVSCCSLLRGLSSGWSSPLLPAVPCNPKNK  AIFTVDAKTTEILVANDKACGLLGYSQDLIGQKLTQFFLRSD  SDVVEALSEEHEADGHAADVFGTVVDIISRSGEKIPVSVWMK  RMRQERRLCVVVLEPVERVSTWVAFQSDGTVTSCDSLFAHLH  GYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSVGRAR  DGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISG  LITLLPDGTIHINGINHSFALTFLGYGKTELLGKNITFLIPGFYS  YMDLAYNSSQLPDLASCLDVGNESGCGERTLDPWQGDPAEG  GQDPRINVLGGHVPRDEIRKLMSQDIFTGTQTELIAGGQ  LLSCLSPQAPAGVDNVPEGSLPVHGEQALPKDQQTALGREEP  VAIESPGQDLLGESRSEPVDVKPFASCEDSEAPVPAEDGGSDA  GMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKQQLAGGS  LLMHCPCYGSEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWL  GVENDREELQTCCLIKEQLSQLSLAGALDVPHAEVLPTECQAVT  APVSSCDLGGRLCGGCTGSSSACYALATDLPGGLEAVEAQEV  DVNSFSWNLKELFFSDQTDQTSNCS CATSELRETPSSLAVGS  DPDVGSLQEQQSCVLDRELLLLTGTCVDLGQRRFRESVCVGH  DPTEPLEVCLVSSEHYAASDRES PGHVPSTLDAGPEDTCPSAE  EPRLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYHRDGLRL  SIQFEVRRVELQGPTPLFCCWLVDLLHSQRDSAARTRFLIAS  LPGSTHSTAELTGPSLVEVLRARPFEEPPKAVELEGLAACE  GEYSQKYSTMSPLGSGAFGFVWTAVDKEKNKEVVVKFIKKEKV  LEDWCIEDPKLGKVTLEIAILSRVEHANI IKVLDIFENQGFQ  LVMEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\QSRLV  SAVGYLRLKDIHRDIKDENVIAEDFTIKLIDFGSAAYLERG  KLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTLVTFE  ENPFCELEETVEAAIHPPYLVSKEMLSVSGLLQVPERRTTL  EKLVTDPWVTQPVNLADYTWEVFRVNKPESGVL SAASLEMGN  RSLSDVAQAQELCGGPVPGEAPNGQGLHPGDPRL LTS</p>
383	1122	177	1365	<p>PGTSAATCRFLSPPVISLSFTGLCISDLVVAVNGVWILVETFM  LKGGNFFSKHVPWSYLVFLTIYGVELFLKVAGLGPVEYLSGGW  NLFDFSVTVF AFLGLLALALNMEPFYFIVVLRPLQLRLFLK  ERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIV  FPNCCNTSTVADAYRWRNHTVGNRTVVEEGYYYLNNFDNILNS  FVTLFELTVVNNWYIIMEGVTSQTS HWSRLYFMTFYIVTMVVM  TIIVAFILEAFVFRMNYSRKNQDSEVDGGITLKEIKISKEELVA  VLELYREARGASSDVTRLLETLSQMERYQQHSMVFLGRRSRTK  SDLSLKMYYEEIQEWYEEHAREQEQRQLSSSAAPAAQPPGS  RQRSQTVT</p>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
384	1123	1	986	LAGVGTQAPPRP PGGEMAAGQNGHEEWVGSAYLFVSSLDKVV LSDAYAHPQQKVAVYRALQAALAESGGSPDVLQMLKIHRS DPQ LIVQLRF CGRQPCGRFLRAYREGALRAALQ RSLAALAQHSVP LQL\DLRAGAERLEALLADEERCLSCILAQQPDRLRDEELAEL EDALRN LKCGSGARGGDGEVASAPLQPPVPSLSEVKPPPPPP AQTF LFQGPV VNRPLSLKDQQT FARSVGLKWRKVGRSLQRGC RALRDPALDSLAYEYEREGLYEQAFQLLRRFVQAEGRRA TLQR LVEALEENELTSLAEDLLGLTDPNGGLA
385	1124	2409	399	SSKPKLKKRFS LRSVGRSVRGSVRGILQWRGTVDPPSSAGPLE TSSGPPVLGGNSNSNSGGAGTVGRGLVSDGTSPGERWTHRFE RLRLSRGGGALKD GAGMVQREELLSFMGAEEAAPDPAGVGRGG GVAGPPSGGGQPQWQKCRLLLRSEGGGGSRLEFFVPPKAS RPRLSIPCSSITDVRTTTALEMPDRENTFVVKVEGPSEYIMET VDAQHV KAWVSDIQECLSPGPCPATSPRPM TLPLAGT SFLTR ENTDSLELSCLNHSESLPSQDLLLGPSESNDRLSQGAYGGLSD RPSASISPSSASIAASHFDSMELLPELPRIPIEEGPPAGTV HPLSAPYPLDTPETATGSFLFQG\EP EGGEQDPLSGYPWFH GMLSR LKAAQLVLTGGTGS HGVFLVRQSETRRGEYVLT FNFQG KAKHLRLSLNEEGQCRVQHLWFQSI FDMLEHFRVHPIPLESGG SSDVVLVSYPSSQRQQGEQSR SAGEEVPVHPRSEAGSRLGAM RGCAREMDATPNASCTLMPFGASDC\EP TTSHPDPQPEPPSW TDPQPQGE E\EASR\APGSGGQAAAAAKERQEKEKAGG\GGV PEE\LVPV V*LV PVGELGEGHRPQAQEAQRLGPGGDAGVPP\ MVQLQQSPLGG\DGEEGGHPR\AI\NNQYSFV
386	1125	2204	1042	FRAPVGTAA RSPQV VIRR LPPGLTKEQLEEQRLPLPAHDYFEF FAADLSLYPHLYSRAYINFRNPDDILLFRDRFDGYIFLDSKDP EYKKFLETYCV EEKTSANPETLLGEMEAKTRELIARRTTPLL EYIKNRKLEKQRI REEKREERRRRELEKKRLREEEKR RRRREE RCKKKETDKQKIAEKEVRIKLLKKPEKGEEPTTEKPKERGE IDTGGGKQESCAPGAVVKARPMEGSLEEPQETSHSGSDKEHRD VERSQE QESEAQRYHVD DGRHRAHHEPERLSRRSEDEQRWGK GPGQDRGKKGSQDSGAPGEAMERLGRAQRCD DSPAPRKERLAN KDRPALQLYDPGARFRARECGGNRRICKAEGSGTGPEKREEAE
387	1126	176	800	GVWGVCVSGLLQVGSQRAQAWRAWSPMETPLTGTFLWPHIPQG LFFDDSYGFYPGQVLIGPAKIFSSVQWLSGVKPV LSTKSKFRV VVEEVQVVELKVTWITKSF CPGGTDSVSPP/PSVITQENLGRV KRLGCFDHAQR/HAWGALSVCLPSQGRASQDCLGMSRKKLRPG GGLYGQEGEAPVEEAGCADHVMLPRHPVFP GPFHGRPR



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
388	1127	1	2017	FRDSSPSCSAFEFHCLSGECIHSSWRCDGGPDCKDKSDEENCAV ATCRPDEFQCSGNCIHGSRQCDREYDCKDMSDEVCVNVTLCE EGPNKFKCHSGECITLDKVCNMARDCRDWSDEPIKECGTNECL DNNGGCSHVCNDLKIGYECLCPDGFQQLVAQRRCEIDECQDPD TCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAVGSIAYLFFTN RHEVRKMTLDRSEYTSILIPNLRNVVALDTEVASNRIYWSDL SQ RMICSTQLDRAHGVSSYDTVISRDIQAPDGLAVDWIHSNIYWT DSVLGTVSVADTKGVKRTKLFRENGSKPRAIVDPVHGFMWYT DWGTPAKIKKGGNGVDIYSLVTENIQWPNGITLDLLSGRLYW VDSKLHSISSIDVNGGNRKTILEDEKRLAHPFSLAVFEDKVF TDIINEAIFSANRLTGSDVNLLAENLLSPEDMVLFNHNTQPRG VNW CERTTSLNNGGCQYLCLPAPQINPHSPKFTCACPDGMLLAR DMRSCLTEG\EA AVATQETSTVRLKVSSTAVRTQHTTTRPVPD TSRLPGATPGLTTVEIVTMSHQALGDVAG\RGN\EKKPSSVRA LSIVLP IV\LLVFLCLGVFLLWKNWRLKNINSINFDPVYQKT TEDEVHICHNQDGYSYPSRQMVSLDDVA
389	1128	2299	1148	RIPGLGPPGSPPPPPHVRGMPGCPGCGMAGPRLLFLTALAL ELLGRAGGSQPALRSRGATACRLDNKESSESWGALLSGERLDT WICSLGSLMVGLSGVFPLLVIPLEMGTMRLSEAGAWRLKQLL SFALGGLLGNVFLHLLPEAWAYTCSASPGGEGQSLQQQQQLGL WVIAGILTFLALEKMFLDSKEEGTSQAPNKDPTAAAAALNGGH CLAQPAEPGLGAVVRSIKVSGYLNLLANTIDNFTHGLAVAAS FLVSKKIGLLTTMAILLHEIPHEVGDFAILLRAGFDRWSAAKL QLSTALGGLLGAGFAICTQSPKGVEETAAWLPLFTSGGFLYIA LVNVLPDLLEEDPWRSLLQQLLLL CAGIVVMVLFSLFVD
390	1129	1	523	GKVSAGQAGADRTLRRAPRFRFSQEPTGNSAYPQLRPFLDPQG RDLKPSALVPPTSRHTGRRPWLHTQPLPGPQGRWGPCT/TPA CVDRVLESEEGRREYLAFPTSKSSGQKGRKELLKGNRRIDYM LHAEGLCPDWKAEEVEFSFITQLSGLTDHLPVAMRLMVSSGE EEA
391	1130	1459	765	PCGGIRLSASEAATLFGYLVVPAGGGGTFLGGFFVNKRLRLRGS AVIKFCLFCTVVSLLGILVFSLHCPSPVPMAGVTASYGGSLLPE GHLNLTAPCNAACSCQPEHYSFVCGSDGLMYFSLCHAGCPAAT ETNVDGQKVSGAAAYRCPPLDPGKGPPCLPLVIGAIVGLPRC TETVAVSLRIFPLVLAM\HCREMHFNLSKAPPSGFHIRCNFL YIPQQHSC TNGNSTMCP
392	1131	1668	962	LLRKVGAPGGARGVIRLLDWFERPDGFLLVLERPEPA\QD\LF DFITERGALDEPLARRF\FAQVLA AVRHCHSCGVVHRDIKDN LLVDLRS GELKLIDFGSGALLKDTVYTFDFGTRVYSPPEWIRY HRYHGRSATVWSLGVLLYDMVCGDIPFEQDEEILRGRLLFRRR VSPECQQLIRWCLSLRPSEPSLDQIAAHPWMLGADGGAPESC DLRLCTLDPDDVASTTSSSESL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
393	1132	3	817	GKNSQKASPVDDDEQLSVCLSGFLDEVMMKKYGSVLPLSEKEVLG RLKDVFNEDFSNRKPFINREITNYRARHQKCNFRIFYNKHMLD MDDLATLDGQNLNDQVINMYGELIMDAVPDKVHFFNSFFHRQ LVTKGYNGVKRWTKKVDLFKKSLLLPIHLEVHWSLITVTLSN RIISFYDSQGIHFKFCVENIRKYLLTEAREKNR\NLNQGWQTA VTKCIPQQKNDSDCGFVLQYCKCLAL\KQPFQFSQEDMPVR KRIYKELCECLMD
394	1133	1252	628	PPGG*QGSAAKHR/FP/KGYRHPALEARLGRRRTVQEARALLR CRRAGISAPVFFVDYASNCLYMEEIEGSVTVRDYIQSTMETE K\TPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLE QLNIVLIDFGLSFISALPEDKGVLDLYVLEKAPLSTHPNTETVF EAFLLSYSTSSKKARPVLKKLDEVRLRGKKRSMVG
395	1134	2	1595	RACVFRPEDMMQGEAHPASLIDRTIKMRKETEARKVVLAWGL LNVSMAGMIYTEMGTGLISSYNNVTYWPLWYIELALASLFSLN ALFDFWRYFKYTVAPTSLVVSPGQQTLLGLKTAVVQTTTPPHDL AATQIPPAPPPSPSIQGGSVLSYSPSRSPSTSPKFTTSCMTGYS PQLQGLSSGGSGSYSPGVITYSPVSGYNKLASFSPSPSPYPTT VGPVLESSGLRSRYRSSPTVYNSPTDKEDYMTDLRLDTFLRSE EEKQHRVKLGSPDSTSPSSSPTFWNYSRSMGDYAQTLKKFQYQ LACRSQAPCANKDEADLSSKQAAEEVWARVAMNRQLLDHMDSW TAKFRNWINETILVPLVQEIESVSTQMRRMGCELOIGEASIT SLKQAAALVKAPLIPTLNTIVQYLDLTPNQEYLFERIKELSQQG CMSSFRWNRGGDFKGRKWDTLPTDSAIIMHVFCYLD SRLPP HPKYPDGKTFTSQHFVQTPNKPDTNENVFCTYQSAINPPHYE LIYQRHVYIPAKGQK
396	1135	16	1542	SSAVEFINRNNNSVVQVLLAAGADPNLGDDFSSVYKTAKEQGIH SLEVLITREDDFNNRLNRRASFKGCTALHYAVLADDYRTVKEL LDGGANPLQRNEMGHTPLDYAREGEVMKLLRTSEAKYQEKQRK REAEERRRFPLEQRLKEHIGQESAIATVGAAIRRKENGWYDE EHPLVFLFLGSSGIGKTELAKQTAKYMHKDAKKGFI RLDMSEF QERHEVAKFIGSPPGYVGHEEGGQLTKKLKQCPNAVVLDFEVD KAHPDVLTIMLQLFDEGRITDGKGKTIDCKDAIFIMTSNVASD EIAQHALQLRQEALEMSRNRIENLGDVQISDKITISKNFEN VIRPILKAHFRRDEFLGRINEIVYFLPFCHSEL IQLVNKELNF WAKRAKQRHNITLLWDREVADVLVDGYNVHYGARS IKHEVERR VGNQLAAAYEQDLLP\GGCTLRITVEDSDKQLLKSPELPSPQA EKRLPKLRLEIIDKDSKTRRLDIRAPLHPEKVCNTI
397	1136	1848	1602	SSCDRERHGSLGMMSGSFILCLALVTRWSPQASSVPLAVYESK TRKSYSRQDRDGGKDRSQGMGLSLLVETRKLLLSANQG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
398	1137	1497	717	HTPMA/FFL/SFLSTSET/VYTFVILPKMLINLLSVARTISFN CCALQMFFFLGFAITNCLLLGVMGYDRYAAICHPLHYPTLMSW QVCGKLAAACAIGGFLASLTVVNLVFSLPFCSTNKVNHYFCDI SAVILLACTNTDVNGFVIFICGVLVLVVPFLFICVSYFCILRT ILKIPSAEGRRKAFSTCASHLSVVIVHYGCASFIYLRPTANYV SNKDRLVTVTYTIVTPLLNPVMSLRNKDVLAIKRVLGKKGS LKLYN
399	1138	2	1185	RPPAATRYPREKLKSMTSRDNYKAGSREAA\AAAAAIAAAAA AAAAAEPYPVSGAKRKYLEDSDPERSDYEEQQEQEEEEARKVK SGIROMRLFSQDECAKIEARIDEVVSRAEKGLYNEHTVDRAPL RNKYFFGEGYTYGAQLQKRGPGQERLYPPGDVDEIPEWVHQLV IQKLVEHRVIEGFGVNSAVINDYQPGGCIVSHVDPIHIFERPI VSVSFFSDSALCFGCKFQFKPIRVSEPVLSLPVRRGSVTVLSG YAADEITHCIRPQDIKERRAVIILRKTRLDAPRLETKSLSSSV LPPSYASDRLSGNNRDPALKPKRSHRKADPDAAHRPRILEMDK EENRRSVLLPTHRRRGSFSENWYRKSYESSEDCSEAAGSPAR KVKMRRH
400	1139	60	1699	VTWHFYFCDHKNHGYIIPQMAADRSRQKCMSQSLDLSLAKAA KKKLQALSNRLFEELAMDVYDEVDRRENDVWLATQNHSTLVT ERSAVPFLPVNPEYSATRNQGRQKLARFNAREFATLIIDILSE AKRRQQGKSLSSPTDNLELSLRSQSDLDQHDYDSVASDETD QEPLRSTGATRSNRARSMDSSDLSDGAVT\LQEYLELKKALAT SEAKVQQLMKVNSSLSDEL\RRLQREHFAP\IHKLQAE NLQ RQPPGPVPTPPLPSERAHTPMAPGGSTHRRDRQAFSMEPGS ALKPFGGPPGDELTTTLQPFHSTELEDDAIYSVHVPAGLYRIR KGVASAVPFTPSSPLLSCSQEGSRHTSKLSRHGSGADSDYEN TQSGDPLLGLEGKRFLELGKEEDFHPELES LDGDLDPGLPSTE DVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIH LAVTEMA SLFPKRPALPEVRSSLRLNLNASAYRLQSECRKTVPPEPGAPVD FQLLTQQVIQCAVDIAKAAKQLVTITTTREKKQ

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
401	1140	1	1863	RYLSYGS GPKRFPLVDVLQYALEFASSKPVCTSPVDDIDASSP PSGSIPSQTL PSTTEQQGALSSSELPSTSPSSVAAISSRSVIHK PFTQSRIPDLPMPAPRHITTEELSVLESCLHRWRTEIENDT RDLQESISRIRHTIELMYSKSMIQVPYRLHAVLVHEGQANAG HYWAYIFDHRESRWMKYNDIAVTKSSWEELVRDSFGGYRNASA YCLMYINDKAQFLIQEEFN/K/ETGQPLVG IETLPPDLRDFVE EDNQRFKEKELEEWDAQLAQKALQEKLLASQKLRETSVTTAQ AAGDPKYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETV LQSAIKLEYARLVKLAQEDTPPETDYRLHHVVVFYFIONQAPKK IIEKTLLEQFGDRNLSFDERCHNIMKVAQAKLEMIPKEEVNLE EYEEWHQDYRKFRETTMYLIIGLENFQRESYIDSLLFLICAYQ NNKELLSKGLYRGHDEELISHYRRECLLKLNEQAELFESGED REVNNGLIIMNEFIVPFLPLLLVDEMEEKDILAVEDMNRNWC YLGQEMEPHLQEKLTDFLPKLLDCSMEIKSFHEPPKLPSTH ELCERFARIMLSLSRTPADGR
402	1141	1	465	AQVYVRMDSFDEDLARPSGLLAQERKLCRDLVHSNKKEQEFRS IFQHIQSAQSQRSPSELFAQH\VPVHVHVKHEHFGSSGMTLH ERFT\KYLKRG\TEQEAANKKSPEIHRRIDISPSTRKHGLA HDEMKS PREPGYKDGHN SKNELQRVNFY
403	1142	2	369	TYTFCFSLMI\ILLTTIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTPVPHGFETHTLQEHNLANYLFFMYLINKDET EHTGQESYVWVKMYQERCWEFFPAGDCFRKQYEDQLN
404	1143	3115	557	FRRKGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWFSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLSKSFVVTSVVAFPTDSKTVQRTQDNCSFGLH ARGVELMRFTTPGFDPSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYPGHPNIDCTWNIEVPNNQHVKVRKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTNSNKNITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCS CDAGHQFTCKNFKCKPLFWVCDLND GDNSDEQGCSCP\AQTFRC SNGKCLSKSQCCNGKDDCGDGSDE ASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCS DGSDE KDCDCGLRSFTRQARVVGTTDADEGEWPQVSLHALGQGHICG ASLISPWLVSAAHCYIDDRGFRYS DPTQWTAFLGLHDQSQRS APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR PICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVI NQTTCE NLLPQQITPRMCMVGLSGGVDSCQGD SGGPLSSVEA DGRIFQAGVVSWGDGCAQRNKP GVTYRLPLFRDWIKENTGV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
405	1144	1	424	RHEEDLGNLWENTRFTDCSFFVRGQEFKAHKSVLAARSPVFNA MFEHEMEESKKNRVEINDLDPEVFKEMMRFIYTGAPNLDKMA DNLLAAADKYALERLKVMEKALCSNLSVENVADTLVLADLHS \AEQLKAQAIDFINRCSVLRLGCKDGKNWNSNQATDIMETSG GKSMIQSHPHLVAEAFRALASAQGPQFGIPRKRLQS*NLGNL WENTRFTDCSFFVRGQEFKAHKSVLAARSPVFNAMFEHEMEES KKNRVEINDLDPEVFKEMMRFIYTGAPNLDKMA DNLLAAADK YALERLKVMEKALCSNLSVENVADTLVLADLHSGRTVESTSH RLY
406	1145	1	1021	QRGGIPGKFQEDSGSVDWALGPFWGIFQADFGCMRFYLSAQTS DPVLRM*WGSPISHPSTSLCPGGGAGQTTGSLCLGQQCCPLS CPNIPSRHKRWRL*AALVAGSRGSC TLR*RTPLPVTRNLP R/CHLHLHPTGDLRVHVHQLHGHVPPGAALLQCGGCDLRG EAAGLLFLGHACLRGSVNLRRDQWLPV\PYSRLCFSGAREGHL PSLLAMIHVRHCTPIPALLC\PIKVNLLIPVAYLVFWAFLLV FSFISEHMCVGVVIIILTGVP IFFLGVFWRSKPKCVHRLTES MTHWQELCFVVYPQDAPEEEENGPCPPSLLPATDKPSKPKQ
407	1146	2	1280	AAALVAEYLALLEDRHRLPVGCVSFQNISSNVLEESATISDDIL SPDEEGFCSGKHFTLGLVGLLEQAAGYFTMGGLYEAVNEVYK NLIPILEAHRDYKKLAHVHGLQEAFTKIMHQSSGWERVFGTY FRVGFYGAHFGLDEQEFVYKEPSITKLAEISHRLEEFYTERF GDDVVEI IKDSNPVDKSKLDSQKAYIQITYVEPYFDTYELKDR VTYFDRNYGLRTFLFCTPFTPDGRAHGELEQHKRKTLLSTDH AFPIKTRIRVCHREETVLTP\VEVAIEDMQKKTRELAFAEQ DPPDAKMLQMVLGSGVPTVNOGPLEVAQVFLAEIPEDPKLFR HHNKLRLCFKDF\*KKCEDALRKKNKALIGPDQKEYHRELERNY CRLREALQPLLTQRLPQLMAPTPPGLRNSLNRASFRKADL
408	1147	55	651	GEGQQWQSTPLSPLOPTVADFLNLAWWTSAAAW*VLSGRWVEK VLPGREGSEEK*GMASSADHLHSAPRALQ\SLFQQLLYGLIY HSWFQAGR*GFGGASSSPGPQSELRRHLHGEQGVYD*GRPETLP GSVGGAEALWALADPAEAGSPETRESSVMKQTQYYFGSVNA SYNAIIDCGNCSRCWQWGGRGQGRNL
409	1148	1855	904	VAGIPACFDN/FTEALAEATACRMGYSSKPTFRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSLHCLACGESLKTPRV VGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFR KHTDVFNWKVRAGSDKLGSPSLAVAKIIIEFNPMYPKDNDI ALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWFTKQ NGGKMSDILLQASVQVIDSTRCNADDAQGEVTEKMMACAGIPE GGVDTQGDGSGPLMYQSDQWHVVGIVSWGCGGPGSTPGVYT KVSAYLNWIYNVWKAEL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
410	1149	3	964	TISTVRWNSRIGMVLGVAIQKRAV\PGLY\AFEEAYARADKEA PRPCHKGSWCSSNQLCRECQAFMAHTMPKLFKAFMS SAYNAYR AVYAVAHGLHQLLGCASGACSRGRVYPWQLLEQIHKVHFLHKK DTVAFNDNRDPLSSYNIIAWDWNPGPKWTFTVLGSSTWSPVQLN INETKIQWHGKDNQVPKSVCSDDCLEGHQRVVTGFHHCCEFCV PCGAGTFLNKS/SYLGKDLPENYNEAKCVTFSLFNFSWIAF FTTASVYDGKYLPAANMMAGLSSLSGFGGYFLPKCYVILCRP DLNSTEHFQASIQDYTRRCGST
411	1150	2	1378	VARGAFHPKMGSPFSPKPGSERLSFVSAKQSTGQDTEAELQD ATLAHLGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQ AEAQKVTFSDPTTVALCISKEGRPPARISWLSSLDWEAKETQ VSGTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEPAI PVTLSVRYPPEVSISGYDDNWYLGRTDNLCDVRSNPEPTGY DWSTTSGTFTPSAVAQGSQVLVIHAVDSLNTTFVCTVTNAVGM GRAEQVIFVRETPTNTAGAGATGGIIGGIIAIIATADA\TGIL ICROQRKEQTLQGAEEDEDELEGGPPSYKPPTPKAKLEAQEMPSQ LFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGP LHPGATSLGSPIPVPPGPPAVEDVSLDLEDEEGEEEEYYLDKI NPIYDALSYSSPSDSYQGGKGFVMSRAMYV
412	1151	1	1828	GTRLREDKNHNMVAGCTEVEVKSTEEAFVFWRGQKKRRIAN THLNRESSRSHSVFNILVQAPLDADGDNVLQEKEQITISQLS LVDLAGSERTNRTAEGRNRLREAGNINQSLMTLRTCMDVLREN QMYGTNKMVPYRDSKLTFLFKNYFDGEGKVRMIVCVNPKAEDY EENLQVMRFAEVTQEEVEVARPVDKAI CGLTPGRRYRNQPRGP\ IGNEPLVTDVVLQSFPLPSC EILDINDEQTLPRLI EALEKRH NLRQMMIDEFNKQSNFAKALLQEFDNAVL SKENHMQGLNEKE KMISGQKLEIERLEKKNKTLEYKIEILEKTTTIIYEDKRNLOQ ELETQNKQLQRQFSDKRRLEARLQGMVTETTMKWEKERRVA AKQLEMQNKLWVKDEKLKQLKAI VTEPKTEKPERPSRERDREK VTQRSVSPSPVPLLFPDQNAPIRLRHRRRSRSAGDRWVDHKP ASNMQTETVMQPHVPHAITVSVANEKALAKCEKYM LTHQELAS DGEIETKLIKGDYKTRGGGQSVQFTDIETLKQESPNGSRKRR SSTVAPAQPDGAESEWTDVETRCVAVEMRAGSQLGPGYQHHA QPKRKKP
413	1152	1	336	PFSSSSVSSKGSDFPGTLDPPFGSGSFNSAEGFADFSQMS/KGK STPVSQLGSADFPEAPDPFQPLGADSGDPFQSKKGFDPFSGK DPFVPSA AKPSKASASGFADFTSVS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
414	1153	1	1334	MSLMVVSMAVCGLFLVQRAGPHMGGQDKPFLSAWPSAVVPRGG HVTLRCHYRHRFNNFMYLKEDRIHIPFIHGRIFQESFNMSPV TAHAGNYTCRGSHPHSPTGWSAPSNPVVIMVTGNHRKPSLLAH PGPLVKSGERVILQCWSDIMFEHFFLHKEGISKDPSRLVQGIH DGVSKANFSIGPMQDLAGTYRCYGSVTHSPYQLSAPSDPLDI VITGLYEKPSLSAQPGPTVLAGEVTLSCSSRSSYDMYHLSRE GEAHERRFSAGPKVNGTFQADFPLGPATHGGTYRCFGSFRDSP YEWSNSDPLLVSVTGNPSNSWSPSPTEPSSETGNPRHLHVLI TSVVIILFILLFLHHRWCN\KKNAAVMDQESAGNRTANSE DSDEQDPQEVYTYQLNHCVFTRQKITRPSQRPKTPPTDIIVYT ELPNAESRSKVVSCP
415	1154	1	1570	MSLRVHTLPTLLGAVVRPGCRELLCLLMITVTVPGASGVCPT ACICATDIVSCTNKNLSKVPGNLFRILIKRLDLSYNRIGLLDSE WIPVSFAKLNTLILRHNNITSISTGSFSTTPNLKCLDLSSNKL KT\VKNAVQELKVLEVLNLYNNHISYLDPSAFGGLSQLQKLY LSGNFLTQFPMDLYVGRFKLAELMFLDVSYNRIPSPMPHHINL VPGKQLRGIYLGHPFVCD\CSLVSLLVFYRRHFSSVMDFKN DYTCRLWSDSRHSRQVLLQLQDSFMNCSDSIINGSFRALGFIE AQVGERLMVHCDSTGNANTDFIIVGPDNRLLEPDKEMENFYV FHNGSLVIESPRFEDAGVYSCIAMNKQRLNETVDVTINVSF TVSRSHAHEAFNTAFTTLAACVASIVLVLLYLYLTPCPCKCKT KRQKNMLHQSNHSSILSPGPASDASADERKAGAGKRVVFLEP LKDTAAGQNGKVRFLPSEAVIAEGILKSTRKSDSDSVNSVFS DTPFVAST
416	1155	2	1928	ASDFIRSLDHCYLSLEGVFSHKFDFELQDVSSVNEVDLLTTG LLCKYTAQRFKPKYKFFHKSFOEYTAGRRLSSLLTSHEPEEVT KNGYGLQKMSISDITSTYSSLLRYTCGSSVEATRAVMKHLAA VYQHGCILLGLSIAKRPLWRQESLQSVKNTTEQEILKAININSF VECGIHLQESTSKSALSQEFEAFFQGSLYINSGNIPDYLF FFEHLNPNCASALDFIKLGFYGGAMASWEKAAEDTGGIHMEAP ETYIPSRVSLFFNWKQEFRTLEVTLRDFSKLNKQDIRYLGI FSSATSRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTI EDERHITSVTNLKTLSDHDLQNRPLPGGLTDSLGNLKNLTCLI MDNIKMNEDAIKLAEGGLKNLKKMCLFHLTHLSDIGEGMDYIV KSLSEPCDLEEIQLVSCCLSANAVKILAQNHLNVLKSLIDL SENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLS LLKHLEEVQVLVGLGNWRLTDTEIRILGAFFGKNPLKNFQQ LNLAGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEFLPDPA LVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFKLVT
417	1156	342	718	ASDRKVAMTCDCFWFRMTLDQHASCEVGTERTERQAG\GLVMF DPSGFPTGEKVLQDDEFTCDLFRFLQLLCEGHNSGL*VPGTSD DTKA*IMFSSQ*QEPVSSNYASF*QQIILEHGSALGSG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
418	1157	1	135	EITHIVGETAAFLCPRLRLRRGGKDGSPKPGFLASVIPVDRRP GE*DITHIVGETAAFLCPRLRLRRGGKDGSPKPGFLASVIPVD RRPGE
419	1158	173	943	SKFIFYVDSQSMIFFFQTPTRHKVLIMEFCPCGSLYTVLEEPS NAYGLPESEFLIVLRDVGGMNHLRENGIVHRDIKPGNIMRVI GEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYLHPDMYERA VLRKDHQ\KKYGAT\VDLW\SIGVTIFYQGKPTGS\LAI*HPFE GASVRNKASDGIKIITGKLLGAIS\GVQSKKNG\PI\DWEW EDMPVSCSPSSGVLRVPNLPPVLA\NILESRSRKKCWGF*PSF LQEN
420	1159	987	500	GSTISCERSLRSLWTAHWALPEMDSRIPYDDYPVVFLPAYENP PAWIPPHERVHHPDYNNELTQFLPRTITLKKPPGAQLGFNIRG GKASQLGIFISKVIPDSDAHRAGLQEGDQVLAVNDVDFQDIEH SKAVEILKTAREISMRVRFFPYNYHRQKERTVH
421	1160	3	890	HEQVSALHRRRIKAIVEVAAMCGVNIICFQEAWTMPFAFCTREK LPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILERDSEHGD VLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYMEGNLGH PVFQTQFGRIAVNICYGRHPLNWLMYSSINGAEIIFNPSATIG ALSESLWPTEARNAAIANHCFTCAINRVGTEHFPNEFTSGDGK KAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDLNL CQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
422	1161	5214	352	MAKSGGCGAGAGVGGGNGALTWVNNAAKKEESETANKNDSSKK LSVERVYQKKTQLEHILLRPDITYIGSVEPLTQFMWYDEDVGM NCREVTFVPGLYKIFDEILVNAADNKQORDKNTCIKVSIDPES NIISIWNNKGKIPVVEHKVEKVYPALIFGQLLTSSNYDDDEK KVTGGRNGYGAKLCNIFSTKFTVETACKKEYKHSFKQTWMNNMM KTSEAKIKHFDGEDYTCTTFQPDLSKFKMEKLDKDIVALMTRR AYDLAGSCRGVKVMFNGKKLPVNGFRSYVDLYVKDKLDETGVA LKVIHELNERWDVCLTLSEKGFQQISFVNSIATTKGGRHVDY VVDQVVGKLEIVVKKKNKAGVSVKPFQVKNHIWVFINCLINP TFDSQTKENMTLQPKSFGSKCQLSEKFFKAASNCGIVESILNW VKFKAQTQLNKKCSSVKYSKIKGIPKLDDANDAGGKHSLECTL ILTEGDSAKSLAVSGLGVIGRDYGVFPLRGKILNVREASHKQ IMENAEINNIKIVGLQYKKSYYDAQSLKTLRYGKIMIMTDQD QDGSNIKGLLINFIIHNWPSLLKHGFLEEFITPIVKASKNKQE LSFYSIPEFDEWKKHIENQKAWKIKYYKGLGTSTAKEKEYFA DMERHRILFRYAGPEDDAITLAFSKKKIDDRKEWLTNFMEDR RQRLHGLPEQFLYGTATKHLTYNDFINKELILFNSNDNERSI PSLVDGFKPGQRKVLFTCFKRNDKREVKVAQLAGSVAEMSAYH HGEQALMMTIVNLAQNFGVGSNNINLLQPIGQFGRHLHGKDA SPRYIFTMLSTLARLLFPAVDDNLLKFLYDDNQVRPEWYIPI IPMVLINGAEGIGTGWACKLPNYDAREIVNNVRMLDGLDPHP MLPNYKNFKGTIQELGQNQYAVSGEIVVDRNTVEITELPVRT WTQVYKEQVLEPMLNGTDKTPALISDYKEYHTDITVKFVVKMT EEKLAQAEAAAGLHKVFKLQTTLTCSNMVLFDHMGCLKKYETVQ DILKEFFDLRLSYGLRKEWLVGMLGAFTKLNNQARFILEKI QGKITI*NRSKKDLIQMLVQRGYESDPVKAWKEAQEAAEED TONQHDDSSSDSGTPSGPDFNYILNMSLWSLTKEKVEELIKQR DAKGREVNDLKRKSPSDLWKEDLAAFVEELDKVESQEREDVLA GMSGKAIKGVKPKVKKLQLEETMPSPYGRIIPEITAMKAD ASKKLLKKKKGDLDTAAVKVEFDEEFSGAPVEGAGEEALTPSV PINKGPKPKREKKEPGTRVRKTPTSSGKPSAKKVKKRNPWSDD ESKSESLEETEPVVI PRDSSLRRAAAERP KYTFDFSEEDDD ADDDDDNDNDLEELKVKASPI TNDGEDEFVPSDGLDKDEYTF PGKSKATPEKSLHDKKSQDFGNLFSFPSYSQKSEDDSAKFDSN EEDSASVFSPSFGLKQTDKVPSTVAACKGKPSSTVPKPKRA PKQKKVVEAVNSDSDSEFGIPKKTTPKKGKGRGAKKRKASGSE NEGDPYNGRKTSTTSKKPKKTSFDQSDVDIFPSDFPTEPPS LPRTGRARKEVKYFAESDEEDDDVDFAMFN 423 1162 1 219 KGCLAASFNCIFLYTGELYPTMIR*VEA*WENDSLFLGKDILL CTGQTPELNQVHPSPKAPPNTHHCKAHSSH

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
424	1163	1454	446	ENSFECKDCGKAFSRGYQLSHHQKIHTGEKPYECKECKKAFRWGNQLTQHQQKIHTGEKPYECKDCGKAFRWGSSLVIHKRIHTGEKPYECKDCGKAFRRGDELTHQHFHTGEKDYECKDCGKTFSRVYKLIQHKRIHSGEKPYECKDCGKAFCGSSLIQHKRIHTGEKPYEQECGKAFTRVNYLTQHQQKIHTGEKPHECKECKGAFRWGSSLVKHERIHTGEKPYKCTECGKAFNCGYHLTQHERIHTGETPYKCKECGKAFIYGSSLVKHERIHTGVKPYGCTECGKSFSHGHQLTQHOKTHSGAKSYECKECKGACNHLNHLREHQRHNS
425	1164	826	407	HQYLDLPLHVMITILLKSHFFTMLKRPVGGSSSFASLPFYHQSILLRKNQMKRKKTQQDLTHINWTLQAVSIQTCIWLQKKPSSYFHQLPNQVL*PENSGPESCLYDLAAVVVHHGSG
426	1165	464	29	XLDPDTLPVATLLMDVMFYSGVVKDPMATGDDCGHIRFFSFSLIEGYISLVMVDVQTQRRFPSNLLFTSASGELWKMVRIGGQPLGFGPVWESGPTGPTSPLILPVTSSSHRQAASQVTTTKQGQWLC LKRPSARSPDHATCLG*
427	1166	649	901	EAPLTSVCFSLERRFGSSSNTTSFGTLASQNAPTFGSLSQQTSGFGTQSSGFGSGFGSGTGGSFGSNNNS*VSPFLSLTLIKSIK
428	1167	3	340	EEPQGSPIWVWLAGSLTSVSCFLPFQRMRIKPHQGQYIGEMSF LQHHKGECRPQKD*ARQENPCGPCSERRKHLLGQDPKTCCKSC KNTDSRCKARPLELNERTCRCDKPRR
429	1168	355	1312	TLWAGPGLCPQSHSSSSVPAPWEPHVERALRTDRNQQRPLLS ASWAPAPARPLFLTSPVLLPKSRAIPAARDPS*AGIFCLLEMA GGQASVVIIGSAGVLGCRWGSSGKSHSLSPSRKGNLHLLSQEP QTTVVHNATDGIKGSTESCNTTTTEDEDLKVRKQEI IKITEQLI EAINNGDFEAYTKICDPGLTSFEPEALGNLVEGMDFKFYFEN REWVRAADILLPAPLPLCLCLLLTFSSQLPTFPLFDLRAALLL CMLVPLCPDGCRCQAPLKALLLSSKCHSFCSCFVAVPVTTIKLT YFLPGA VAYACNPNTLGG
430	1169	439	728	ERAGAGGAAACRAGTRSGATSRTPWPLHRQLSMMLMLAQSNPQ LFALMGTRAGIARELERVEQQSRLEQLSAAELQSRNQHWADW LQAYRARLGQ
431	1170	3	440	NGTLFIMVMHIKDLVSDYKE*WL*RKPLPW*EALLLRDCFFF* VTENGADPNPYVKTYLLPDNHKTSKRKTKISRKTRNPTFNEML VYSGYSKETLRQRELQLSVLSAESLRENFFLGGVTLPLKDFNL SKETVKWYQLTAATYL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
432	1171	433	1824	LHRIMQLAVVVSQVLENGSSVLVCLLEGGWDITAQVTSVLQQLS DPFYRTLLEGFQMLVEKEWLSFGHKFSQRS\$TLNLCQSGFAPV FLQFLDCVHQVHNQYPTEFEFNLYLKFLAFHYVSNRKFITLL DSDYERLEHGTFLFDDKGEKHAKKGVCIWECIDRMHKRSPIFFN YLYSPLEIEALKPNVNVSSLKKWDYIETLSTGSPSYDWMMLT PKHFPSEDSDLAGEAGPRSQRRTVWPCYDDVSCTQPDALTSIF SEIEKLEHKLNQAPEKWQQLWERVTVDLKEPRTDRSQRHLSR SPGIVSTNLPSYQKRSLHLDPSSMGEEQNSSISPSNGVERR ATLYSQYTSKNDENRSFEGTLYKRGALLKGWKPRWFVLDVTKH QLRYDSDGEDTSCKGHIDLAEMVIPA GPSMGAPKHTSDKAF FDLKTSKRVYNFCAQDQSAQQWMDKIQSCISDA
433	1172	1714	946	EVEGPRRVSAPETLGMEE\$SVRPSVFVVDGQTDIPFTRLGRS HRRQSCSVARVGLGLLLLLMGAGLAVQGWFLQLHWRLGEMVT RLPDGPAGSWEQLIQERRSHEVNPAHLTGANS\$LTGSGGPLL WETQLGLAFLRGLSYHDGALVVTKAGYYYIYSKVQLGGVGCPL GLASTITHGLYKRTPRYPEELELLVSQQSPCGRATSSSRVWWD SSFLGGVVHLEAGEEVVRVLDERLVRLRDGTRSYFGAFMV
434	1173	16	367	QSAELGPRRREGSR\$RPSCTKASKPWRRRPGGPT\$GLG*GPLSP GPYQCRPSLPAQLYPQSLMAAATLRTP\$TQVSAASSRPHTPSPT HVLKPSVRGACSSPRCPG\$GTLRR\$WVGPF\$
435	1174	27	1139	LWWPPLSRHAAHRQWPGPTAPRGLGHKVKGRGASPAAMW\$CSW FNGTGLVEELPACQDLQLGLSLLSLLGLVVGVPVGLCYNALLV LANLH\$KASMTMPDVYFVNMAVAGLVLSALAPVHLLGPPSSRW ALWSVGGEVHVALQIPFN\$SSLVAMYSTALLSLDHYIERALPR TYMASVYNTRHVC\$FVWGGALLTSF\$SLLFYICSHV\$TRALEC AKMQNAEAADATLVF\$IGYVVPALATLYALVLLSRVREDTPLD RDTGRLEPSAHRLLVATVCTQFGLWTPHYLILLGHTV\$ISR\$GK PVD\$HYLGLLHFVKDFSKLLAF\$SS\$FVTPLLYR\$MNQ\$F\$PSKL QRLMKKLPCGDRH\$CSPDHMGVQQVLA
436	1175	322	756	SESEFTLMP\$SLPTTNCVH\$SLQMIPL\$SPAPNQELVLGLCYMS YLAFLYMTDFCCLYF\$STVYAP\$FKYICVHTDTHICVCVCIYL SSV\$KSSAEADGVLP\$RRHPASLLIVFATSISE\$SLLIFS\$Q KTEAKLIVFAVSLAAK
437	1176	2	153	FFFLRQSLT\$SPRLECSGATSASPSAGITGMSH\$SQPIVNFLR ACIPISK
438	1177	1	692	RQHAEEGR\$RNP\$KTGLTLERVGP\$ESSPYLLRRHQ\$RQGE\$EHY HSCVQLAPTRGLEES/GHG\$PL/\$SLAGGPRVGGV/AAAATEAPR MEWKVKVRS\$D\$TRYVAKRPVRDRL\$KARALKIREERSGMTTDD DAVSEMKMG\$RYSKEERKQHLIRAREQRK\$REFMMQ\$SRLECLR EQONGDSKPELNI\$IALSHR\$KTMKKR\$NKKILDN\$WITTIQ\$EMLAHG ARSADGKRVYNPLLSVTTV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
439	1178	2	616	SDRGCSAAAGRNMNTAVGVQAQRPLGQRQPRRSFFESFIRTLII TCVALAVVLSSVSI CDGHWLLAEDRLFGLWHFCTTTNQSVPIC FRDLGQAHVPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLC EDKHSQCKWVMGSILLVSVFLSSGGLLGFVILLRNQVTLIGF TLMFWCEFTASFLFLNAISGLHINSITHPWE
440	1179	2	540	QILPNLYLGSARDSANLESLAKLGIRYILNVTNPNPFEEKNG DFHYKQPIPSDHWSONLSRFFPEAIEFIDEALSQNCVGVHCL AGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNF GQLLDFERSLRLEERHSQEQSGGQASAAASNPPSFFTTPTSDG AFELAPT
441	1180	940	463	RKSLHENKLRLEQKVEVLEAKKEELETENQVLNRQNVPFEDY TRLQKRLKDIQRRHNEFRSLILVPMNPPTASINPVSFQSSAMG SKHGTTISSYAGGTTSGKTLSTSQKTRRTGNNTKKTRGTWI FRMMFLENRQIKRGEVGDVSKLDILTCCI
442	1181	1	986	GRPGAGASELFPSTTDLSSVKQNACLTCVDFVTVHVCMGFWG IGPGALSTSCIPYPLSHGPGSVKAEMLMYSQKDPILLCVRLA VLLAVTLTVPVVLPFIRRALQQLLFPKAFSWPRHVAIALILL VLVNVLVICVPTIRDFGVIGSTSAFSLIFILPSIFYLRIVPS EVEPFLSWPKIQALCFGVLGVLFMAVSLGFMFANWATGQSRMS GH*SGPAGPGPCAHAHGGVRAAP*GPSCPTCGGWFP*TWLSE AGDSRGCRLAHFPPPGQCQAWIMALIPTPTWEEEEEEEEEEEE EEEEEEEEEEARSWSLCPAQSSLPPPG
443	1182	460	27	INELRYHLEESRDKNVLLCLEERDWDPLAIDNLMQSNQSK KTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIFILLEPV LQHSQYLRRLRQRI CKSSILQWPDNPKAEGLFWQTLRNVLN DSRYNNMYVDSIKQY
444	1183	1682	230	DDPIKTSWTPPRYVLSMSEERHERVRKKYHILVEGDGIPPIK SFKEMKFPAAILRGLKKKGIIHPTPIQIQIPIILSGRDMIGI AFTGSGKTLVFTLPVIMFCLEQEKRLPFSKREGPYGLICPSR ELARQTHGILEYYCRLLQEDSSPLLRCALCIGGMSVKEQMETI RHGVHMMVATPGRIMDLLQKKMVSLDICRYALDEADRMIDMG FEGDIRTIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPVTI NVGRAGAASLDVIQEVEYVKEEAKMVYLLECLQKTPPVLI FAEKKADVDAIHEYLLKGVAVAIHGGKDQEERTKAIEAFREGK KDVLVATDVASKGLDFPAIQHVINYDMPEEIEYVHRIGRTGR SGNTGIATTFINKACDESVMIDLKALLLEAKQKVPVQLVHLC GDESMLDIGGERGCAFCGGLGHRITDCPKLEAMQTKQVSNIGR KDYLAHSSMDF
445	1184	1	375	IETTPQSEDNANSQDNMQPETSSQQQLLSPTLSDRGGSQD AADAGKPQRKFGQWRLPSAPKPI SHSVSSVNLRFGRRTTMKSV VCKMNPMTDAASCSEVKKWWT RQLTVESDESDDLDDI
446	1185	2	223	NDRFSACYFTLKLKEAAVRQREALKLTKNATDSYISVNLRD VYARSIMELRLKGRERASTRSSGGDDFWF

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
447	1186	2	1031	FTVFILGITIRPLVEFLDVKRSNKKQQA VSEEIYCR LFDHVKT GIEDVCGHWGHNFWRDKFKKFD DKYLRLKLLIRENQPKSSIVSL YKLEIKHAIEMAETGMISTVPTFASLND CREEKIRKVTSSSET DEIRELLSRNLYQIRQRTLSYNRHSLTADT SERQAKEILIRRR HSLRESIRKDSSLNREHRASTSTSR YLSLPKNTKLPEKLQKRR TISIADGNSSSDADAGTTVLNLQPRARRFLPEQFSKKS PQSY KMEWKNEVDVDSGRDMPSTPPTPHSREKGTQTSGLLQQP LLSK DQSGSEREDSLTEGIPPKPPPRLVWRASEPGSRKARFGSEKP
448	1187	3	444	HEEASGLSVWMGKQMEPLHAVPPAAILLISLLVAVFTECTSN VATTTFLFLPIFASMSRSIGLNPLYIMLPCTLSASFAMLPVAT PPNAIVFTYGH LKVADMVKTGVIMNIIGVFCVFLAVNTWGRAI FDLDHFPDWANVTHIET
449	1188	3	125	HELENNWLQHEKAPTEEGKKELLALSNNANPSLLERHCAYL
450	1189	1	188	GNI IYMYMQPGARSSQDQ GKFLTLYNIVTPLLNPLIYTLRNR EVKGALGRLLLGKRELKGE
451	1190	10	1879	PLEQRSNCRVDPRVRTHMTASDTSSLVQSHTYKKREPADV PYQ TGQLHPAIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPW DSAKKDENRMKNRYGNI IAYDHSRVRLQTIEGDTNSDYINGNY IDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLV EVGRVKCKKYWPDDEIYKDIKVTLIETELLA EYVIRTFAVEK RGVHEIREIRQFHFTGWPDHGVVYHATGLLG FVRQVKS KSPPS AGPLVVHCSAGAGRTGCFIVIDIMLDM AEREGVVDIYNCVREL RSRRVMNVQTEEQYVF IHDAIL EACLCGDTSPASQVRS LYD MNKLDPQTNSSQIKEEFRTLNMVPTL RVEDCSIALPRNHEK NRCMDILPPDRCLPFLITIDGES SNYINAALMDSYKQPSAFIV TQHPLPNTVKDFWRLVLDYHCTSVVMLNDVDP AQLCPQYWPEN GVHRHGPIQVEFVSADLEEDIISRI FRIYNAARPQDGYRMVQQ FQFLGWPMYRDTPVSKRSFLKLI RQVDKWQE EYNGGEGRTVVH CLNGGGRSGTFC AISIVCEMLRHQRTVDVFH AVKTLRNNKPNM VDLLDQYKFCYEVALEYLNSG
452	1191	603	342	PLTYNKKYTPWWGDALGWLLALSSMVCIPAWSLYRLGTLKGP FRERIRQLMCPAEDLPQRNPAGPSAPATPRTSLLRLTELESHC
453	1192	120	449	TLSESGALFSLGPPPLSLKSSSAPRPYSTLRDCLEHFAELFDL GFPNPLAERII FETHQIH FANCSLGQPTFS DPPEDVLLAMIIA PICLIPFLITLVVWRSKDSEAQA
454	1193	1838	1066	CEEREQEKKDDVDVALLPTIVEKVILPKLTVIAENMWDPFSTTQ TSRMVGITLKLINGYPSVVNAENKNTQVYLKALLLRMRRTLDD DVFMPLYPKNVLENKNSGPYLFFQRQFWSSVKLLGNFLQWYGI FSNKTQLQELS IDGLLNRYILMAFQNSEYGD DS IKKAQNVINCF PKQWFMNLKGERTISQLENFCRYLVHLADTIYRNSIGCS DVEK RNARENKQIVKLLASVRALDHAMSVASDHN VKEFKSLIEGK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
455	1194	112	1361	TPFCFLCSLVFRSRVWAEPCCLIDAAKEEYNGVIEEFLATGEKL FGPYVWGRYDLLFMPPSPFPGGMENPCLTFVTPCLLAGDRSLA DVIIEHISHSWFGNLVTNANWGEFWLNEGFMYAQRRISTILF GAAYTCLEAATGRALLRQHMDITGEENPLNKLRVKIEPGVDPD DTYNETPYEKGFCFVSYLAHLVGDQDQFDSFLKAYVHEFKFRS ILADDFLDYLEYFPELKKRVDIIPGFEFDRWLNTPGWPPYL PDLSPGDSLMPKPAEELAQLWAAEELDMKAEAVAI SPWKTYQL VYFLDKILQKSPPLPGNVKKLGDTPSISNARNAELRLRWGQI VLKNDHQEDFWKVEFLHNQKQKYTLPLYHAMMGSEVAQTL AKETFASTASQLHSNVVNYVQQIVAPKGS
456	1195	1	889	CASGSSGWRPVLWAGFTMASAELDYTIEIPDQPCWSQKNSPS PGGKEAETRQPVVILLGWGGCKDKNLAKYSAIYHKRGCI VIRY TAPWHMVFFSES LGIPSLRVLAQKLELLFDYIEIEKEPLL FHV FSNGGVMLYRYVLELLQTRRFCLRVVGTIFDSAPGDSNLVGA LRALAA ILERRAAMLRLLLLVAFALVVVLFHVL LAPITALFHT HFYDRLQDAGSRWPELYLYSRADEVVLARDIERMVEARLARRV LARSVD FVSSAHVSHLRDYPYTYTSLCVD FMR \NWVRC
457	1196	2	295	PRVRDRLPSTGVRDRKGDKPWKESGGSVEAPRMGFTHPGHLS GCQSSLASGETGTGSADPPGGPRPGLTRRAPVKDTPGRAPAD AAPAGPSSCLG
458	1197	1299	682	QGR TSCIGLYTYQRRICKYRDQYNWFFLARPTTFAT IENLKYF LLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSL LNIPEKCP EQGGM IWKI SEDKQLAVCLKYAGVFAENAEDADGK DVFN TKS VGLS I KEAMTYHPNQVVEGCCSDMAVTFNGLTPNQM HVMYGVYRLRAFG \HIFNDALVFLPPNGSDND
459	1198	779	61	HEGKPTRGRGRGGS LSTRGRGSEVPDSAHLAPTPLFSES GCCG LRSRFLTDCKMEEGNLGLIKMVHLLVLSGAWGMQMWTFVS GFLFRSLPRHTFGLVQSKLFPFYFHISMGC AFINLCILASQH AWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAMWALQT VEKERGLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHG LSSLCNLGCVLSNGLCLA \ALPWK
460	1199	517	815	KQLDKQLRADPSGSLPPLPPSPPPPLEAGGRPPEVP/PRGPSA VPSFPSVSGDWGGPVEAG/EGGQQGRGRARARPCSLPPLPPS PVCRLSGSRAPLGCDG
461	1200	1	583	RNQLSSQKSVPVVPILKSLPLWAI VVAHFSYNWTFYTLTLLP TYMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRKW NFSTLCVRRIFSLIGMIGPAVFLVAAGFIGDYS LAVAF LTIS TTLGGFCSSGFS INHLDIAPSYAGILLGITNTFATIPGMVGPV IAKSLTPDMGISLHRPGWSAVA
462	1201	25	383	GPSGTTHASAHSGHPGSPRGSLSRHPSSQLAGPGVEGEGTQK PRDYIILAILSCFCPMWPVNIVAFAYAVMSRNSLQQGDVDGAQ RLGRVAKLLSIVALVGGVLIIASCVINLGVYK
463	1202	573	372	SLFLSFPLSPFKMTLNDAMRNKARLSITGSTGENGRVMTPEFP KAVHAVPVXSPGMGMNVSVTDLS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
464	1203	2018	491	DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPPEVADGGV VDSGVYAVPPPAEREAPAEGRKLSASSTGSTRSSQSASSLEVA GPGREPLELEVAVEALARLQQGVSAATVAHLLDLAGSAGATGSW RSPSEPQEPLVQDLQAAVAQSAVHELLEFARSAGVNAHTS DRALHAKLSRQLQKMEDVHQTVAHGQALDAGRGGSGATLEDL DRLVACSRAPEDAKQLASFLHGNASLLFRRTKATAPGPEGGG TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGGWME DYDYVHLQGKEEFKTKELLEKGSITRQKSQLELQQLKQFE RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLLFY EQCEANLTTLTNAVDAAFTAVATNQPPKIFVAHSKFVILSAHK LVFIGDTLRQAKAADVRSQVTHYSNLLCDLLRGIVATTKAAA LQYPSPSAAQDMVERVKELGHSTQQFRRVLGQLAAA
465	1204	299	189	EMEEPQKSYVNTMDLERDEPLKSTGPGQISVSEFSCHCCYDILV NPPTLNCGHSCFRHCLALWWASSKKTECPECREKWEFGPKVSI LLRDAIEKLFPPDAIRLRFEDIQQNNDIVQSLAAFQKYGNDQIP LAPNTGRANQQMGGGFFSGVLTALTGVAVVLLVYHWSRESEH DLLVHKAVAKWTAEVVLWLEQLGPWASLYRERFLSERVNGRL LLTLTEEEFSKTPYTIENSSHRAILMELERVKALGVKPPQNL WEYKAVNPGRSLFLLYALKSSPRLSLLYLYFDYTDFTFLPFIH TICPLQEDSSGEDIIVTKLLDLKEPTWKQWREFLVKYSFLPYQL IAEFAWDWLEVHYWTSRFLIINAMLLSVLELFSFWRIWRSSEL K*VGFRFLRLGVAALGSVEVAGLRGVVKGERPLLYGHGAGARF PHSVLLLPVAKPLPLPLPRGLC
466	1205	2	242	EKARMIYEDYISILSPKEVSLDSRVREVINRNLDPNPHMYED AQLQIYTLMRDSSFPRFLNSQIYKSFVESTAGSSSES
467	1206	2	619	LYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAPEVL AQKPYSKAVDCWSIGVIAIYLLCGYPPFYDENDSKLFEQILKA EYEFDSPLYWDDISDAKDFIRNLMKDPNKRYTCEQAARHPWI AGDTALNKNIHESVSAQIRKNFAKSKWRQAFNATAVVRHMRKL HLGSSLDSSNASVSSSLSLASQKDCASGTFHAL
468	1207	1	352	RTRGGAVSFEDFIKGLSILLRGTQVEKLNWAFNLYDINKDGYI TKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVETFFQKMDKN KDGVVTTIDEFIESCQKDNIMRSMQLFENVI
469	1208	3	1015	PRSPPEHHTPAWHEGRSLGPIMASMADRNMKLFSGRVVPAGGEE TFENWLTQVNGVLPDWNMSEEEKLKRIMKTLRGPAEVMRVLQ ATNPNLVADFLRAMKLVFGESESSVTAHGKFFNTLQAQGEKA SLYVIRLEVQLQNAIQAGIIAEKDANRTRLQQLLLGGELSRDL RLRLKDFLRMYANEQERLPNFLELIKMVREEDWDADFIRKR PKRSESMVERAVSPVAFQGSPPPIVIGSADCNVIEIDDTLDDSD EDVILVESQDPPPLPSWGAPPLRDRARPQDEVVIDSPHNSRAQ FPSTSGSGSGYKNGPGEMRRARKRKHTIRCSYCGEE
470	1209	1543	1351	SVACTVPLRSMSPDPQDFDKEPDSSTKHSTPSNSSNPSPGPPS PNSPHRSQPLEGLEQPACDT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
471	1210	3	952	YSAVEFAERGSGGSSGDELREDDEPVKKRGRKGRGRGPPSSSD SEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQ AKPVKVERTRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKF ALKVDSFDVKRCLNALEELGTLQVTSQILQKNTDVVATLKKIR RYKANKDVMKAAEVYTRLSRVLGPKIEAVQKVNKAGMEKEK AEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGES AEDKEHEEGRDSEEGPRCGSSEDLHDSVREGPDLDPRGSDRQE RERARGDSEALDEES
472	1211	5204	2901	LAELSSLSVLRSLSHNSISHIAEGAFKGLRSLRVLDLDHNEISG TIEDTSGAFSGLDLSKLTFLGNKIKSVAKRAFSGLEGLEHLN LGGNAIRSVQFDADFVKMKNLKHSSDSFLCDCQLKWLPWWL IGRMLQAFVTATCAHPESLKGQSIFSVPPESFVCDLFPQII TQPETTMAMVGKDIRFTCSAASSSSSPMTFAWKDNEVLTNAD MENFVHVHAQDGEVMEYTTILHLRQVTFGHEGRYQCVITNHFG STYSHKARLTVNVLPSTFKTPHDITIRTTTMMARLECAATGHPN PQIAWQKDGTDFFPAARERRMHVMPDDDDVFFITDVKIDDAGVY SCTAQNSAGSISANATLTVLETPSLVVPLEDVSVGETVALQ CKATGNPPPRITWFKGDRPLSLTERHHLTPDNQLLVQNVVAE DAGRYTCEMSNTLGTERRAHSQSVLPAAGCRKDGTTVGIFTIA VVSSIVLTSVLVWCIIYQTRKKSEEYSVTNTDETVVPPDVPSY LSSQGTLSDRQETVVRTEGGPQANGHIESNGVCPRDASHFPEP DTHSVACRQPKLCAGSAYHKKPWKAMEKAEGTPGPHKMEHGGR VVCSDCNTVEVDCYSRGQAFHPQPVSRDSAQPSAPNGPEPGGSD QEHSPPHQCSRTAAGSCPECQGSLYPSNHDRLTAVKKKPMAS LDGKGDSWTLARLYHPDSTELQPASSLTSGSPERAEAYLLV SNGHLPKACDASPESTPLTGQLPGKQRVPLLLAPKS



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
473	1212	2	2466	AAAGAARRVSVRCGRSGPGPGRGAAGLSPADIALASEQGASCS VRAPERKLRMKLLWQAKMSSIQDWGEEVEEGAVYHVT LKRVQI QQAANKGARWLGVGDQLPPGHTVSQYETCKIRTIKAGTLEKL VENLLTAFGDNDFTYISIFLSTYRGFASTKEVLELLLDYRGNL TSPNCEEDGSQSSSESKMVRNAIASILRAWLDQCAEDFREPP HFPCLOKLLDYLTRMMPGSDPERRAQNLLQFQKQEVETDNGL PNTISFSLIEEEEELEGGESA EFTCFSEDLVAEQLTYMDAQLFK KVVPHHCLGCIWSRRDKKENKHLAPTIRATISQENTLT KCVVS TILGGKELKTQORAKIIEKWINIAHECRLLKNFSSLRAIVSAL QSNSIYRLKKTWAAVPRDRMLMFEELSDIFSDHNNHLTSRELL MKEGTSKFANLDSSSVKENQKRTQRRQLQKDMGVMQGTVPYLG TFLTDLTMLDTALQDYIEGGLINF EKRRREFEVIAQIKLLQSA CNSYCMTPDQKFIQWFQRQQLLTEESYALSCEIEAAADASTT SPKPWKSMVKRLNLLFLGADMITSPPTKEQPKSTASGSSGES MDSVSVSSCESNHSEAE EGYITPMDTPDEPQKKLSESSSYCSS IHMDTNFLQGMSSLINPLSSPPSCNNNPKIHKRSVSVTSITS TVLPPVYNQONEDTCIIRISVEDNNGNMYKSIMLTSQDKTPAV IQRAMLKHNLDSDPAEEYELVQVISEDKELVIPDSANVFYAMN SQVNFDFILRKKNSMEEQVKLSRSTSLTLPR TAKRG CWSNRHS KITL
474	1213	1	867	AREKMDSCIEAFGTTKQKRALNTRMRNVGNESLNRAVAKAAE TIIIDTKGVTALVSDAIHNDLQDDSLYLPPCYDDAAKPEDVYKF EDLLSPA EYEALQSPSEAFRNV TSEEILK MIEENSHCTFVIEA LKSLPSDVESRDRQARCIWFLDTLIK FRAHRVVKRKSALGPGV PHIINTKLLKHFTCLTYNNGRLRLNISDSMKAKITAYVILAL HIHDFQIDLTVLQRD LK LSEKRMMEIAKAMRLKISKRRVSVAA GSEEDHKLGTLSLPLPPAQTSDRLAKRRKIT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
475	1214	2	2621	LSLFGSRALGRSGARAMAKAKKVGARRKASGAPAGARGGPAKANSNPFEVKVNRQKFQILGRKTRHDVGLPGVSRARALRKRTQTL LKEYKERDKSNVFRDKRFGEYNSNMSPEEKMMKRFALQQRRHHEKKS IYNLNEDEELTHYGQSLADIEKHNDIVDSDSAEDRGTL SGELTAAHFGGGGGLLHKKTQQEGEEREKPKSRKELIEELIAK SKQEKRRERQAQREDALELTEKLDQDWKEIQTL LSHKTPKSENRRDKKEKPKPDAYDMMVRELGFEMKAQPSNRMKTEAELAKEEQEHLRKLEAERLRRMLGKDEDENVKKPKHMSADDLNDGFVLDKDDR RLLSYKDGKMNVEEDVQEEQSKEASDPESNEEEGDSSGGEDTE ESDSPDSHLDLESNVESEEEENEKPAKEQRQTPGKGLISGKERAGKATRDDELPTFAAPESYEELRSLLLGRSMEEQLLVVERIQKCNHPSLAEGNKAKLEKLFGLLEYVGDLDATDDPPDLTVIDKLVV HLYHLCQMFPEASDAIKFVLRDAMHEMEEMIETKGRAALPGL DVLIYLYKITGLLFPTSDFWHPVVT PALVCLSQLLT KCPILSLQ DVVKGLFVCCLFLEYVALSQRFIPELINFLGILYIATPNKAS QGSTLVHPFRALGKNSSELLVVSAREDVATWQSSLSLRWASRL RAPTSTEANHIRLSCLAVGLALLKRCVLMYGSLSFHAIMGPL RALLTDHLADCSHPQELQELCQSTLTEMESQQLCRPLTCEKS KPVPLKLFTPRLVKVLEFGRKQGSSKEEQERKRLIHKHKREFK GAVREIRKDNQFLARMQLSEIMERDAERKRKVKQLFNSLATQE GEWKALKRKKFKK
476	1215	3	961	LTKQEDCCGSIGTAWGQSKCHKCPQLQYTGVOQKPGPVRGEVGA DCPQGYKRLNSTHCQD INECAMPGVCRHGDCLNNPGSYRCVCP PGHSLGPSRTQCIADKPEEKSLCFRLVSPHQCHPLTTRLTR QLCCCSVGKAWGARCQRCPTDGTAAFKEICPAGKGYHILTSHQ TLTIQGESDFSLFLHPDGPPKQQLPESPSQAPPPEDTEEERG VT TDSVPVSEERSVQQSHPTATTTPARPYPELISRPSPTMRWF LPDLPPSRSAVEIAPTQVTETDECRLNQNICGHGECVPGPPDY SCHCNPGYRSHPPQHRVCV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F= Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
477	1216	3652	1207	MAGGHCGSFPAAGSGEIVQLNVGGTRFSTSRQTLMWIPDSF FSSLLSGRISTLRDETGAIFIDRDPAAFAPILNFLRTKELDLR GVSINVLRHEAEFYGITPLVRRLLLCEELERSSCGSVLFHGYL PPPGIPSRKINNTVRSADSRNGLNSTEGEARGNGTQPVLSGTG EETVRLGFPVDPKVLIVAGHHNWIVAAYAHFAVWYRIKESG WQQVFTSPYLDWTIERVALNAKVVGPHGDKDKMVAVASESI ILWSVQDGGSGSEIGVSLGVVPDALFFIGNQLVATSHTGKVG VWNAVTOHQVQDVVPITSYDTAGSFLLLCNNGSIYYIDMQK FPLRMKDNLLVTELYHDPNDAITALS VYLT PKTSVSGNWIE IAYGTSSGAVRVIVQHPETVGGPQLFQTFTVHRSPVTKIMLS EKHLVSVCADNNHVRTWTVTRFRGMISTQPGSTPLASFKILSL EETESHGYSYSGNDIGPFGERRDQQVFIQKVVPITNKL FVRLS STGKRICEIQAVDCTTISFTGRECEGSSRMGSRPRYLFTGH TNGSIQMWDLTTAMDVMNKSEDKDVGGPTEEBLLKLLDQCDLS TSRCATPNISPATSVVQSHLRESNSSLQLQHHDTHAEATYG SMRPYRESPLLARARTESFHSYRDFQITINLRNVERAVPENG NLGP IQAEVKGATGECNISERKSPGVEIKSLRELD SGLEVHKI AEGFSESKKRSEDENENKIEFRKKGGFEGGGFLGRKKVPYLA SSPSTDGGTDSPGTASPSPTKTTSPRHKKS DSSGQEYSL
478	1217	1	1379	RRPTRPILTDELFRKTIQLPHLKTILNGNKLETLSLVSCFAN NTPLEHLDSLQNLQHKNDENC SWPETVNMNLSYNKLSDSVF RCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDL PGC SHFSRLSVLNIEMNFILSPSLDFVQSCQEVKTLNAGRNP RCTCELKNFIQLETYSEVMVWSDSYTCEYPLNLRGTRLKDV HLHELSCNTALLIVTIVIMLVGLAVAFCC LHFDPWYLRML GQCTQTWHRVRKTTQEQLKRNVRFHAFISYSEHDSLWVKNELI PNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI FVL SPNFVQNEWCHYEFYFAHNL FHENSDHIIILILEPIPFYCIP TRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNLAT REMYELQTFTELNEESRGSTISLMRTDCL
479	1218	1	1099	PTRPPTRPPTRPLLTSPWTSTGRMWSHLNRLLEWSIFSSVTCR KAVLDCEAMKTNEFPSPCLDSKTKVVMKGQNVSMFC SHKNKSL QITYSLFRKTHLGTQDGKGEPAIFNL SITEAHESGPYKCKAQ VTSCSKYSRDFSFTIVDPVTS PVLNIMVIQTETDRHITLHCLS VNGSLPINYTF FENHVAISPASKYDREPAEFNLTKKNPGEEE EYRCEAKNRLPNYATYSHPVTMPSTGGDSCPFCLKLLLPGLLL LLVVIILILAFWVLPKYKTRKAMRNVPDRGDTAMEVGIYAN ILEKQAKEESVPEVGSRPCVSTAQDEAKHSQELQYATPVFQEV APREQEACDSYKSGYVYSELNF
480	1219	1	293	FFFFEERTGSHSVGHPRMEYSGVSMHCSLNLGSSNSPSSA SQDARTTGACQHAQLIGFFFF\ VETASPVVTHAG/LKHLVSRN PSAVTSQSARIKT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
481	1220	1	727	NREGARKIQNKWLRPSRSHRTPEVSVPERYSYGTSSSSKRTE GSCRRRRQSSSSANSQQGQWETGSPPTKRQRRSRGRPSGAKR RRRGAPAAPQQQSEPARPSSEGKVTCDIRLRVRAEYCEHGPAL EQGVASRRPQALARQLDVFQATAVLRSDLGSVVCDIKFSEL SYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLLVSV DEADYEAGRRLLLMEEEGRRPTEAS
482	1221	1	1321	APNTAELRI CRVNKNCGSVRGGDEIFLLCDKVQKDDIEVRFVL NDWEAKGIFSQADVHRQVAIVFKTPPYCKAITEPVTVMQLRR PSDQEVSESMDFRYLPDEKDTYGNKAKKQKTTLLFQKLCQDHV ETGFRHVDQDGLELLTSGDPPTLASQSAGITVNFPERPRPGLL GSIGEGRYFKKEPNLFSHDAVVREMPGTGVSSQAESYPPSPGPI SSGLSHHASMAPLPSSSWSSVAHPTPRSGNTNPLSSFSTRITLP SNSQGIPPFILRIPVGNDLNASNACIYNNADDIVGMEASSMP DLYGISDPNMLSNCSVNMMTSSDSMGETDNPRLLSMNLNPS CNSVLDPRDLRQLHQMSSSSMSAGANSNTTVFVSQSDAFEGSD FSCADNSMINESGPSNSTNPNSHGFBVQDSQYSGIGSMQNEQLS DSFPYEFFQV
483	1222	1	1311	RRLSLDLQLGLPLGRDPPQECSTFSPTDSGEEPGQLSPGVQFQ RRQNQRFRSMEDVSKRLSLPMDIRLPQEFQLQKLMESPDLPKP LSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLT ENLVALKEIRLEHEEGAPCTAIREVSLKLNKLANIVTLHDLI HTDRSLTLVFEYLDSDLKQYLDHCGNLMMSMHNKIFMFQLLRG LAYCHHRKILHRDLKPQNLLINERGELKLADFGLARAKSVPTK TYSNEVVTWYRPPDVLLGSTYESTPIDMWGVGCIHYEMATGR PLFPGSTVKEELHKINRLLGTPTEETWPGVTAFSEFRTYSFPC YLPQPLINHAPRLD TDGIHLLSSLLLYESKSRMSAEALSHSY FRSLGERVHQLED TASIFSLKEIQLQKDPGYRGLAFQPPGRGK NRRQSI F
484	1223	807	356	CTPHGSSSSWKIPLWPRHMSPLHSCLPVGTSTSSGPLAVPRDC FHLCLWGQLLLISCLACGQGCVRVAGGQHVPGQALGTLSP VSLLTWAGPSLDWPHPGSLVTPRCPI LPAVPVLVKGLGGWPPT RPSRAAPVSGPWDQLPYFPGL
485	1224	1199	370	LISPVWGNIQRSRSVPLFPSSGLVLGGIWARGPLLALLASFNI SVLNAECYLKQILHPTSHFTVSETPPLSGNDTDSLSCDSGSSA TSTPCVSRLVTGHHWASKNGRHLVGLIEDYEALLKQISQGR LLAEMDIQTQEAPSSTSQELGTGPHAPLSKFVSSVSTAKLT LEEAYRRLKLLWRVSLPEDGQCPLHCEQIGEMKAEVTKLHKKL FEQEKQLQNTMKLLQLSKRQEKVIFDQLVVTHKILRKARGNLE LRPGGAHPGTCSPSRPGS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
486	1225	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEACQRRQQLPVTFTGNKQKVLGKALSIRFPLMTIEEFAAGPAQSGILSDREVVNLFHLFTVNPKEPRVEYIDRPRCCLRGKECCINRFQQVESRWGYSSTSDRIRFTVNRRIISIVGFGLYGSIHGPTDYQVNIQIIIEYEKKQTLGQNDTGFS CDGTANTFRVMFKEPIEILPNVCYTACATLKGPD SHYGTGKLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIPEIIFYT
487	1226	1193	372	SVWWNSEVKDWMQKKRRGLRNSRATAGDIAHYRDYVVKKGLGHNFVSGAVVTAVEWGTPDPSSCGAQDSSPLFQVSGFLTRNQAQQPFFSLWARNVVLATGTFD SPARLGIPGEALPFIHHELSALEAA TRVGAVTPASDPVLIIGAGLSAADAVLYARHYNIPVIHAFRRADVDDPGLVFNQLPKMLYPEYHKVHQMMREQSILSPSPYEGYRSLPRHQLLCFKEDCQAVFQDLEGVEKVFVGSVLVLVLIGSHPDLSFLPGAG\LTQLQWILTSR
488	1227	756	1016	KLRPFIFSNQSLWLHSYEGAELEKTFIKGSWATFWVKVASCWACVLLYLGLLLAPLCWPPTQKPQPLILRRRRRHRIISPDNKYPPV
489	1228	1	747	QLIHLSHGYQIHWTDYINVTGTRPEFGTRAHKS LAGAE LKTLKDFVTVLAKLFPGRPVVKLLLEMLQEWLASLPLDRIPYNAVLDLVNNKMRISGIFLTNHIKWVGCQGSRELRGYPCSLWKLFHTLTVEASTHPDALVGTGFEDDPQAVLQTMRRYVHTFFGCKEKGHEHFEEMAKESMDSVKTPDQAILWLWKKHNMVNGRLAGEKPLGMGGSARAEGGPGPGTARTARLPWGLSLSFAASCHPLC
490	1229	4797	2398	HGGATFINAFVTTPMCPSRSSMLTGKVVHNHNVYTNNECSSPSWQAMHEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWEWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLITNESINYFKMSKRMYPHRPVMVISHAEPHGPEDSAPQFSKLYPNASQHITPSYNYAPNMDKHWIMQYTGPMPLIHMEFTNILQRKRLQTLMSVDDSLVERLYNMLVETGELENTYIIYTADHGYHIGQFGLVKGKSMFYDFDIRVPFFIRGPSVEPGSIVPQIVLNIDLAPTILDLIAGLDTPPDVDGKSVLKLDPKPGNRFRFNKAKIWRDTFLVERGKFLRKKEESSKNIQQSNHLPKYERVKELCQARYQTACEQPGQKWQCIEDTSGKLRIHKCKGPSDLLTVRQSTRNLYARGFHDKDKESCRESGYRASRSQRKSQRQFLRNQGT PKYKPRFVHTRQTRSLSVFEFEGEIIDINLEEEELQVLQPRNIAKRHDEGHKGPRLDQASSGGNRGRMLADSSNAVGPPTTVRVTHKCFILPND SIHCERELYQSARAWKDHKAYIDEEIEALQDKIKNLREVRGHLKRRKPEECSCSKQSYYNKEKGVKQKQKLSHLHPFKEAAQEVDSKLQLFKENNRKRKKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNNNTYWC LRTVNEHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQCNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
491	1230	2480	385	HLLIAQELADRVGEGRACWSLGNAYVSMGRPAQALTFAKKHLQ ISQEIGDRHGELTARMNVAQLQLVLGRLTSPAASEKPDLAGYE AQGARPKRTQRLSAETWDLRLPLEREQNGDSHSHSGDWGRGPSR DSLPLPVRSRKYQEGPDAERRPREGSHSPLDSADVVRVHPRTS IPRAPSSDEECFFDLLTKFQSSRMDQRCPLDDGQAGAAEATA APTLEDRIAQPSMTASPQTEEFFDLIASSQSRRLDDQRASVGS LPGLRITHSNAGHLRGHGEPQEPGDDFFNMLIKYQSSRIDQQR CPPPDVLPRGPTMPDEDFFSLIQRVQAKRMDEQRVDLAGGPGA GGRRPARAPAAVPAWCELRPCAHRQAHPAPTGRSSHSHSVL PRPLPRTGTGHAAPRPPRPRATGSGQAARGGRACFHPGLAPMA LSFLPSAPAAAGRTGPSACRPRPGAVRLPHPLPQALPVLPCPAK CETLLSPSPSPKVSLSRLLGPPRTGPCSVPELVLGWPCDRHA PPLQLRPGAGLPPSLSPHSPARGQQPQKAPQTTHGRPGCSGSP EVPPAESQGPAGASTGAGPISKAEGMAGHELHRSKTPSQEKQ GLVLGMLTGSKSSAQSGWEVAPGSVTLTQVGGWSVEAGEASLS STLQTPHMRTPLLPPAGGDDITALSMGRGLTGHQVRDPRTGRT CWSLRWAPGA
492	1231	3	398	NSAADLAI FALWGLKPVVYLLASSFLGLGLHPISGHFVAEHY FLKGHETYSYGYPLNWITFNVGYHVEHDFPSIPGYNLPLVRK IAPEYYDHL PQHHSWVKVLWDFVFE DSLGPYARVKRVYRLAKD GL
493	1232	1	214	QESGFSCCKGPGQNVAVTRAHPDSQGRRRRPERGARGGQVFYNS EYGELSEPSEEDHCSPSARVTFFTDNSY
494	1233	3	443	VIVHARPIRTRASKYYIPEAVYGLPAYPAYAGGGGFVLSGATL HRLAGACAQVELFPIDDVFLGMCLQRLRLTPEPHPAFRTFGIP QPSAAPHLSTFDPCFYRELVVVHGLSAAIWLWMLLHGHGPHG ACAHQPQVAAGPFQWDS
495	1234	1	897	MASAACSMDPIDSFELLDLLFDRQDGLLRHVELGEGWGHVKDQ VLNPNPDSDDFLSSILGSGDSLPSPLWSPEGSDSGISEDLP SDPQDTPPRSGPATSPAGCHPAQPGKGPCLSYHPGNSCSTTTPGP VIQQQHHLGASYLLRPGAGHCQELVLTEDEKKLLAKEGITLPT QLPLTKYEERVLKKIRRKIRNKQSAQESRKKKKEYIDGLETRS CCCPLPSSSSPPSALLAPTKPRALGTLRLYECSPELCTTMLPP AWLLMLCQAPRPQDPDPRLTQPEKSLQEAPGQTGASRTPRT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
496	1235	4235	940	ARGRRSRPVWAASWGGGRPAARRRPRGLAATMGFELDRFDGD VDPDLKCALCHKVLEDPLTTPCGHVFCAGCVLPWVVQEGSCPA RCRGRLSAKELNHVLPKRLILKLDIKCAYATRGCGRVVKLQQ LPEHLERCDFAPARCRHAGCGQVLLRRDVEAHMRDACDARPVG RCQEGCGLPLTHGEQRAGGHCCARALRAHNGALQARLGAHKA LKKEALRAGKREKSLVAQLAAQLELQMTALRYQKKFTEYSAR LDSLSRCVAAPPGGKGEETKSLTLVLHRDSGSLGFNIIGGRPS VDNHDGSSSEGI FVSKI VDSGPAAKEGGLQIHDR IIEVNGRDL SRATHDQAVEAFKTAKEPIVVQVLRRTPTKMTFPPSESQSLVD TGTQTDITFEHIMALTKMSSPSPVLDPYLLPEEHPSAHEYD PNDYIGDIHQEMDREELELEEVLDLYRMNSQDKLGLTVCYRTDD EDDIGIYI SEIDPNSIAAKDGRIREGDRI IQINGIEVQNREEA VALLTSEENKNFSLIARAELQLDEGWMDDRDNDLDDLHMDM LEEQHHQAMQFTASVLQKKHDEDDGTTDTATILSNQHEKDSG VGR TDESTRNDESSESEQENNGDDATASSNPLAQQRKLTCSQDTL GSGDL PFSNKSFI SPECTGAAYLGIPVDECERFRELLELKCQV KSATPYGLYYPGGLDAGKSDPESVDKELELLNEELRSIELEC LSIVRAHKMQQLKEQYRESWMLHNSGFRNYNTSIDVRRHELSD ITELPEKSDKSSAYNTGESCRSTPLTLEISPDNSLRRAAEG ISCPSSGAVGTTEAYGPASKNLLSITEDPEVGTPTYSPSLKE LDPNQPLESKERRASDGSRSPTPSQKLGSAYLPSYHHSYPYKHA HIPAHQHYQSYMQLIQKSAVEYAQSQMSLVSMCKDLSSPTP SEPRMEWKVKIRSDGTRYITKRPVRDRLLRERALKIREERSGM TTDDDAVSEMKGRIYSKEERKQHLVKAKEQRRRREFMMQSRL DCLKEQQAADDRKEMNILELSHKMMKKRNKKIFDNWMTIQEL LTHGTSKSPDGTRVYNSFLSVTTV
497	1236	2	157	FFFLVEMGFCHVGQGLTLIGSSNLPASASKSAGITGVSHCAR PDFKSCVE
498	1237	1	211	LAGRKVLLFVSGYVVGWGPITWLLMSEVLPLRARGVASGLCVL ASWLTAFLTKSFLPGGVSVQPQAPGP
499	1238	2	345	FWAPGPPGVGAAGDASTRLRESCPSPPGRLRRTTAPWSSQ ARAAAPAPSSSCRGPDGASSPRDLPWRPWKILRRTPLSGDVEL SQVHPDQRILRRFILSRTCNTIPGMAE
500	1239	1	523	MRRFLSKVYSFPMRKLILFLVFPVVRQTPTQHFKNQFPALHWE HELGLAFTKNRMNYTNKFLIPESGDYFIYSQVTFRGMTSECS EIRQAGRPNKPDSITVVTIKVTDSYPEPTQLMGTKSVCEVGS NWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAF LL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
501	1240	2	1277	FVWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGSSRVISHY AGQDATDPFVAFHINKGLVKYMNSSLIGELSPQPSFEPTKN KELTDEFREL RATVERMGLMKANHVFFLLYLLHILLDGAAWL TLWVFGTSFLPFLLCVLLSAVQAQAGWLQHDFGHSVSTSK WNHLHHFVIGHLKGAPASWWNHMHFQHHAKPNCFRKDPDINM HPFFALGKILSVELGKQKKKYPYNNHQKYFFLIGPPALLPL YFQWYIFYFVIQRKKWDLAWMITFYVRFFLTYPVLLGLKAFL GLFFIVRFLESNWFVWVTQMNHIMHIDHNRMDWVSTQLQAT CNVHKSAFNDWFSGHLNFQIEHHLFPTMPRHNHYKVAPLVQSL CAKHGIEYQSKPLLSAFADI IHSLKESGQLWLDAYLHQ
502	1241	999	540	QCGGIPYNTTQFLMNDRDPEEPNLDVPHGISHPGSSGESEAGD SDGRGRAHGEFQRKDFSETYERFHTESLQGRSKQELVRDYLEL EKRLSQAEETRRLLQQLQACTGQQSCRQVEELAAEVQRLRTEN QRLRQENQMWNREGCRCDEEPT
503	1242	1448	875	SPERSSLSVGREKAMEVPPAPRSFLCRALCLFPRVFAAEAVT ADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKD\VTGSLF RINVLRLGLVAGGIIGALLGTPVGGLLMAFQKYSGETVQERKQ KDRKALHELKLEEWKGRLOVTEHLPEKIESSLQEDEPENDAKK IEALLNLPRNPSVIDKQDKD
504	1243	149	1293	RSGLAVTEMVPWVRTMGQKLKQRLRLDVGREICRQYPLFCFL LLCLSAASLLLNRYIHILMIFWSFVAGVVTFCYSLGPDSSLNPN IFFTIKYKPKQLGLQELFPQGHSCAVCGKVKCKRHRPSLLEN YQPWLDLKISSKVDASLSEVLELVLENFVYPWYRDVTDDES FV DELRITLRFASVLIRRIHKVDIPSIITKKLLKAAMKHIEVIV KARQKVKNTTEFLQQAAL EYGP EHLVALRSRDELHYLRKLTE LLFPYILPPKATDCRSLTLLIREILSGSVFLPSLDFLADPDTV NHLLIIFIDDSPPEKATEPASPLVPFLQKFAEPRNKKPSVLKL ELKQIREQQDLLFRFMNFKQEGAVHVLHVLFDCCGI
505	1244	2	1116	QSLAEVLQQLGASSELQAVLSYIFPTYGVTNHSFAFSMHALLV NHYMKGGFYPRGVTSEIAFHTIPVIQRAGGAVLTATVQSVLL DSAGKACGVSVKKGHELVNIYCPIVVSNAFLNTYEHLLPGNA RCLPGVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYVY YD TDMDQAMERYVSMPREEAAEHIPLFFAFPSAKDPTWEDRF PGRSTMIMLIPTAYEWFEEWQAEKKGK\RGSDYETFKNSFVEA SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGAD HDLGRHLHPCVMASLRASPIPNLYLTGQDIFTGGLVGLALQAL LCSSTILKRNLYSDLKNLDSIRAQKKKN
506	1245	1759	873	RPQETRVLQVSCGRAHSLVLTDRGVFSMGNNSSYGQCGRKVVE NEIYSESHRVHRMQDFDQGVVQVACQGDHSLFLTDKGEVYSCG WGADGQTGLGHYNITSSPTKLGGDLAGVNVIVATYGDCCCLAV SADGGLFGWGNSEYLQLASVTDSTQVNVPRCLHFSVGKVRQA ACCGTGCAVLNNEGHEVFWGYGILGKGNLVESAVPEMIPPTL FGLTEFNPEIQVSRIRCGLSHFAALTNKGELFWGKNIRGCLG IGRLEDQYFPWRVTMPGEPVDVACGVDHMTLAKSFI



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
507	1246	520	2	LPFREWLMTIVVLSLSAAAVAAAFMAKCRMVLSRRYFCSHFVMSA SRARIRSSFSRTSSRRAGALYSGMLAGWFFPCFCWVLSASSSL SSQVRSRLRSICSRFSHADCSWVRACCSFSTFSTYACFSRNSSS SLMTLAWALLKAWSRISMCLRWSSLAVRTAANSISNFSFSFKN
508	1247	1	1083	MQAVRATASQSLSCARAPREPTQHALRAHWFPAAAVQPSPHS GVAAAAGTWSSAFRGEHPLVSSGLLLGVREQSFRLRLSKAGTH MYLEHTSHCPHDDDDTAMDTPLPRPRPLLAVERTGQRPWLWAPS LELPKPDMPQLPAGAFLEEVAEGTPAQTESEPKVLDPEEDLLC IAKTFSYLRESGWYSGSITASEARQHLQKMPGTFVLVDSTHP SYLFTLSVKTRGPTNVRIEYADSSFRLDNCLSRPRIAAPPD VVSLVQHYVASCTADTRSDSPDPAPTPALEMPKEDAPSDPALP APPPATAVHLKLVPFVRSSARSLOHLCLVINRLVADVDCI PLPRRMADYLRQYPPQL
509	1248	2	841	FVDIFQRWKECRGKSPAQAELS YLNKAKWLEMYGVDMMHVVRGR DGCEYSLGLTPTGILIFEGANKIGLFFWPKITKMDFKKSKLTL VVVEDDDQGREQEHFVFRLDSARTCKHLWKCAVEHHAFFRLR TPGNSKSNRSDFIRLGSRRFRFSGRTEYQATHGSRLRRTSTFER KPSKRYPSRRHSTFKASNPVIAAQLCSKTNPVHNYQPQYHPN IHPSQPRWPHSPNVRPSFQDDRSWKASASGDDSHFDYVHDQ NQKNLGGMQSMYRDKLMTAL
510	1249	2	763	GGIRLIQKLTWRSRQDRENCAMKGKHKDECHNFIKVFVPRND EMVFVCGTNAFNPFCRYRVSIFYVICFF*STFLPSLICC*S* NLSAFQ*FVLSLVQ*KNKDRILQMEF*YK*NSIAFKRAR*IDM TLAIYFSFV\LSTL*YDGEEISGLARCPFDARQTNGALFADGK LYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKE/PHFL YAIK/Y/GNYVYFSFREIVAT**LG/KA VDS/RVARYEKQLVG PTV
511	1250	1555	629	ARALARERESESARADDVTLGVSAI LAVDRGGNLSA\DGWAY IDVEVRRPWFVGPGRSSGNGSTAYGLVGSRWLSPFHTGG AVSLPRRPRGPGPVLGVARPCLRCVLRPE\HYEPGSHYSGFAG RDASRAFTVGDCEAGLVDDVSDLSAAEMLTLHNWLSFYEKNY VCVGRVTGRFYGEDGLPTALTQVEAAITRGLEANKLQLEKQ TFPPCNAEWSSARGSLWCSQKSGGVSRDWIGVPRKLYKPGAK EPRCVCVVRTTGPSPGQMPDNPPHRNRGDLDPNLAETGCPPL AITCSFPL
512	1251	1100	798	YFIICRDGVLLFCPGWSQTPGAQAILLHWATQAGMTDMSHSA QPIYLFYILIRTRSHYVAQAGQLLDSNDSNPVASQNVGITGMS HHAWLKIVLYFCII

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
513	1252	3	1395	PAARPPSLVRLSPSPPKPRARARAPQSVEPAAPLVARGSSPPA RPAPAMVRRAPYRSGAGGPLGGRGRPPRPLVVAVRSRSP ASPRGPQPPR\IRARSAPPMEGARVFGALGPFGSSPGLTLGG LAVSEHRLSNKLLAWSGVLEWQEKRRPYSDSTAKLRKRTLPCQA YVNQGENLETDQWPQKLIMQLIPQQLLTTLGPLFRNSQLAQFH FTNRDCDSLKGLCRIMGNFAGCMLFPHISPCEVRVLMLLYSS KKKIFMGLIPYDQSGFVSAIRQVITTRKQAVGPGGVNSGPVQI VNNKFLAWSGVMEWQEPPEPNSRSKRWLPSHVYVNQGEILRT EQWPRKLYMQLIPQQLLTTLVPLFRNSRLVQHFHTKDLETLS LCRIMDNFAGCVHFSYKASCEIRVLMLLYSSEKKIFIGLIPH DQGNFVNGIRRVIANQQQVLQRNLEQEQQQRMGG
514	1253	320	964	GRPALGREAPPQAGLSSTPPPCSETCTMGPHSILRTVHCRPTK TPPEPSAEPHPLSLTSSNTSLAGTSLGRDLTPGGKPPSGQT PRNPESPRHLGSPRGRRLASPTPTGSGRSGPASRGQRRSLC AAQDPTSEGASVGAMEAGLGPPTAAPRGVVSEAAESLGGTSLW GAWGRPPAGPSGLAGRRSRREALRPDRKEASVMAAVSAIQP
515	1254	704	107	PGVPTHGWPRSRVLTRVRGSRGSGKMAAAVLAAGLRAARRAV AATGVRGGQVRGAAGVTDGNEVAKAQATPGGAAPTIFSRILD KSLPADILYEDQCLVFRDVAPQAPVHFLVIPKKPIPRISQAE EEDQQ/LTYVPPLSL*LLGHLLLVAKQTAKAEGLDGGRYLVIN DGKLAQSVYHLHIHVLGGRQLQWPPG
516	1255	2299	924	VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAAPFLVAFAYWNH YLSCTSPSCYRPLCRLNFGNLNVENLALLVLTYSSEDF/T WVPG*GRSGEVFPEGTGLPLPHSDLPTS WCGHSLQCGSQSSFP PAIHENAFIVFIASSLGHMLLTICILWRLTKKHTVSQE\DGLSL AGAPRQPRRKSRTSVLRIRVMVRWELSSNGNPGRGVLGLGLGL GNKLRVVGQNLGL*HCVVVVWETGE*KRWRLOMGIE*GVASRR Q*VRNSVRGLVCHNSSAPPMYMGFFSPTVFGGGVGG*LVHTFI LHPPEVEAAGIPLLLGPSLPQRQGREHIVVILAAPACAPFHDR *WEPREIRPSP*ELGLRGEPTLSYPASCRVIRQPI*DRKSYS WKQRLFIIINFISFFSALAVYFRHNMYCEAGVYTI FAILEYTVV LTNMAFHMTAWWDFGNKELLITSQPEEKRF
517	1256	3	254	IDLLEIRNGPRSHESFQEMDLNDDWKLSDDEVKAYLKKEFEKH GAVVNESHHDALVEDIFDKEDDKDGFISAREFTYKHDEL
518	1257	2	611	PRVRGRVGKEGAAAKPRSLRRFQLLSWSVCGGNKDPWVQELM SCLDLKECGHAYSGIVAHQKHLPTSPPI SQASEGASSDIHTP AQMLLSTLQSTQRP TLVGSLS SDKELTRPNETIHTAGHSLA AGPEAGENQKQPEKNAGPTARTSATVPVLCCLLAIIFILTAALS YVLCRRRGQSPQSSPDLVHYIPVAPDSNT
519	1258	1002	418	LIISNFLKAKQKPGSTPNLQQKKSQARLAPDIVSASQYRKFE FQTGILLIYELLHQPNPFVRAQLRERDYRQEDLPPLPALSLYS PGLQQLAHLLEADPIKRIRIGEAKRVLQCLLWGPRREL VQQP GTSEALCGTLHNWIDMKRALMMMKFAEKAVDRRRGVELEDWL CCQYLASAEPGALLQSLKLLQLL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
520	1259	2	2019	KRGLIVVMAHEMIGTQIVTERGVALLESgtekvLLIDSRPFVEYNTSHILEAININCSKLMKRRLLQODKVLITELIQHSAKHKVDIDCSQKVVVYDQSSQDVASLSSDCFLT VLLGKLEKSFNSVHLLAGGFAEFSRCFPGLCEGKSTLVPTCISQPCLPVANIGPTRILPNLYLGCQRDVLNKLMOQNGIGYVLNASNTCPKPDFIPESHFLRVPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRSATIAIAYIMKRMDMSLDEAYRFVKEKRPTTISPNNFLGQLLDYEKKIKNQGTASGPKSKLLHLLEKPNPVPVAVSEGQKQKSETPLSPPCADSATSEAAAGQRPVHPASVPSVPSVQPSLLEDSPVLQALSGHLHLSADRLEDNKLKRSFSLDIKSVSYASMAASLHGFSSSEDALEYYPSTTLDGTNKLQCFSPVQEL/CGADSRNQSS**GGSQ/PSPRSCRPPGLQTARASDCIRSEPAAVAPPRGPFYLHCIEVGAWRTITTPASFSAFPP\PAAPHEVCWPGP*GLA\PDILAPQTSTPSLTSSWYFATESSHFYASAIYGGSASYSAYSQSQLPTCGDQVYSVRRRQKPSDRADSRRSWHEESPFQKQFKRRSCQMEFGE SIMSENRSREELGKVGSGSSFSGSMETIEVS
521	1260	20	803	ASSSKRVSQRKMLQLWKLVLCCGVLGTSESLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAELNNVISKLLPTNTDIFGLKISNSLILDVKAEPIDGKGLNLSFPVTANVTEAGPIIDQIIN\LRASLDLLTAVTIETDPQTHHPVAGLGE CARDPTSISLCLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTLQTLI
522	1261	1246	411	CSLRRPRSAEPDADHVPLLGLLRLQLRAARQPGAMRPGGPAA SPQRLRGLLLLLLLQLPAPSSASEIPKQKQKQALRQREVVDLYNGMCLQGPGVPGRDGSPGANGIPGTPGI PGRDGFKEGECRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAI IYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWGTCSDYPKGDASTGWNVSRIIEELPK
523	1262	2009	921	MHSAMLGTRVNLVSDFWRVMMRVLCWLVRQDSRHQRIRLPHLEAVVIGRGPETKITDKKCSRQQVQLKAECNKG YVKVQGVNPTSIDSVVIGKDQEVKLQPGQVLHVMNELYPYIVEFEEEAKNPGLETHRKRKRSGNSDSIERDAAQEAEGTGLEPGSNSGQCSVPLKKGKDAPIKKESLGHWSQGLKISMQDPKMQVYKDEQVVVIKDKYPKARYHWLVLPWTSISSLKAVAR\EHLELLKHMHTVGEKVIVDFAGSSKLRFRLGYHAIPSMHVHLHVISQDFDSPCLKNKKHWN SFNTEYFLESQAVIEMVQEA GRVTVRDGMPPELLKPLRCHECQQLLPSIPQLKEHLRKHWIQ

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
524	1263	2067	198	DMSDTSSESGAGLTRFQAEASEKDSSSMQTLTQNVETPKASKALEVSEDEVKVS KASGVSKATEVSKTPEAREAPATQASS TTQLTDTQVLAENKSLAADTKQNADPQAVTMPATEKKVSH VADTKVNTKAQETEAAPSQAPADEPEPEPESAAAQSQENQDTRPK VKAKKARKVKHLDGEEDGSSDQSQASGTTGRRVSKALMASMA RRASRGPIAFWARRASRTRLACFGPGEPLSPWRSP\KARRQR GFAVRVAKFQ\SSQEPPEAPPW\DVALLQGRAN\DLVKYLLAK DQTKIPIKRS\DKLKDIIKEYTDVYPEII\ERAGYSLE\KVFG IQLKEIDKNDHLYILLSTLEPTDAGILGTTKDSPKLGLLMVLL SIIIF\MNGNRS\SEAVIWEVLR/RSLGLRLGIHHS\LLGDVK\ KLITDEV\VKQKYL\DYARVPHSNP\EYEFFWG\LRSYEDQ QR*KSKFKACK\VQK\KDPK\EWAAQSPPGKAR/ERMEAD\LK AAS*GSPWKPRLRAEIKARMGIGLGSENAAGPCNWDEADIGPW AKARIQAGAEAKAKAQESGSASTGASTSTNNSASASASTSGGF SAGASLTATLTFLGLFAGLGGAGASTSGSSGACGFSYK
525	1264	1	1397	ARPPVCTGSTMSLTVVSMACVGFLLQGAWPLMGQDKPFLSA RPSTVVPRGGHVALQCHYRRGFNNFMYKEDRSHVPIFHGRIF QESFIMGPVTPAHAGTYRCRGSRPHSLTGWSAPSNPLVIMVTG NHRKPSLLAHPGPLLKSGETVILQCWSDIMFEHFFLHKEGISK DPSRLVGQIHDGVSKANFSIGPMMLALAGTYRCYGSVTHTPYQ LSAPSDPLDIVVTGPYEKPSLSAQPGPKVQAGESVTLSCSSRS SYDMYHLSREGGAHERRLPAVRKVNRTFQADFLGPATHGGTY RCFGSRHSPYEWSDPSDPLLVSVTGNPSSSWSPTEPSSKSG NLRHLHLIGTSVVKIPFTILLFFLLHRWCSNKK\NAAVMDQE PAGNR\VNSEDSDQDHQEVSY*LEHCVFTQRKITRPSQRPK TPPTDTSMYIELPNAEPRSKVFCPRAPQSGLEGIF

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F= Phenylalanine, G=Glycine, H= Histidine, I= Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q= Glutamine, R= Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
526	1265	6657	988	<p>LHNLRLRYFSGLIYTYSGLFCVVVNPYKHLPIYSEKIVDMYKG</p> <p>KKRHMPPHIYAIADTAYRSMQLQDREDQSILCTGESGAGKTEN</p> <p>TKKVIQYLAVVASSHKGKDTSTITGELEKQLLQANPILAEFGN</p> <p>AKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLEKSRAIR</p> <p>QARDERTFHIYYMIAGAKEKMRSDLLLEGFNNTFLSNGFVP</p> <p>IPAAQDDFMFQETVEAMAIMGFSEEEQLSILKVVSSVLQGNL</p> <p>VFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIK</p> <p>VGRDVVQKAQTKEQADFAVEALAKATYERLFRWILTRVNKALD</p> <p>KTHRQASFLGILDIAGFEIFEVNSFEQLCINYTNEKLQQLFN</p> <p>HTMFIL\EQEYQREGIEWNFIDFGLDLQPCIELIERPNNPPG</p> <p>VLALLDEECWFPKATDKSFVEKLCTEQGSHPKFKPKQLKDKT</p> <p>EFSSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLLNASSDKFVA</p> <p>DLWKDVDRIVGLDQMAKMTESLPSASKTKKGMFRTVGQLYKE</p> <p>QLGKLMTTLRNTTPNFVRCIIIPNHEKRSGLDAFLVLEQLRCN</p> <p>GVLEGIRICRQGFNRIVFQEFRQRYEILAANAIPKGFMDGKQ</p> <p>ACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEERDLKITD</p> <p>VIMAFQAMCRGYLARKAFARQQQLTAMKVIQRNCAAYIKLRN</p> <p>WQWCRLFTKV*PLLQVTRQE*EMQAKEDQLQKTKERQQKAENE</p> <p>LKELEQKHSQLTEENLLQEQQLAETELYAEAEEMRVRLAAKK</p> <p>QELEEILHEMEARLEEEEDRGQQLQAEKKMAQQLDLEEQL</p> <p>EEEEARQKLQLEKVTAEAKIKKLEDEILVMDDQNNKLSKERKL</p> <p>LEERISDLTTLNLAEEEEKAKNLTCLKNKHESMISEFVRLKKE</p> <p>EKSRLQELKLRKLEGDASDFHEQIADLQAQIAELKMQLAkke</p> <p>EELQAALARLDDEIAQKNNALKKIRELEGHISDLQEDLDSERA</p> <p>ARNKAQKQKRDLEGELEALKTELEDTLSTATQQLRAKREQE</p> <p>VTVLKR\ALNEETRSHEAQVQEMRQKHAQAVQSLTEQLEQ\*K</p> <p>RAKANLDKNKQTLKENTD\LAGELRVLGQA\KQVEVHRMKKL</p> <p>QAQVQELQSKCSGERARAELENDKVHK\QNEVESVTG\MLNE</p> <p>ABGKAIKLAKDVASLSSQL\QDTQELLQEESSRQKLNVT\SLR</p> <p>\QLEEBERNLQDQLDEEMEAQNLERHISTLNIQLSDSKKLLQ</p> <p>DFASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLEKTKNR</p> <p>LQQELDDLVDLDNRQQLVSNLEKKQKQKFDQLLAEEKNIS SKY</p> <p>ADERDRVEAEAREKETKALSL\ARALEEALEAKEELERTNKML</p> <p>KA\EMGRPGSASKD\DVQELSHDL\EKSK\RALGDPRLLEEMK</p> <p>T\QLEELGRTELASPRRDA\KLRLEVMQAPSRASFER\DLQA</p> <p>RTEQNE\ESRR\HLQRQLHEYETELEDERKQRALAAAKIKLG</p> <p>WDPVRTL DL*ADSAIKGRGGKAIKQLRKLQAQMKDFQRELEDA</p> <p>\RASRDEIF\ATA\KENEKKAksLEA\DLMQQLQ\DLAAEEG</p> <p>RKQ\ADLE\KEELAEEL\ASSLSGRNALQDEKRRLEARIAQLE</p> <p>EELEEEQGNMEAMSDRVKATQQAQELSNEATERSTAQKNES</p> <p>ARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEE</p> <p>QVEQEAREKQAATKSLKQKDKKLEILLQVEDERKMAEQYKEQ</p> <p>AEKGNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESN</p> <p>EAMGREVNALSKLRRGNETS FVPSRRSGGRRVIENADGSEEE</p> <p>TDTRDADFNGTKASE</p>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
527	1266	1	775	KLHFAKSLNSELSCSTREAMQDEGDYITLNIKTRKPALVSVGP ASSSWWRVMA LILLILCVGMVVLVALGIWSVMQRNYLQDENE NRTGTLQQLAKRFCQYVVKQSELKGTFGHKCSPCDTNWRYYG DSCYGFRRHNLTWEEKQYCTDMNATLLKIDNRNIVEYIKAR\ THLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNC AYFHNGKMHPTFCENKHYL\MCE\RKAGHDPRTWQLPLMPKRW TG
528	1267	1053	424	NQGLRDVGLCRTCLVNKIFASSILGKSHHSLVSNQGHNA PW KAAGS\LPLKAAYC\QGFSPCDCLKYG\SWDEKDLMPQPDTH KGSVLRWISKRGKPLAVEME EGHCL\CLPLGTECLGVKP\IVH LFNSEMG EK\RPVAG\ARHVGSSAALLFFTPLRCLGGEKHKSG LRARPGIVPSLELNYDIDSFAHMF /SVDLLLIITLLSYIIPF C
529	1268	1435	1560	MWURLAPTQAIWRAAGCCMRFSRRRSTCCCLASCIFLLYKIVR GDQPAARRRQRRRAAPSAPPQAARLHPPPKLRRFDGVQDPAP YSWAINGKVFVDVTQRPANFLRGPRGPETLSDWESQFTFKYHHV GKLLKEGEEPTVYSDEE EPKDESARKND*
530	1269	705	166	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCL GASPTPGEVQRHLQTHGIDNGELDFSTFLTIMHMQIKQEDPK KEILLAMLMDKEKKGYVMASDLRSKLTSLGEKLT HKEV\DDL FRE\ADIEPNGKVKYDEFIHKI/TLLPGRDLLKEENGRASPGP ENLEQLIFL
531	1270	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRTWNPVNPESPRI PAPRLPKRM SGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRF ASWDEMNVLAHGLLQLGQGLREHAERTS QLSALERRLSACGS ACQGTGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH KVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKR LPEMAQPVDPAHNVSRHLRLPRDCQELFQVGERQSGLFEIQPQ GSPFFLVNCKMTSDGGWTVIQRHDGSDVFNRPWEAYKAGFGD PHGEFWLGLEKVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL GGEDTAYSLQLTAPVAGQLGATTVP PPSGLSVPFSTWDQDHLR RDKNCAKSLSGGWVFGTCSHNLNGQYFRSIPQQRQKLKKGIF WKTWRGRYYPLQATTMLIQPMAAEAS
532	1271	1276	90	ALDFGDCSQWPRPQDTMKQLPVLEPGDKPRKATWYTLTVPGDS PCARVGHSCSYLPPVGN AKRGKVFIVGGANPNRSFSDVHTMDL GKHQWDLDTCKGLLPRIYEHASFIP SCTPDRIWVFGGANQSGNR NCLQVLNPETRTWTTP EVTSPPPSPRTFHTSSAAIGNQLYVFG GGERGAQPVDTKLHVFDANTLTWSQPETLGNPPSPRHGHVMV AAGTKLFIHGGLAGDRFYDDLHCIDISDMKWQKLNPTGAA\PA GCAS/HTPAVAMGK\HVYI\FGMT PAGAPGTQCTQYHTEEQH WDPCCLKF\DTPSYPPGTIGTHSHVVSFPW\PVT CASEKEDS\N SLTLNHEAEKEDSADKVM SHSGDSHEESQTATLLCLVFGGMNT EGEIYDDCIVTVVD

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
533	1272	1169	639	GFSIGKATDRMDAFRKAKNRAVHHLHYIERVEDHTIFHDISLR FKRTHIKMKKQPKGYGLRCHRAIITICRLIGIKDMYAKVSGSI NMLSLTQGLFRGLSRQETHQQLADKKGLHVVEIREECGPLPIV VASPRGFLRKDPEPEDEVDPVKLDWEDVKTAQGMKRSVWSNLK RAAT
534	1273	25	1396	ADPHTTVIRFFPAASATKRVLPVLRVSSPRTWNPVNPESPRI PAPRLPKRMMSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRF ASWDEMNVLAHGLLQGLQGLREHAERTSRLSALERRLSACGS ACQGTGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH KVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKR LPEMAQFVDPAHNVSRHLRLPRDCQELFQVGERQSGLFQIQPQ GSPFFLVNCKMTSDGGWTVIQRRHDGSDVFNRPWEAYKAGFGD PHGEFWLGLKGVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL GGEDTAYSLQLTAPVAGQLGATTVPSPGLSVFSTWQDHDHLR RDKNCAKSLSGGWFGTCSHSLNNGQYFRSIPQQRQKLKKGIF WKTWRGRYYPLQATTMLIQPMAAEAAS
535	1274	23	1102	TLRSRPAGEAGYLGWDPEQAGEGSALSRLPGAMAALMTPGTGAP PAPGDFSGEGSQGLPDPSPEPKQLPELIRMKRDGGRLSEADIR GFVAAVVNGSAQGAQIGAWGGLGVPDPDWEVSPRDFGSLGVRR CPTTSTGPRVPHRCGLPPSRVPPHTRG\MLMAIRLRGMDLEET SVLTQALAQSGQQLLEWPEAWRQQLVDKHSTGGVGDKVSLVLAP ALAACGCKVINHLLSRREP IPHMQQPVHPQAAPNLKPGPKPPR PYQGFSPPCSPAQFSPPRSPAQRLGPLWLQTRPLGAGKRSTDG IQTPFPLGPQTAPPREELRTSLPLPQALFPQGQVPTSSPTDTS QPRKLPFHSLTSLTWSAPL
536	1275	3	439	RALRELERVTHGLAEAGRDREDVSTELYRALEAVRLQNSEGS CEPCPTSWLPFGGSCYYFSVPKTTWAEAQGHCADASAHLA/IV GGLGEQDFLSRDTSALEYWIGRRRAVQHLRKVQGYSWVDGVPLS FR*/WEG/HPGETWGPQVRL
537	1276	1	564	RWPRSWPPRAGAARGAAEAAMVGALCGCWFRLLGGARPLIPLGP TVVQTSMSRSQVALLGLSLLLMLLLYVGLPGPPEQTSCLWGDP NVTVLAGLTPGNSPIFYREVLPLNQAHREVEV\CCFMERPLTLT RGSSWAHCSYCHRGATGPWPLTFQVLGTRHLQRRQAQRQGGQR CWSGRCGTWRYRMPCW

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
538	1277	102	1549	QENQLEKKMKFLIFAFFGGVHLLSLCSGKAICKNGISKRTFEE IKEEIASCGDVAKAIINLAVYGKAQNRSYERLALLVDTVGPRL SGSKNLEKAIQIMYQNLQDDGLEKVHLEPVRI PHWERGEESAV MLEPRIHKIAIILGLGSSIGTPPEGITAEVLVVTSTFDELQRRAS EARGKIVVYNQPYINYSRTVQYRTQGAVEAAKVGALASLIRSV ASFSIYSPHTGIEYQDGVPKIPTACITVEDAEMMSRMASHGI KIVIQLKMGAKTYPDTDSFNTVAEITGSKYPEQVVLVSGHLD WDVGQGMDDGGGAFISWEALSLIKDLGLRPKRTLRLVLWTAE EQGGVGAFQYYQLHKVNISNYSVMESDAGTFLPTGLQFTGSE KARAIMEEVMSLLQPLNITQVLSHGEGTDINFWIQAGVPGASL LDDLYKYFFHHSHGDTMTVHGIQTQMNVA\AAV\WAVVSYV\ VADMEEMPLRS
539	1278	2438	1148	TKPRRRRHQPASQRQRPWSSDSTGDLARGKGRKEENKGS DRV SLAPPSLRPPMMCQSEARQGP ELRAAKWLHFPQLALRRRLGQL SCMSRPALKLRSWPLTLVLYLLPFGALRPLSRVGRVPVSRVAL YKSVPTRLLSRAWGRLNQVELPHWLRRPVVSLYIWTFGVMKE AAVEDLHHYRNLS EFFRRKLKPQARPVCGLHVSISPDSGRILN FGQVKNCVEQVKGVTYSLESFLGPRMCTEDLPFPAAASCD SF KNQLVTREGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFP SLMSVNPGMARWIKELFCHNERVLTGDWKHGFSLTAVGAT\ NWGSIRIYFDRDLHTNSPRHSKGSYNDFS FVTHTNREGVPMRK GEHLGEFNLGSTIVLIFEAPKDFNQLKTGQKI\RFGEALGSL
540	1279	3	1911	LPERAFGPRTPRAPRRRRRRLLSPPPRPPPDLREPRAPGPW LCPSRAGTAQDPARIRERRGRVAGGAAGPAMELRARGWLLCA AAALVACARGDPASKRSRSCGEVRQIYGA GFSSS\DVPAEIS GEHLRICPQGYTCCTSEMEENLANRSHAELETALRDSSRVLQA MLATQLRSFDDHFQHLNDSERTLQATFPGAFGELYTQNARAF RDLYSELRLYYRGANLHLEETLAEFWARLLERLFKQLHPQLLL PDDYLDCLGKQAEALRPF\GEAP\RELRLRAT\RA\FVAAR\S FVQGLGVAS\DVVRKVAQVPLG\PEC\SRVIEAGSYC\ALHC VGVPGARPCPDYCRNVLKGCLANQADLDAEWRNLLDSMVLITD KFWGTSGVESVIGSVHTWLAEAINALQDNRDTLTAKVIQCGCN PKVNPQGP GPPEKRRRGKLAPRERPPSGTLEKLVSEAKQLRD VQDFWISLPGTLCSEKMALSTASDDRCWNGMARGVYLPEVMGD GLANQINNPEVEVDITKPDMTIRQQIMQLKIMTNRLRSAYNGN DVDFQDASDDGSGSGSGDGCLDDLCGRKVSRSKSSSRTPPLTHA LPGLSEQEGQKTSAA SCPQPPTFLPLLLFLALTVARPRWR
541	1280	590	189	ATELTRAGMEASALTKSA\VTSVAKVVR\VASGSAVVLP LARI ATSCD*RVGGP/VQAVPMVL\SAMGLQLRAGIASSSIAAKMS AAAIA\NGGGVSPGQPLWLLLQSLGATGL\SGLTKFILGSIGS AIA\AVIARFY



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
542	1281	41	1415	TNGRNLLHHWILGVCGMHPHHQETLKKNRVVLAKQLLSELLE HLLKDIITLEMRELIIQAKVGSFSQNVELLNLLPKRGPQAFDA FCEALRETKQGHLEDMLLTTLSGLQHVLPPLSCDYDLSLPFPV CESCPYKKLRLSTDTVEHSLDNKDGVPCLQVKPCTPEFYQTH FQLAYRLQSRPRGLALVLSNVHFTGEKELEFRSGGDVDHSTLV TLFKLLGYDVHVLCDQTAQEMQEKLQNFAPLPAHRVTDSCIVA LLSHGVEGAIYGVGDKLLQLQEVFQLFDNANCPSLQNKPKMFF IQACRGAIGSLGHLFFFATAATASLAL\ETDRGVDQQDGKNHA GSPGCEESDAGKEKLPKMRLPTRSDMICGYACLKGTAAMRNTK RGSWYIEALAQVFSEACDMHVADMLVKVNALIKDREGYAPGT EFHRCKEMSEYCSLTLRHLVLPFPGHPPT
543	1282	862	275	VRGKEVMAALCRTRAVAAESHFLRVFLFRPFRGVGTESGSES GSSNAKEPKTRAGGFASALERHSELLQKVEPLQKGSPPKNVESF ASMLRHSPLTQMGPADKLVIGRIFHIVENDL\YIDFGGKFHC VCRRPEVDGEKY\QKGTRVR\LRLLDLELTSRFLGATTD\TTV LEANAVLLGIQESKDSRSKEEHLEKYI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
544	1283	2	4503	IPGASPAPRRAPLRLGLRLASGWARAPGGVSPVPGPGMGDA PTMARQAALVLELTFQLCAPETETPEVGCTFEEGSDPAVPC SQAQYDDFQWEQVRIHPGTRAPADLPHGSYLMVNTSQHAPGQR AHVIFQSLSENDTHCVQFSYFLYSRDGHSPGTLGVYVRVNGGP LGSVWNMTGSHGRQWHQAEALAVSTFWPNEYQVLFREALISPDR RGYMGDDILLLSYPCAKAPHFSRLGDVEVNAGQNASFQCM GRAAEAEERFLLQRQSGALVPAAGVRHISHRRFLATFPLAAVSR AEQDLYRCVSQAPRGRGTSLNFAEFMV/KEPPTPIAPPQLLRA GPTYLIIQLNTNSIIGDGPVIRKEIEYRMARGPWAHVAVSLQ TYKLWHLDPDTEYEISVLLTRPGDGGTGRPGPPLISRTKCAEP MRAPKGLAFAEIQARQLTLQWEPLGYNVTRCHTYTVSLCYHYT LGSSHNQTI\RECVKTEQGVSRVTMKNLLPYRNVHVRVLVTNP EGRKEGKEVTFQTDDEVPSGIAAESLTFTPLEDMI FLKWEPEQ EPNGLITQYEISYQSI ESSDPVNVPGPRRTISKLRNETYHVF SNLHPGTTYLFSVRARTGKGFGQAALTEITNISAPSFYDADM PSPLGESENTITVLLRPAQGRGAPISVYQVIVVEEQGSRLRR EPGGQDCFPVPLTFEAALARGLDYFGAELAASSLPEAMPFTV GDNKTYRGFWNPPEPRKAYLIYFQAASHLKGETRLNCIRIAR KAACKESKRPLEVSQRSEEMGLILGICAGGLAVLILLGAIIV IIRKGRDHYAYSYPKPVNMTKATVNYRQEKTHMMSAVDRSFT DQSTLQEDERLGLSFMDTHGYSTRGDQRSGGVTEASSLLGGSP RRPCGRKGSPTYHTGQLHPAVRVADLLQHINQMKTAEGYGFQKE YESFFEGWDATKKKDKVKGSRQEPMPAYDRHRVKLHPLMGDPN ADYINANYIDIRINREGYHRSNHFIATQGPKPEMVYDFWRMVW QEHCSSIVMITKLVEVGRVKCSRYWPEDSDTYGDIKIMLVKTE TLAEYVVRTFALERRGYSARHEVRQFHTAWPEHGVPHYATGL LAFIRRVKASTPPDAGPIVIHCSAGTGRGTGCYIVLDVMLDMAE CEGVVDIYNCVKTLCSRRVNMIQTEEQYIFIHDAILEACLCE TTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPPLDV EECSIALLPNRDKNRSMDVLPDRCLPFLISTDGSNNYINA ALTDYSYTRSAAFIVTLHPLQSTTPDFWGLVYDYGCTSI VMLNQ LNQSNSAWPCLQYWPEPGRQYGLMEVEFMSTADEDLVARVF RVQNISRLQEGHLLVRHFQFLRWSAYRDTPDSSKKAFLHLLAEG DKWQAESGDGRITIVHCLNGGGRSGTFCA\CATVLEMIRCHNLV DVFFAAKTLRNYKPNMVETMDQYHFCYDVALEYLEGLESR

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
545	1284	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLARGKGRKEENKGS DRV SLAPPSLRRPMMCQSEARQGPRLRAAKWLHFPQLALRRRLGQL SCMSRPALKLRSWPLTVLYYLLPFGALRPLSRVGVWRPVSRVAL YKSVPTRLLSRAWGRNLNQVELPHWLRRPVVSLYIWTFGVNMKE AAVEDLHHYRNLSFFRRKLKPQARPVCGLHVSIVSPSDGRILN FGQVKNCVEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCSF KNQLVTREGNELYHCVIYLAPGDYHCFHSPDWTVSHRRHFP SLMSVNPGMARWIKELFCHNERVVLTGDWKHGFSLTAVGAT\ NWGSIRIYFDRDLHTNSPRHSGSYNDFSFTHTNREGVPMAL RGEHLG/QSFNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALG SL
546	1285	185	3057	AELGLFGSLRFSSLLHFPFRPRSPASACGPGEGRMERGLPLLC AVLALVLAPAGAFRNDKCGDTIKIESPGYLTSPGYPHSYHPSE KCEWLIQAPDPYQRIMINFNPHFDLEDRCCKDYVEVFDGENE NGHFRGKFCGKIAPPPVSSGPFLFIKFVSDYETHGAGFSIRY EIFKRGPECSQNYTTPSGVIKSPGFPPEKYPNSLECTYI\VFAP KMSEIIL\DFESFDLEPDSNPPGGMFCRYDRLEIWDGFPDVG HIGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVL QSSVSEDFKCMELGMESGEIHSQITASSQYSTNWSAERSRL NYPENGWTPGEDSYREWIQVDLGLLRFTVAVGTQGAISKETKK KYYVKTYKIDVSSNGEDWITKEGNKPVLFQGNINPTDVVAV FPKPLITRFVRIKPATWETGISMRFVYGCKITDYPSCGMLGM VSGLISDSQITSSNQDRNWPENIRLVTSRSGWALPPAPHSY INEWLQIDLGEKIVRGII IQGGKHRENKVMRKFKIGYSNNG SDWKMIMDDSKRKAKSFEGNNNYDTPELRTFPALSTRFIRIYP ERATHGGLGLRMELLCGEVEAPTAGPTTPNGNLVDECDQAN CHSGTGDDFQLTGGTTVLATEKPTVIDSTIQSEFFTYGFNCEF GWGSHKTFCHWEHDNHVQLKWSVLTSTGTPIQDHTGDGNFIYS QADENQKGVARLVSPVVYSQNSAHCMTFWYHMSGSHVGTLRV KLRYQKPEEYDQLVWMAIGHQGDHWKEGRVLLHKSILKLYQVIF EGEIGKGNLGGIAVDDISINNHSQEDCAKPADLDKKNPEIKI DETGSTPGYEGEGEDKNISRKPGNVLKTLEPILITIIAMSAL GVLLGAVCGVVLVYCACWHNGMSERNLSALENYNFEVLDGVKLLK KDKLNTQSTYSEA
547	1286	3	521	HEGSALTWASHYQERLNSEQSLNEWTAMADLES LRPPSAEPG GSVCGGEGGLGGGEGRIMQWGAWWRGGERAP*LRGSAPRSSEGEQ MEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPLQ/PVP *LHRQPDAAAGGTAGPSLPHLPPPLPGLRVERSKPGGAEEQV GL
548	1287	1742	1200	MAALDLRAELDSLVLQLLGDLEELEGKRTVLNARVEEGWLSLA KARYAMGAKSVGPLQYASHMEPQVCLHASEAQEGLQKFVVR GVHAPEVEGPREAGLRRRKGPCTKPEPESSEAPQDPLNWFIL VPHSLRQAQASFRDGLQLAADIASLQNRIDWGRSOLRGLQEK KQLEPGAA*

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
549	1288	1	649	HSDVGAATAVLPLLTAVLGVTVVTRRDTEGPGRAALVHLTGSP RQKVGTSGREGLPGLGASCAESELERETQEPRSRGRCIFGAAR WRQVPLASPQRPFLLSPGPRLRHMGPLVSWAPPALWVLGCCAL LLSLWALCTACRRPEDAVAPRKRARRQRARLQGSATAAEAVSA KLSRGPWGPQGTDPSSPPVPTADPPLLPQQVGHQTARAAP G
550	1289	433	632	LTGPGQRLAGTTEGPRRCRGSSQAPTPTWKLVDTRLCAAAPWL ASRAPGHYSQMLLVN*PCRKDWLVSKWMRTFVCGQSPAMTDRP RSEAGRDRRAKALPGLIPGSNPNEACGHQALCSSSVASVQG PWLLPNASSPPTPGQPQP
551	1290	102	612	KHRLCSLEQLMTLISAAREYEIEFIYAISPGLDITFSNPKEVS TLKRKLDQVSQFGCRSFALLFDDIDHNMCAADKEVFSSFAHAQ VSITNEIYQYLGEPEFTFLFCPT/EYCI*WLYI*LVFLEYITYK GPWAPFSLHFPPPLVCKSRNLFLEDIFQDPKLEKF*ELINDN
552	1291	269	565	TSALTQGLERIPDQLGYLVLSEGAVALSSGDLENDEQAASATS ELVSTACGFRHLRGMNVFPKRLSVVFGEHTLLVTVSGQRFV KRONRGREPIDV
553	1292	660	233	AKRAERTSRLQGLQHPSPPYPATLGVTGQDRTLQLOHQCPA GRKSRKKKSKATQLSPEDRVEDALPPSKAPSRTRAKRDLPKR TATQRPEGTSLQQDPEAPTVPKKGRKGRQAASGHCRPRKVK DIPSLPEPGTSAS
554	1293	590	323	RKSSWLGAHAACNPSSLGGPGRQITRSGVRDQPGQYGETPSL LKIQTLAGRGGACL*SHILRRLRQKNRLNLGGRGCSELSRHC APA
555	1294	1	242	AWNSARGAVSPLWVPGCFLTSLVTWIGAAPLILSRIVGGWECE KHSQPWQVLVASRGRAVCGGVLVHPQWVLTAAHCIRK
556	1295	1074	230	AEMADDLGDEWWENQPTGAGSSPEASDGEGEDTEVMQOETVP VPVPSEKTKQPKCEFLIQPKERKENTTKTRKRRKKKITDVLAK SEPKPGLPEDLQKLMKDYSSRRLVIELEELNLPDSCFLKAND LTHSLSSYLKEICPKVWKLKRNHSEKKSVMILICSSAVRALE LIRSMTAFRGDGKVIKLFKHKIKVQAQVKLLEKRVVHLGVGTP GRIKELVKQGGNLNLSPLKFLVFDWNWRDQKLRRMDIPEIRKE VFELLEMVLSLCKSESILKGLF
557	1296	929	289	RPGTAIWVVECEHGRPIAESEGEGRGHSPPGPCSVAGFLRGR LGRNLEIMGSTWGS PGWVRLALCLTGLVLSLYALHVKAARARD RDYRALCDVGTAISCSRVFSSRWGRGFLVEHVLGQDSILNQS NSIFGCIFYTLQLLLGLRTRWASVLMLLSSLVSLAGSVYLA WILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRH

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
558	1297	2	1063	ESPAPPAPFRPAMA AVALMPPELLLLLLLLLASPPAASAPSARDPF APQLGDTQNCQLRCRDRDLGPQPSQAGLEGASESPYDRAVLIS ACERGCRLFSICRFVARSSKPNATQTECEAACVEAYVKEAEQQ ACSHGCWSQPAEPEPEQKRKVL EAPSGALSLLDLFSTLCNDLV NSAQGFVSSWTYYLQTDNGKVVFQTPQPIVESLGFQGGRLQR VEVTWRGSHPEALEVHVDPVGPLDKVRKAKIRVKTSSKAKVES EEPQDNDFLSCMSRRSGLPRWILACCLFLSVLWMLWLS CSTLV TAPGQHLKFQPLTLEQHKGFMMEPDWPLYPPPSHACEDSLPPY KLKLDLTKL
559	1298	2	485	FPELGTSLSAMRFLAATFLLALSTAAQAEVPQFKDCGSVDGV IKEVNVSPCPTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHG ILMGVPVFPFPIPEPDGCKSGINCPIQKDKTYSYLNKLPVKSEY PSIKLVVEWQLQDDKNQSLFCWEIPVQIVSHL
560	1299	1304	919	APETFRVCVWRLQGLTFIAFTELQAKVIDTQQVKLADIQIEQL NRTKKHAHLTDTEIMTLVDETNMYEGVGRMFIQSKEAHSQ LEKQKIAEEKIKELEQKKS YLERSVKEADNIREMLMARRAQ
561	1300	3	799	HSLLLGTRVRDASSKIQGEYTLTLRKGGNNKLSRVFHRDGHY FSEPLTFCSVVDLINHYRHESLAQYNALDTRLLYPVSKYQV RAGLGAREGSTWLAPGLSFLGRPDQAMHLPFRHVSP\ DQIVK EDSVEAVGAQLKVYHQYQDKSREYDQLYEYTRTSQELQMKR TAIEAFNETIKIFEEQQTQEKCSKEYLERFRREGN/QTKEMQ RIILLNSERLKSRIA\ EI HESPHRSWEQQLLVPRASDNKRD/ID KPH* TSLKPD L
562	1301	1772	301	AAAAAGRGSSGRRRRRPGALFASLGVLGPRPPPGIPRTRA CSMGGVGEPGREGPAQPGAPLPTFCWEQIRAHQDQPGDKWLVI ERRVYDISRWAQRHPGGSRLIGHHGAEDATDAFRAFHQDLNFV RKFLQPLLIGELAPEEPSQDGPLNAQLVEDFRALHQAEDMKL FDASPTFFAFLGHILAMEVLAWLLIYLLGPGWVPSALAAFIL AISQAQSWCLQHDLGHASIFKKS WNNHVAQKFVMGQLKGFSAH WWNFRHFQHHAKPNI FHKDPDVTVPVFLGESSVEYGKKRR YLPYNQOHL YFFLIGPPLLTLVNFEVENLAYMLVCMQWADLLW AASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHWFVWITQMN HIPKEIGHEKHRDWSSQLAATCNVEPSLFTNWFSGHLNFQIE HHLFPRMPRHNYSRVAPLVKSLCAKHGLSYEVKPFALTALVDIV RSLKKS GDIWLDAYLHQ
563	1302	424	93	KSRATRLRESAEMTGFLPPASRGTRRSCSRSRKRQTRRRRNP SSFVASCP TLLPFACVPGASPTTLA FPPVLTGPSTDGIPFAL SLQRVPFVLPSPQVASLPLGHSRG
564	1303	1	414	IQYRSDLELHSITMKKSGVLFLLGIILLVLIGVQGTPVVRKGR CSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIATLKNGVQT CLNPDSADVKKELIKKWEKQVSQKKKQKNGKKHQKKVKLVKRS QRSRQKKT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
565	1304	7	3007	IPGSTISCRGCCGKWPVQEADEPPRAALRGRFPALLTRHCPSPRAEKEKRSLLRRCGCRPLLVELAGPAGQAVEVLPHFESLGKQEKIPNKMSAFRNHCPHLDVSGEITKEDLIQKSLGTCQDCKVQGPNLWACLENRCSYVGCESQVDHSTIHSQETKHYLTVNLTTLRVWCYACSKVEFLDRKLGTPSLPHVRQPHQIQENSVQDFKIPSNTTLKKTPLVAVFDDLDIEADEEDELRRAGLTGLKNIGNTCYMNAAALQALSNCPPPLTQFFLDCCGLARTDKKPAICKSYLKLMTLWYKSRPGSVVPTTLFQGIKTVNPTFRGYSQQDAQEFLRCLMDLLHEELKEQVMEVEEDPQTITTEETMEEDKSQSDVDFQSCESCNSDR AENENGSRCFSEDNNETTMLIQDDENNSEMSKDWQKEKMCNKI NKVNSEGEFDKDRDSISETVDLNNQETVKVQIHSRASEYITDV HSNDLSTPQILPSNEGVPNRLSASPPKSGNLWPLAPPKKQAQ SASPKRKKQHKKYRSVISDIFDGTIISSVQCLTCDRVSVTLET FQDLSLPIPGKEDLAKLHSSSSHPTSIVKAGSCGEAYAPQGWIA FFM EYVKRFVWSCVPSWFWGPPVTLQDCLAFFARDELKGDNM YSCEKCKKLNRNGVKFKVQNFPEILCIHLKRFRHELMFSTKIS THVSFPLEGLDLQPFLLAKDSPAQIVTYDLSVICHHGTAASSGH YIAYCRNNLNLWYEFDDQSVTEVSESTVQNAEAYVLFYRKSS EEAQKERRRISNLLNIMEPSLLQFYISRQWLNKFKTFAEPGPI SNNDFLCIHGGVPPRKAGYIEDLVMLPQNIWDNLYSRYGGGP AVNHLYICHTCQIEAEKIEKRRKTELEIFIRLNRAFQKEDSPA TFYCISMQWFREWESFVKGKDGDPPGPIDNTKIAVTKCGNVML RQGADSGQISEETWNFLQSIYGGGPEVILRPPVHVDPDILQA EEKIEVETRSL
566	1305	28	450	SPSAAGGLAWVSLALGSGSRGRDHSGSGVGTAMAGALVRKAAD YVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGR MTFALCCYSLTFMRFAVKVQPRNWLLFACHATNEVAQLIQGGR LIKHEMTKTASA
567	1306	133	1292	LGSROAAGTMRGQRSLLLGPARLCLRLLLLLGYRRRCPPLLRG LVQRWRYGKVCRLSLLYNSFGGSDTAVDAAFEPPVYWLVDNVIR WFGVVVVLVIVLTGSIVAIAYLCVLPILRTYSVPRLCWHFF YSHWNLIIVFHYQAITTPPGYPPQGRNDIATVSIKKKCIYP KPARTHCSICNRCVLKMDHHCPLNNCVGHYNHRYFFSFCFF MTLGCVCYCSYGSWDLFREAYAAIEKMKQLDKNKLQAVANQTYH QTPPPTFSFRERMTHKSLVYLWFLCSSVALALGALTVWHAVLI SRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWKVFLG VDTGRHWLTRVLLPSSHLPHGNGMSWEPPWVTAHSASVMAV
568	1307	66	962	ATRRRAAEAGMAAVLQRVERLSNRVVRVLGCNPGPMTLQGTNT YLVGTGPRRILIDTGEPAIPEYISCLKQALTEFNIAIQEIVVT HWRDHSGGIGDICKSINNDTTYCIKKLPRNPQOREEIIIGNGEQ QYVYLKGDGVIKTEGATLRVLYTPGHTDDHMLALLEENAI FS GDCILGEGTTVFEDLYDMNSLKELLKIKADIIYPGHGPVIHN AEAKIQQYISHRNIREQQILTLFRENFEKSFTVMELVKIIYKN TPENLHEMAKHNLHLKKLEKEGKIFSNTDPDKKWKHAHL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
569	1308	96	1017	ELHRAGQVAGGARRSRRESMELERIVSAALLAFVQTHLPEADL SGLDEVIFSYVLGVLEDLGPGSPSEENFDMFAFTMEMEAYVPG FAHIPRGTIGDMMQKLSGQLSDARNKENLQPSSSGVQGVPI PEPLQRPEMLKEETRSSAAAAADTQDEATGAEELLPGVDVLL EVFPTCSVEQAQWVLAKARGDLEEAVQMLVEGKEEGPAWEGP NQDLPRRLRGPQKDELKSFILQKYMVDS AEDQKIHRPMAKPE APKKLIRYIDNQVVSTKGERFKDVRNPEAEEMKATYINLKPAR KYRFH
570	1309	3	526	FITGKGIVAILRCLQFNETLTTELRFHNQRHMLGHHAEIMEIARL LKANNTLLKMGYHFEFGPRMVVTNLLTRNQDKQRQKRQEEQK QQQLKEQKKLIAMLENGLGPPGMWELLGGPKPDSRMQEFFQP PPPRPPNPQNVFQSQRSEMMKKPSQAPKYRTDPSFRVVKLR IQ
571	1310	3	1858	GGRAGTQCCWRAGARLRGISPSPALPEAPGLCRVRAGLGAGAL GRSPAGRRRRGPRVSSSPAPHPRRVLCRCLLFLFFSCHDRRGD SQPYQALKYSSKSHPSGDRHEKMRDAGDPSPPNKMLRRSDS PENKYS DSTGHSKAKNVHTRVRERDGGTSYSPQENSHNHSAL HSSNFTFFLIPSN*PQGKTFRIAPYDS\ADDW/SLEHISSSGE KYYNCRTEVSQWGKTPKSGLERGQRQKEANKMAVNSFPKDRD YRREVMQATATSGFASGKSTSGDKPVSHSCTTPSTSSASGLNP TSAPPTSASA\VPVSP\VPQ\SPIPPLLQDPNLLRQLL\PALE ATLQLNNSNVDI\SIINEVLTGDTVQASLQTIHKCLTAGPSV FKITSLISQAQLSTQAQASNQSPMSLTSDASSPR\SYVSPRN KAHLKLNTVPIQTFGFSTPPVSSQPKVSTPVVKQGPVSQSATQ QPVTADKQQGHEPVSPRSLQRSSSQSPSPGNHTSNSSNASN ATVVPQNSSARSTCSLTPALAAHFSENLIKHVQGW PADHA EKQ ASRLREBAHNMGTIHMSEICTELKNLRS LVRVCEIQATLREQR ILFLRQQIKELEKLNQNSFMV
572	1311	2	1165	VAPECRGAYPFRAMMPGTALKAVLLAVLLVGLQTATGRLLSGQ PVCRRGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGDWIGLRRREEKQSNSTACQDL YAWTDGSISQFRNWWYDEPSCGSEVCVMYHQPSAPAGIGGPY MFQWNDRCNMKNNFICKYSDEKPAVPSREAEGETELTTPVL PEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLLVTTTV CWVWICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIR KQSEADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPS ESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENEIYGY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
573	1312	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILRCRRLPEPSPFLT QPNLAQSQPPAPVPVTDPSVTMHPAVFLSLPDLRCSLLLLVTW VFTPVTTEITSLDTENIDEILNNADVALVNFYADWCRFSQMLH PIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYP TLKLFNRNGMMMKREYRGQRSVKALADYIRQQKSDPIQEIRDLA EITTLDRSKRNIIGYFEQKDSDNRYRVFERVANILHDDCAFLSA FGDVSKPERYSGDNIYKPPGHSAPDMVYLGAMTNFDVTYNWI QDKCVPLVREITFENGEEELTEEGLPFLILFHKEDTESLEIFQ NEVARQLISEKGTINFLHADCDKFRHPLLHIQKTPADCPVIAI DSFRHMYVFGDFKDVLPGLKQFVFDLHSGKLHREFHHGPD TDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
574	1313	928	142	LTPSVGPVFPGRPTRPLASFPFVPLHRCSAGSQPPGVPVEGLI RIYSMRFCPPYSHRTRLVLKAKDIRHEVVNINLRNKPEWYYTKH PFGHIPVLETSQCQLIYESVIACEYLD DAYPGRKLFPYDPYER ARQKMLLELFCKVPHLTKECLVALRCGRECTNLKAALRQEFNS LEEILEYQNTTFFGGTCIS MIDYLLWPWFERLDVYGILDCVSH TPALRLWISAMKWDPTVCALLMDKSI FQGFNLNLYFQNNPNAFD FGLC
575	1314	884	363	NTATNMTQPNAGTRKYSVPAISVHTSSSSSFAYDREFLRTLPGF LIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVF FLIIYITMTYTRI PQVPWTTVGLCFNGSAFVLYLSAAVVDASS VSPERDSHNFNNSWAASSFFAFLVTICYAGNTYFSFI AWRSTI Q
576	1315	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGG SSRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRSRRR HQKRYRRYSRSYSRSRSRSRRYRERRYGFTRRYRSPSRYR SRSRSRSRSGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWR DRSRTSRSRSTPFLRSEKDRMELLEIAKTNAAKALGTTNIDL ASLRTVPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQ I



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R= Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
577	1316	265	2300	AEGSTMDLTGMGIQLQNPNHPTGLLCKANQMRLAGTLCDVVI MVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQ QILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLET IQASDDNDTEATMADGGAEKKDKRKARYLKNIFISKHSSEESG YASVAGQSLPGPMVDQSPSVSTSFGLSAMSPTKAAVDSLMTIG QSLLOQTLPAGPEEPTLAGGGRHPGVAEVKTEMQVDEVPS QDSPGAAESSISGGMGDKVEERGKEGPGTPTRSSVITSARELH YGRESAEQVPPPAEAGQAPTGRPEHPAPPPKHLGIYSVLPN HKADAVLSMPSSVTSGLVHQPALAVSMDFTYGGLLPQGFQIR ELFSKLGELAVGMKSESRTIGEQCSCGVELPDNEAVEQHRKL HSGMKTGYGCELCGKRFLDSLRLRMHLLAHSAGAKAFVCDQCGA QFSKEDALETHRQTHGTDMAVFCLLCGKRFQAQSAQQHMEV HAGVRSYICSECNRTFPSTALKRHLRSHTGDHPYCEFCGSC FRDESTLKSHKRIHTGEKPYECNGCGKKFSLKHQLETHYRVHT GEKPFCEKLCQRSRDYSAMIKHLRTHNGASPYQCTICTEYCP SLSSMQKHMKGHKPEEIPPDWRIEKTYLYLCYV
578	1317	686	908	IWEAPTLLFTLAGGRALGHPPMQKGSQGCALPHPLPGASLPAQ PGPADHRGWECRIGGEASVFTHLFLPHSPT
579	1318	150	1204	ASGSPAPSSSSAMAAACGPGAAGYCLLLGLHLFLLTAGPALGW NDPDRMLLRDVKALTLHYDRYTTSSRLDPIQLKCVGGTAGCD SYTPKVIQCQKNGWDGYDVQWECKTDLDIAYKFGKTVVSCGY ESSEDQYVLRGSCGLEYNLDYTELGLOKLKESGKHGFASFSD YYYKWSADSCNMSGLITIVVLLGIAFVVYKFLSDGQYSPPP YSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGF GSAFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDS WYYPSPPSYPGTWNRAYSPLHGGSGSYSVCSNSDTKTRTASG YGGTRRR
580	1319	1208	276	GRCGAMAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGV NNPFLPQASRLQAKRDPSVSGPVHLFRLSGKCFSLVESTYKY EFCPFHNVTQHEQTFRWNAYSGILGIHWEIANNFTGMWMR DGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFTETPL VCHPHALLVYPTLPEALQRQWDQVEQDLADELITPQGHEKLLR TLFEDAGYLKTPENEPTQLEGGPDSLGFETLENCRAHKELS KEIKRLKGLLTQHGIPTPTETSNEHLGHETPRAKSPEQLR GDPGLRGS
581	1320	1074	132	NSFWSVFLVQEETEVARCNAQHRLRQSRDSKPDPSFRSQPID SSISFAGSDIQPLFSFASVDGTQVGEAEWAGPWAEATLLPGP GNRWPPRAGLSGNWLEEDGDWPSLPEVVGVSERELFRDALGA GCRILLICEMQLTHQLDLFPECRVTLFLKDVKNAGDLRRKAM EGTIDGSLINPTVIVDPFQILVAANKAVHLYKLGMKTRTLST EIIIFNLSPMNNISEALKKFGISANDTSILIVYIEEGEKQINQE YLISQVEGHQVSLKNLPEIMNITEVKKIYKLSSQEESIGTLLD AIIICRMSTKDV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
582	1321	5021	7694	<p>Q R S W A G P G A G P E A G T R P P A R G R R R Q P G N V D P R R R A P Q L R S Q M Q</p> <p>V A M A R A T T A T G N R L W P G L L I M L G S L C H R G S P C G L S T H I E I G H R</p> <p>A L E F L Q L H N G R V N Y R E L L L E H Q D A Y Q A G I V F P D C F Y P S I C K G G</p> <p>K F H D V S E S T H W T P F L N A S V H Y I R E N Y P L P W E K D T E K L V A F L F G</p> <p>I T S H M A A D V S W H S L G L E Q G F L R T M G A I D F H G S Y S E A H S A G D F G</p> <p>G D V L S Q F E F N F N Y L A R R W Y V P V K D L L G I Y E K L Y G R K V I T E N V I</p> <p>V D C S H I Q F L E M Y G E M L A V S K L Y P T Y S T K S P F L V E Q F Q E Y F L G G</p> <p>L D D M A F W S T N I Y H L T I F M L E N G T S D C N L P E N P L F I A C G G Q Q N H</p> <p>T Q G S K M Q K N D F H R N L T T S L T E S V D R N I N Y T E R G V F F S V N S W T P</p> <p>D S M S F I Y K A L E R N I R T M F I G G S Q L S Q K H V S S P L A S Y F L S F P Y A</p> <p>R L G W A M T S A D L N Q D G H G D L V V G A P G Y S R P G H I H I G R V Y L I Y G N</p> <p>D L G L P P V D L D L D K E A H R I L E G F Q P S G R F G S A L A V L D F N V D G V P</p> <p>D L A V G A P S V G S E Q L T Y K G A V Y V Y F G S K Q G M S S S P N I T I S C Q D</p> <p>I Y C N L G W T L L A A D V N G D S E P D L V I G S P F A P G G G K Q K G I V A A F Y</p> <p>S G P S L S D K E K L N V E A A N W T V R G E E D F S W F G Y S L H G V T V D N R T L</p> <p>L L V G S P T W K N A S R L G H L L H I R D E K K S L G R V Y G Y F P P N G Q S W F T</p> <p>I S G D K A M G K L G T S L S S G H V L M N G T L K Q V L L V G A P T Y D D V S K V A</p> <p>F L T V T L H Q G G A T R M Y A L T S D A Q P L L L S T F S G D R R F S R F G G V L H</p> <p>L S D L D D D G L D E I I M A A P L R I A D V T S G L I G G E D G R V Y V Y N G K E T</p> <p>T L G D M T G K C K S W I T P C P E E K A Q Y V L I S P E A S S R F G S S L I T V R S</p> <p>K A K N Q V V I A A G R S S L G A R L S G A L H V Y S L G S D</p>
583	1322	1	357	<p>S L R N S A R G L K M A A S A A R G A A A L R R S I N Q P V A F V R R I P W T A A S S</p> <p>Q L K E H F A Q F G H V R R C I L P F D K E T G F H R G L G W V Q F S S E E G L R N A</p> <p>L Q Q E N H I I D G V K V Q V H T R R P K L P Q T S D D E K K D F</p>
584	1323	1205	433	<p>G S S N I H S A S T H G F C H W F S S P S T L K R Q K Q A I R F Q K I R R Q M E A P G</p> <p>A P P R T L T W E A M E Q I R Y L H E E F P E S W S V P R L A E G F D V S T D V I R R</p> <p>V L K S K F L P T L E Q K L Q D Q K V L K K A G L A H S L Q H L R G S G N T S K L L</p> <p>P A G H S V S G S L L M P G H E A S S K D P N H S T A L K V I E S D T H R T N T P R R</p> <p>R K G R N K E I Q D L E E S F V P V A A P L G H P R E L Q K Y S S D S E S P R G T G S</p> <p>G A L P S G Q K L E E L K A E E P D N F S S K V V Q R G R E F F D S N G N F L Y R I</p>
585	1324	134	954	<p>E T R V K T S L E L L R T Q L E P T G T V G N T I M T S Q P V P N E T I I V L P S N V</p> <p>I N F S Q A E K P E P T N Q G D S L K K H L H A E I K V I G T I Q I L C G M M V L S</p> <p>L G I I L A S A S F S P N F T Q V T S T L L N S A Y P F I G P F F F I I S G S L S I A</p> <p>T E K R L T K L L V H S S L V G S I L S A L S A L V G F I I L S V K Q A T L N P A S L</p> <p>Q C E L D K N N I P T R S Y V S Y F Y H D S L Y T T D C Y T A K A S L A G T L S L M L</p> <p>I C T L L E F C L A V L T A V L R W K Q A Y S D F P G S V L F L P H S Y I G N S G M S</p> <p>S K M T H D C G Y E E L L T S</p>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
586	1325	106	1537	EMVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQP LFLTPYIEAGKIQKGRELSLVGPFPGGLNMKSYAGFLT VNKTYN SNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGPYV VTSNMTLRDRDFPWTTLTSMYIDNPVGTGFSFTDDTHGYAVN EDDVARDLYSALIQQFFQIFPEYKNNDFFVTGESYAGKYVPAIA HLIHSLNPVREVKNLNGIAIGDGYSDPESIIGGYAEFLYQIG LLDEKQKKYFQKQCHECIEHIRKQNWFEAFELDKLLDGD LTS DPSYFQNVGTGCSNYNFLRCTEPEDQLYYVKFSLSLPEVRQAIH VGNQTFNDGTIVEKYLRDVTQSVKPWLTEIMNMYKVLINYGQ LDIIVAAALTEERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVA GYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGD PYVG
587	1326	883	541	RDERAKVPFRSTEG\GRRRRRRMEAVVFVFSLLDCCALIFLSV YFIITLSDLECDYINARSCSKLNKWIPELIGHTIVTVLLLM SLHWFIFLLNLPVATWNIYRYIMVPSGNMGVFDPEIHNRGQL KSHMKEAMIKLGFHLLCFFMYLYSMILALIND
588	1327	1126	732	QSPGHGAPCQLSSSHSRNRLSPMARATLSAAPS NRLLRVA LLLLLLVAASRRRAAGAPLATELRQCCLQTLQGIHLKNIQSVKV KSPGPHCAQTEVIATLKNQKACLNPA SPVMVKIIIEKMLKNGK SN
589	1328	197	330	HPLSLVFLALNTGKEKSHPGGGGERPGLAGQGE PDHPAGARDG R
590	1329	1	1575	CTPVARSMATTATCTRTDDYQLFEELGKGAFSVVRR CVKKTSTQEYAAKIINTKKLSARDHQKLEREARICRL LKHPNIVRLHDS ISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILE SVNHIHQHDIVHRDLKPENLLASKCKGA AVKLADFGLAIEVQ GEQQAWFGFAGTPGYLSPEVLRKDPYGPVDI WACGVILYILL VGYPPFWDQHKLYQQIKAGAYDFPSPEWDTVTPEAKNLINQ MLTINPAKRITADQALKHPWVCQRSTVASMHRQETVECLRKF NARRKLKGAILTTMLVSRNFSAAKSLNKKSDGGVKPQSNKN SLVSPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCNTTTED EDLKVRKQEI IKITEQLIEAINNGDFEAYTKICDPGLTSFEPE ALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDA ACIAYIRLTQYIDGQGRPRTSQSEETRVWHRRDGKWLNVHYHC SGAPAAPLQ
591	1330	17	636	NRRTVKMLLELSEEHKEHLAFLPQVDSAVVAEFGRIAVEFLRR GANPKIYEGAARKLNVS SDTVQHGV EGLTYL TESSKLMISEL DFQDSVFLGFSEELNKLLQLYLDNRKEIRTI LSEL\APSLP SYHNLEWRDLVQLASRSLRQQIKPAVTIKLHLNQNGDHNTKVL QTD PATLHLVQQL EQALEEMKTNHCRRVVRNIK
592	1331	1	237	GTSIYLAHRVA\RAWELAQFIHHTSKKADVVLACGDSIVHPED LICCP LTGRSCLCDVHLLSSLLARLGRGYAVSLTNL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
593	1332	2506	1684	RGCGSCGYKPSAGPAWRPRPPPAVSPLRHPEPAKVLFSFSSCPL PALGRTGPSRAARAQSLTMASLFKKKTVDVKEQNRELRGTQ RAIIRDRAALEKQEKQLELEIKKMAKIGNKEACKVLAKQLVHL RKQKTRTFVSSKVTSMSTQTKVMNSQMKMAGAMSTTAKTMOA VNKKMDPQKTLQTMQNFQKENMKMEMTEEMINDTLDDIFDGSD DEEESQDIVNQVLDEIGIEISGKMAKAPSAARSLPSASTSKAT ISDEEIERQLKALGVD
594	1333	905	432	STDGNGAERLFAELRKMNARGLGSELKDSIPVTELSASGPFES HDLLRKGFSCVKNELLPSPLELSEKNFQLNQDKMNFSTLRNI QGLFAPLKLQMEFKAVQQVQRLPFLSSSNLSLDVLRGNDETIG FEDILNDPSQSEVMGEPHLMVEYKLGLL
595	1334	111	117	RNMKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQ ELCQCRPGEGNCSCCKECMLCLGALWDECCDCVGMCPNRYSD TPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIVSFPVAEEL SHHENLVSFLETVNQPHQNVSVPSNNVHAPYSSDK/E*LPTV DFFHSAPSCGLSM*SIIFFEET
596	1335	817	278	VGGVPTWLEGCGSGNPSPRSGGGPGARLTLPALQMTVHNLYLF DRNGVCLHYSEWHRRKKQAGIPKEEYKLMYGMFLSIRSFSVKM SPLDMKDGFLAFQTSRYKLHYETPTGIKVMNTDLGVGPIRD VLHHIYSALYVELVVKNPCLPLGQTVQSELFRSLDSYVRS LP FFSARAG
597	1336	171	881	PGLSQEPGSGMETVVIIVAGVLATIFLASFAALVLVCRQRYCR PRDLLQRYDSKPIVDLIGAMETQSEPSELEDDVVITNPHIEA ILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKM KTSASVSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTAL LLSVSHLVLTNRNACHLTGGLDWIDQSLSAABEHLEVLREAAL ASEPDKGLPGPEGFLQEQAISAI
598	1337	1078	594	VGMELPAVNLLKVILLGHWLLTTWGCIVFSGSYAWANFTTLALG VWAVAQRDSIDAI SMFLGGLLATIFLDIVHISIFYPRVSLTDT GRFGVGMAILSLLLKPLSCCFVYHMYRERGELLVHTGFLGSS QDRSAYQTIDSAAEPADPFAVPEGRSQDARGY
599	1338	717	116	PASRPLLGPDTGGSVANI FKGLVILPEMSLVIRNLQRVIPIRRA PLRSKIEIVRRILGVQKFDLGIICVDNKNIQHINRIYDRNVPTDVL SFPFHEHLKAGEFPQPDFDDYNLGDIFLGVEYIFHQCK ENEDYNDVLTVTATHGLCHLLGFTHTGTEAEWQQMFQKEKAVLD ELGRRGTGRLQPLTPGPLPEGAEGRVPF
600	1339	1	804	LRNALDVLHREVPRVLVNLVDLNPNTIMRQVFLGNPDKCPVQQ A/MLEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYP IKPAIENWGSDFLCTEWKASNSVPTS VHQLRPADIKVVAALGD SLTTAVGARPNNSDLPTS WRGLSWSIGGDGNLEHTTLPNII KKFNPYLLGFSTSTWEGTAGLNVAEGARARDMPAQAWDLVER MKNSPDINLEKDWKLVTLFIGGNDLCHYCENPEAHLATEYVQH IQQALDILSE

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F= Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
601	1340	1	860	VVEFLWSRRPSGSSDPRRRPASKCQMMEERANLMHMMKLSIK VLLQSALSIGRSLDADHAPLQQFFVVMCHKLKHLKVKKSF QNKSFPGPLELVEKLCPEASDIATSVRNLPKLTAVGRGRAWL YLALMQKKLADYLVKVLIDNKHLLSEFYEPALMMEEGMVI LLVGLNVLNLANL\CLKGEDLDSQVGVIDFSLYLKDVQDL DGGKEHERITDVLQDKNYVEELNRHLSCTVGDLDQTKIDGLEKTNSKL QERVSAATDRICSLQEEQQQLREQNELIR
602	1341	60	762	KPEGARRVQFVMGLFGKTQEKPPKELVNEWSLKIRKEMRVVDR QIRDIQREEEKVKRSVKDAKKGQKDVCIVLAKEMIRSRKAVS KLYASKAHMNSVLMGMKNQLAVLRVAGSLQKSTEVMMKAMQSLV KIPEIQATMRELSKEMMKAGIIEEMLEDTFESMDDQEEMEEEA EMEIDRILFEITAGALGKAPSKVTDALPEPEPPGAMAASEDEE EEEEALEAMQSRLATLRS
603	1342	3	456	RWNSIMELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPI LSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQCGCI YKDYRYRNFSQGNIHCSDKGSWCEQQQLCACDKEVAFCLKRNLD TYQKRLRFYWRPHCRGQTPGC
604	1343	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG INLSGFGSEQLDTNDESDVSSALSYILPYLSLRNLGAESILLP FTEQLFNVQDGDRLLSILKNRKSPSQSSLLGNKFKNKIF
605	1344	2	382	LPLTLLLAAPFAHLLLPBGHDQSPCWHPGALSPGTGLPLSWA MANSGQLLGLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQL RSKVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
606	1345	2	987	DPRVRPPLLQPPPPPLLPRLVILKMAPLDLDKYVETARLCKYLP ENDLKRCLDYVCDLLLEESNVQPVSTPVTVCGDHGHQFYDLCE LFRITGGQVPTDNYIFMGDFVDRGYYSLETFTYLLALKAKWPDR ITLLRGNHESRQITQVYGFYDECQTKYGNANAWRYCTKVFDM LTVAAALIDEQILCVHGGSLPDIKTLDQIRTIERNQEIPIHKGAF CDLVWSDPEDVDTWAI SPRGAGWLF GAKVTNEFVHINNLKLCR AHQLVHEGYKFMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVN TREPCLFRAVPDSERVIPRTTTPYFL
607	1346	10	768	SFAGAAARPSTPPASGRGAAPGRPGPSPMDLRAGDSWGM LACTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLA GTYLNYLGPPFNEPDPNPRLGAETLPRATVDLEVWRSNDKL RLTQNYEAYSHLLCYLRGLNRQAATAELRRSLAHFCTSLQGLL GSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL LKEQLQTLWRSKDFNRLKKKMPPAAAVTLHLGAHGF
608	1347	114	700	IKISLKKRSMGSGISGCPFFLWGLLALLGLALVISLIFNISHYV EKQRQDKMYSYSSDHTRVDEYYIEDTPIYGNLDDMISEPM DENCYEQMKARPEKSVNKMQEATPSAQATNETQMCYASLDH SVKGRRKPRKQNTHFSDKDGDEQLHAIDASVSKTTLVDSFSP ESQAV EENIHDDPIRLFGLIRAKREPIN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
609	1348	2	807	VEFHPQRRARAGARAPSMGVLLTQRTLLSLVLALLFPSMASMAA IGSCSKEYRVLLGQLQKQTDLMQDTSRLLDPIYRIQGLDVPKL REHCRERPGAFPSEETLRGLGRRCFLOTLNATLGCVLHRLADL EQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQL LDNSDTAEPTKAGRGASQPPTPTPASDAFQKLEGCRFLHGYH RFMHSVGRVFSKWGESPNRSRRHSPHQALRKGVRRTRPSRK GK RLMTRGQLPR
610	1349	2	418	DFPGRRFRLVWLLVLRLPWRVPGQLDPTTGRRFSEHKLCADDE CSMLMYRGEALEDFTGPD CRFVNFKKGD PVVYVKLARGWPEV WAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTNETDFVCFDGG RDDFHNYNV
611	1350	823	115	SPLGKEGQEEVRVKIKDLNEHIVCCLCAGYFVDATTITTECLHT FCKSCIVKYLQTSKYCPMCNIKIHTQPLNLKLDVRVMDIVY KLVPGLQDSEEKRIREFYQSRGLDRVTQPTGEEPALSNLGLPF SSFHDSKAHYRYDEQLNLCLERLSSGKDKNKSVLQNKYVRCS VRAEVRHLRRVLCHRLMLNPQHVLQLLFDNEVLDPDHMTMKQIWL SRWFGKPSPLLLQYSVKEKRR
612	1351	9	545	LWWYSAHA AVDAMMDVFGVGFPSKVPWKMSAEELNQCPSR WVRLGAEEALRTYSQIGIEATTRARATRKSLHVPYGDGEGE KVDIYFPDESSEATTRARATRKSLHVPYGDGEGEKVDIYFPD ESSEALPFFLFFHGGYQSGRHPGPHGRPGDPQRCVCPEAVSK QQAFSW
613	1352	49	902	GVRMASRGRRPEHGGPPELFYDETEARKYVRNSRMIDIQTRMA GRALELLYLPENKPCYLLDIGCGTGLSGSYLSDEGHYWVGLDI SPAMLDEAVDREIEGDLGLGDMGQGI PFKPGTFDGCISISAVQ WLCNANKKSENPAKRLYCFASLFSVLVRGSRVAVLQLYPENSE QLELITTTQATKAGFSGGMVVDYPNSAKAKFYLCFSGPSTFI PEGLSENQDEVEPRESVFTNERFPLRMSRRGMVRKSRRAWLEK KERHRRQGREVRPDTQYTGRKRKPRF
614	1353	1960	871	TLICRMAGCGEIDHSINMLPTNRKANESCSNTAPSLTVPECAI CLQTCVHPVSLPCKHVFCYLCVKGASWLGKRCALCRQEIPEDF LDKPTLLSPEELKAASRGNGEYAWYIEGRNGWQYDERTSREL EDAFSGKKNTTEMLIAGFLYVADLENMVQYRRNEHGRRRKI KR DIIDIPKKG VAGLRLCDANTVNLARESSADGADSVSAQSGAS VQPLVSSVRPLTSVDGQLTSPATPSPDASTSLED SFAHLQLSG DN TAERSHRGEGEEDHESPSSGRVPAPDTSIETESDASSDSE DVSAVVAQHSLTQQRLLVSNANQTVPDRSDRSGTDRSVAGGGT VSVSVRSRRPDGQCTVTEV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
615	1354	5653	4549	GATPLGSVGGRTGKMDAATLTyDtlRFAEFEDFPETSEPVWIL GRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGW GCMLRCQMIFAQALVCRHLGRDWRWTQRKRQPDsyFsvLNAF IDRKDSYYSIHQIAQMGVGEgKSIGQWYGpNTVAQVLKKLAVF DTWSSLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDR HCNGFPAGAEVTNRPSpWRPLVLLIPLRLGLTDINEAYVETLK HCFMMPQSLGVIGGKPNsAHYFIGYVGEELIYLDpHTTQPAVE PTDGCfIPDESfHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKtFGfLRRFFfSMLG
616	1355	416	65	PTTSNRAITLTAWPKIPFLGICEAKNPRSENMLATILEVACH HLGSGPPPSWELWEQGGPPGNSSRYIEFLNKHTYIKGTLRVYTK KFCMLVIKSFESKSCVCVYDFDSKSSVNVTV
617	1356	2	382	PRVRFRLLHVTSIRSAWILCGIiWILIMASSIMLLDSGSEQNG SVTSCLELNLYKIAKLQTVNYIALVVGCLLPFFTLsICyLLII RVLLKVEVPESGLRVSHRKALtTIIITLIIFFLCFLPYHT
618	1357	3	672	GRHWLGSaQLTDGGSARKPKMAVPAALILRESpmKKAVSLIN AIDTGRFPRLLTRILQKLHLKAESSFSEEEEEKLQAaFSLEKQ DLHLVLETISFILEQAVYHNvKPAALQQQLENIHLRQDKAEAF VNTWSSMGQETVEKFRQRI LAPCKLETVGWQLNLQMAHSAQAK LKSPQAVLQLGVNNEDSKSLEKVLVEFShKELFDfYNKLETIQ AQLDSLt
619	1358	557	208	EASSAKTKRKEEKGPkAKMKLMVLVFTIGLTLllGVQAMPANR LSCYRKILKDHnCHNLPEGVADLTQIDVNVQDHfWDGKGCEMI CYCNfSELLCCPKDVFFGPKISfVIPCNNQ
620	1359	335	1735	KMAEAVFHAPKRKRrvYETYESPLPIPFQDhGpLKEFKIFRA EMINNNVIVRNAEDIEQLYGKGyFGKILSRSRPSFTISDPKL VAKWKDMKTnMPIITSKRYQHSVEWAAELMRQGGDESTVRRI LKDYTKPLEHPPVKRNEEAQVHDKLNSGMVSNMEGTAGGERPS VVNGDSGKSGGVDPREPLGCLQEGSGCHPTTESFEKSvREDA SPLPHVCCCKQDALILQRLHHEDGSQHIGLLHPGDRGDHEY VLVEEAECAMSEREAAPNEELVQRNRLICRRNPYRIFeYLQLS LEEaFFLVYALGCLSIYYEKEPLTIVKLWKAFTVVQPTFRtTY MAYHYFRSKGWVPKVLKYGTDLLLYRKGPpFYHASYSViiEL VDDHFEGSLRRPLSWKSLAALSrvSVNVSKELMLCYLIKpSTM TDKEMESPECMKRIKVQEVILSRWSSRERSDQDDL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
621	1360	5693	4435	RDIWTMNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHNRRRLNLIATAQAQNNQQTEGVKTEESEPLPSCPGSPPLPDDLPLDCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRKDYHSMYMLQISKQLSEEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELADLASGDQSLPMGVLGASERFPPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQSEEGNVSGHGVLSGSDVFEPMSEAGIPQSPDSDSSYSGSHSTDLSLMGSSPVFNQRCCKMRKI
622	1361	15	678	REQILFIEIRDTAKGGETEQQPSLSPLHGGRMPMEMGEGIQSLARETQSHRGRQGWDTWVTRCRESLNRGGAGAGKRAGALAHVFLALIEPNLAEREASEEEVKACSDETVVADLLVKVVVLGAILKIFLREGNVLNQHSMDIEKYSEHYQHDHSPGAEDDAAGGQLRPTAQERRHKEGSRGSPRCKRARKAVGESPGCPRPRVRPRVRPRVRPRV
623	1362	1080	835	GTRGCCREGTAYAKAYQFMASHLSLGKPVSTGSI PRFNKALFNKQAKCKPNHYSFIGLSMLSPENFSIGCKYSVWFSETKGF
624	1363	872	441	GAQGVVRVGIGEVGRVQAPRVSLLSHQGVPRGGTGEAVKEEGRGSSLHPPLPPQGLGEYAAQCASHAFMKGVFTFVTGTGMAGLQMF IQRKFPYPLQWSSLVAVVAGSVVSYGVTTRVESEKCNLWLFLETGQLPKDRSTDQRS
625	1364	1	585	GTSELLCIQRWNWGPAPPPRGLALAPTLOLLVEMGSAKSVPVTPARPPPHNKHARVADPRSPSAGILRTPIQVESSPQGLPAGEQLEGLKHAQDSDPRSPLGKN*GHGWQVQGSDLGSPQPLPPSASHL/YSSRASRCSQPPCLSLPWFGRSSPANTYHVPVTS LCPSPALHYTALQAGIISTSQARAPR
626	1365	36	381	PLLLPRFIDIPCLLCYLTQVTPDDMYAKAFLIKPNATITGTDRKKL\RADETTDFP\TLGTDQIYELLPGKDELNIVKSNHAKRDA*TAYVSGENHILSEP*KNLYPAVNTLSSYP
627	1366	763	1003	SRQPPPLTMTVFLLEFLFLVFFPGCVNQLLSYPWQGGTSLWSSLSFHWLLPQEDSSRLSIFPLRAGSPPPQPAQAPQRI
628	1367	296	1199	KSREQSSLFAADAERSWGGKSCCLLRWRVFGKASHFPRLPLPGEERPETERAWKMEQTWTRDYFAEDDGEMVPRTSHTA/ASVSLTAFLSDTKDRGPPVQSQIWRSGEKVPFVQTYSLRAFEKPPQVQTQALRDFEKHLNDLKKENFSLKLLIYFLEERMQQKYEASREDIYKRNTLKVESLSKRELQDKKQHLDKTWADVENLNSQNEAELRRQFEERQQEMEHHVYELLENKMQLLQEE SRLAKNEARMAALVEAEKECNLELSEKLGVTKNWEDVPGDQVKPDQYTEALAQDK



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
629	1368	191	1116	TRRRGTTWRSRPRRASTRPSTRPRGVASWPWETAGTATTGPGPSARTRRRAARRRRSRPRRAHGGLSQPAGWQSLLSFTILFLAWLAGFSSRLFAVIRFESIIEFDPWFNYRSTHHLASHGFYEF LNWFDERAWYPLGRIVGGTVYPGLMITAGLIHWILNTLINITVH IRDVCVFLAPTFSGLTSTSTFLTLRELWNQAGLLAACFIAIV PGYISRSVAGSFDNEGIAIFALQFTYYLWVKSVKTGSVFWTMC CCLSYFYMVSAWGGYVFIINLIPLHAFVLVLM/Q/RYSKRVIYI *YSTFYIVG
630	1369	852	214	RRLIVVLSDAFLSRAWCSHSF/RVGPARGWVGPSVAPTPLTVP PRREGLCRLLLELTRRPIFITFEGQRRDPAHPALRLLRQHRHLV TLLLWRPGSVTPSSDFWKEVQLALPRKVRYRPVEGDPQTQLQD DKDPMLILRGRVPEGRALDSEVDPDPEGDLGVRGPVFGEPSAP PHTSGVSLGESRSSEVDVSDLGSRNYSARTDFYCLVSKDDM
631	1370	246	1091	LSHEGWRRGREGERINSSVASLAPLCILPDLPSNMHLARLVGS CSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALD GINSGITHAGREVEKVFNGLSNMGSHTGKELDKGVQGLNHGMD KVAHEINHIGIGQAGKEAEKLGHVNNAAAGQAGKEADKAVQGFH TGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAG KELQNAHNGVNOASKEANQLLNGNHQSGSSSHQGGATTTPLAS GASVNTPFINLPALWRSVANIMP
632	1371	3150	2792	SASGGLGMTVEGPEGSEREHRPPEKPPRPPRPLHLSDRSFRRK KDSVESHTPTVDDTRIDADAIVEKIVQSQDFTDGSNTEDSNLR LFVSRDGSATLSGIQLATRVSSGVYEPVVIESH
633	1372	667	993	ERSGWFPQEGTVTAQGPLFWERLSGAVTVSSGYKADMWPSFPQ \VRVGSFLFGILFFSFGSSSLPPGLPPPASLLCCAVQWGARAL FLPCLKERALGMEMRNNTLSFRQ
634	1373	636	2	SSSNLRLSFLINENILGKCFRSGPSCAGPRISPLAAQYECPRP SLLIMASVPKTNKIEPRSYSIIPSCGI\RLGPAINTLIF\QS KRFGPRG\HSAKSIEGAPRGKGRGRAVARLAADRPPAPKIQLR AF*LQQL*YTLLELELPRL LAPDLPSNGSSSLKDLKWTSHNYRA SKESCIVIF\VTSPGREWVICALAAFLGCGS\LSQAPSPES
635	1374	61	519	LRIINTYFCFKFLIVNYIHGTTKARKPHVLGESLISAMSRQEP KMFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGP PGPPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKT GPLGLAGEKGDQGETGKKGPIGPE
636	1375	129	579	FASAMLGSRVDRPKLSVAPSVVLEEDQVLVSPAVDLEAGCRLR DFTEKIMNVKGVILSMLVVSTVIIIVFEFINSTEGSFLWIYH SKNPEVDDSSAQKGWFLSWFNNGIHNYQQGEEDIDKEKGREE TKGRKMTQQSFGYGTGLIQT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
637	1376	127	1376	GSHRFSIASPLDPEVGPHYCDTPTMRTLNFLLWLALACSPVHTT LSKSDAKKAASKTLLLEKSQFSDKPVQDRGLVVTDLKAESVVL HRSYCSAKARDRHAFAGDVLGYVTPWNSHGYDVTKVFGSKFTQI SPVWLQLKRRGREMFVETGLHDVDQGWMAVRKHAKGLHIVPR LLFEDWTYDDFRNVLDSEDEIEELS KTVVQVAKNQHFDDGFVVE VWNQLLSQKRVGLIHMLTHLAEALHQARLLALLVIPPATPGT DQLGMFTHKEFEQLAPVLDGFSLMTYDYSTAHPGPNAPLSWV RACVQVLDPKSKWRSKILLGLNFYGM DYATSKDAREPVVGARY IQTLKDRPRMVWDSQVSEHFF EYKKSRSRGRHVVFYPTLSLQ VRLELARELGVGVS IWELGQGLDYFYDLL
638	1377	998	48	GREGTGWGPAMSEVTRSLRQWGFRRGADFD SWGQLV E AID EYQILARHLQKEAQAQHNNSEFTEEQKKTIGKIATCLELRSA LQSTQSQEEFKLEDLKKLEPILKNILTYNKEFPFDVQVPPLRR ILAPGEEENLEFEDEEEGGAGAGSPDSFPARVPGTLLPRLPS EPGMTLLTIRIEKIGLKDAGQCINPYITVSVKDLNGIDLTPVQ DTPVASRKEDTYVHFNVDI ELQKHVEKLTGAAIFFEFKHYKP KKRFTSTKCF AFMEMDEIKLGPIVIELYKKPTDFKRQLQLLT KKPLYLHLHQTLHKE
639	1378	1298	1569	GSITSEPSLDSLQPLPPGFKRFSCLSLPSSWDYRRPPGLAYF CIFSRDEVSPCWPGCSPSPDLMIRLPRPPSVGITGVSHRAWPT IDNF
640	1379	196	1197	KMPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCLRW DSDILCLPGDIVPAGPVLAPTHLQTELVLRCQKETDCDLCLR VAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVL FQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEV RIWSTYTPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGPCKPRWHKNLVRP PPSQVHSHCRP\CLCK\DAVPYQRGSLKRTHPKQKGKGGGTS AFLVSLTLASSSSSLSSPTSFLYLFHRLDRSLP
641	1380	756	1110	LRLWNRNQMMHNIIVKELIVTFFLGITVVQMLISVTGLKGVEA QNGSESEVFGKYETLVFYWPSLLCLAFLLGRFLHMFVKALRV HLGWELQVEEKSVLEVHQGEHVQQLLRIPRP
642	1381	631	1278	KVNRKLRKKGKISHDKRKSRSKAIGSDTSDIVHIWCPEGMKT SDIKELNIVLPEFEKTHLEHQQRIESKVC KAAIATFYVNVKEQ FIKMLKESQMLTNLKRKNAMISDIEKKRQRMIEVQDELLRLE PQLKQLQTKYDELKERKSSLRNAAYFLSNLKLQYQDYSDVQAAQ EPNVKETYDSSSLPALLFKARTLLGAESHLRNINHLEKLLDQ G
643	1382	1167	755	VWVAMEEPPVREEE*EEGEDEERDEVGPEGALGKSPFQLTAE DVYDISYLLGRELMA LGS DPRVTQLQFKVVRVLEMLEALVNEG SLALEELKMERDHLRKEVEGLRRQSP PASGEWPDSTKRPRRK KRKRCCGY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
644	1383	1	271	PRNDHRLTQSRDSSSKTRAFIVPRFLPAHAGVTSEERTAMKR EGGAHLCSDSLPESSQQQDGNHAPNFSSHGSCRRRRQRRRHDKA LHAR
645	1384	1	499	THASEKSRATMSSWSRQRPKSPGGIOPHVSRTLFLLLLLLAASA WGVTLSPKDCQVFRSDHGSSISCQPPAEIPGYLPADTVHLAVE FFNLTHLPANLLQGASKLQELHLSSNGLESLSPEFLRPVPQRLR VLDLTRNALTGPPGLFQASATLDTLVLENQLEVLE
646	1385	178	675	ERPRIMDLAGLLKSQFLCHLVFCYVFIFASGLIINTIQFTLLL WPINKQLFRKINCRLSYCISSQLVLMLEWWSGTECTIFTDPRA YLKYGKENAIVVLNHF\EI\DFLCGWSLSERFGLLGVSQKCI PPCLTHFFGSAPPLVFLLLVIQNLQKNQSFYLMKWS
647	1386	630	1499	MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNS CICRDDSGTDDSDVTQQQQAENSAVPTADTRSQPRDPVRPPRR GRGPHEPRRKKQNVLDGLVLDLAVIRTLVDNDQEPYSMITLH EMAETDEGWLDVVQSLIRVIPLEDPGLPAVITLLDECPLPTK DALQKLTEILNLNGEVACQDSSHPAKHRNTSAVLGCLAELKLAG PASIGLLSPGILEYLLQCLLQSHPTVMLFALIALEKFAQTSEN KLTISSISSDRL\VTLESW\ANDPDYLKRQVG
648	1387	1	962	RFGTRGLAKSGVVLMAICALTRALRSLNLAPPTVAAPAPSLF PAAQMMNNGLLQQPSALMLLPCRPLVTSVALNANFVSWKSRTK YTITPVKMRKSGGRDHTGRIRVHGIGGGHKQRYRMIDFLRFRP EETKSGPFEEKVIQVRYDPCRSADIALVAGGSRKRWIIATENM QAGDTILNSNHIGRMAVAAREGDAHPLGALPVGTLINNVESEP GRGAQYIRAAGTCGVLLRKVNGTAIQLPSKRQMQVLETCVAT VGRVSNVDHNKRVIGKAGRNRWLGRPNSGRWHRKGGWAGRKI RPLPPMKSYVKLPSASAQS
649	1388	291	714	PVQGARCWLDARRNVRVFSVCCGCGIHGYWAEPCGGCGAMEG LRSSVELDPELTPGKLDEEMVGLPPHDASQVTFHSLDGKTVV CPHFMLGLLLGLLLLTLSVRNQLCVRGERQLAETLHSQVKEKS QLIGKKTDCRD
650	1389	874	2220	GARGRPLAETWPFLTAPVLPGLQITEPTMAEKGDCIASVYGY DLGGRFVDFQPLGFGVNLVLSAVDSRACRKVAVKKIALSDAR SMKHALREIKIIRRLDHDNIVKVYEVLPKGTDLQGLFKFSV AYIVQEYMETDLARLLEQGTIAEEHAKLFMYQLLRGLKYIHS NVLHRDLKPANIFISTEDLVKIGDFGLARIVDQHYS\HKGYL SEGLVTKWYRSPRLLSPNNYTKAIDMWAAGCILAEMLTGRML FAGAHELEQMQLILETIPVIREEDKDELLRVMPFSVSSTWEVK RPLRKLLEPVNSEAIDFLEKILTFNPMDRLEAEMGLQHPYMS YSCPEDEPTSQHPFRIEDEIDDIVLMAANQSQSLSNWDTCSRY PVSLSSDLEWRPDRCDASEVQRDPGRAGSAPLAENVQVDPKRD SHSSSASCQAGRNGVSRYQ

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
651	1390	1	2451	MRTLGTCLATLAGLLLTAAGETFSGGCLFDEPYSTCGYSQSEG DDFNWEQVNTLT KPTSDPWPMSGFMLVNASGRPEGQRAHLLL PQLKENDTHCIDFHYFVSSKSNSPGLLNVYVKVNNGLGNPI WNISGDPTRTWNRAELAISTFWPNFYQVIFEVITSGHQGYLAI DEVKVLGHPCTRTPHFLRIQNVEVNAGQFATFQCSAIGRTVAG DRLWLQGDIDVRDAPLKEIKVTSSRRFIASFNVNTTKRDAGKY RCMI\RTEGGVGISNYAEL\VVKEPPVPIAPPQLASVGATYLV IQLNANSINGDGPVAREVEYCTASGSWNDRQVPDSTSYKIGH LDPDTEYEISVLLTRPGEGGTGSPGPALRTRTKCADPMRGPRK LEVVEVKSQRQITIRWEPFGYNVTRCHSYNLTVHYCYQVGQEQ VREEVSWDTENSHPQHTITNLSPTYTNVSVKLILMNPEGRKESQ ELIVQTDDELPGAVPTESIQGSTFEEKIFLQWREPTQTYGVIT LYEITYKAVSSFDPEIDLNSQSGRVSKLGNETHLFFGLYPGT TYSFTIRASTAKGFGPPATNQFTTKISAPSPMPAYELETPLNQT DNTVTVMKPAHSRGAPVSVYQIVVEEERPRRTKTKTEILKCY FVPIHFQNASLLNSQYYFAAEFPADSLQAAQPFITGDNKTYNG YWNTPLLPHYKSYRIYFQAASRANGETKIDCVQVATKGAATPKP VPEPEKQTDHTVKIAGVIAGILLFVIIIFLGVLVLMKKRLYKHG ASICSASGEASGSFQSWRKAKHKQACPMARAGARERAGGCLKL
652	1391	30	459	GIRQLQLSRASMAARKSWTALRLCATVVVLDVCKGFVQDL DESFKENRNDDIWL VHFYAPWCGHCKKLEPIWNEAGLEMKSIG SPVKAGKMDATSYSSIASIEFGVRGYPTIKLALIRPLPSQQMFE HMHKRHRVFFVYV
653	1392	168	1016	GLVIVISHFSPSPGLLPATQSPAMSDPITLNVGGKLYTTSLAT LTSFPDSMLGAMFSGKMPTKRDSQGNCFIDRDGKVFRIYILNFI RTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKA EKNAMLNITLNQRVQTVHFTVREAPQIYSLSSSSMEVFNANIF STSCLFLKLLGSKLFYCSNGNLSSITSHLQDPNHLTLDWVANV EGLPEEYTKQNLKRLWVPANKQINSFQVFVEEVLKIALSDG FCIDSSHPHALDFMNNKIIRLIRY
654	1393	3	927	SCADNLVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGR RWAIASDDLVPFGFFELVVRVLWWIGILTLYLMHRGKLDCAGG ALLSSYLIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMS KLLYIRLALFFPEMVWASLGAAWVADGVQCDRTVVGIIATVV VSWIIIAATVVSIIIVFDPLGGKMAPYSSAGPSHLDSDSSQL LNLKTAATSVWETRIKLLCCCIKDDHTRVAFSSTAELFSTY FSDTDLVPSDIAAGLALLHQQQDNIRNNQ\DLPRWSAMPQGAP RKLIWMQN
655	1394	1	716	FRAATAAAKNGGGGGGRAGAGDASGTRKKKKGPGPLATAYLVII NVVMTAGWLVIAGVLVRAYLAKGSYHSLYSIEKPLKFFQTGA LLEILHCAIGIVPSSVVLTSFQVMSRVFLIWAIVTHSVKEVQSE DSVL\FVIAWTITEIIRYSFYTFSLNLHPYLIKRRARYTLFIV LYPMGVSGELLTIYAALPFVRQAGLYSISLPNSTKKIFLISQV WWHMLAVSADAKAAEMPAVLKPGP

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
656	1395	72	766	MLTGVGCLVSSSELSCVQCNSWEKSCVNSIASECPSHANTSCI SSSASSSLETVPRLYQNMFCSAENCSEETHITAFTHVHSAEEH FHFVSQCCEGKECSNTSDALDPPLKNVSSNÆECPACYESNGTS CRGKPKWCYEEECVFLVÆELKNDIESKSLVLKGCNSVSNATC QFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKAS LYLLALASLLLRGLLP
657	1396	97	746	VPARRAMEIGTEISRKIRSAIKGKLQELGAYVDEELPDYIMV MVANKKSQDQMTEDLSLFLGNNTIRFTVWLHGVLDKLRVSTE PSSLKSSDTNIFDSNVPSNKSNSFRGDERRHEAAVPP\AIPS ARPEKRSRVSTSSQESKTTNVRQTYDDGAATRLMSTV/KPLR EPAPSEDVIDIKPEPDDLIDEDLNFVQEKPLSQKKPTVTLTGY SSR
658	1397	155	560	ASRVLAAMGLPWGQPHLGLQMLLALNWLRLPSLSLELVPYTP QITAWDLEGKVTATTFSLQPRCVFDGLASADTVWLVAFSN ASRGFQNPETLADIPASPQLLTDGHYMTLPLSPDQLPCGDPMA GSGSAP
659	1398	416	539	NSLNNFFETESCCVAQAGVQWRDLGSLQAPPPGKFRFSC
660	1399	281	736	KSLPLQKHPKPCQEDQGLGRGSLSGHSPLTLLTFLTSCALGD QQLLPPTSGSLCQESMSQSCQMSLRLLLLGKCRSGKSATG NAILGKHVFKSFSDQTVIKMCQRESWVLREKVVVIDTPDLF SSIACAEDKQRNIQHLLLELSAP
661	1400	2	974	FVETTVSVQSAESSDALSWRLPRALASVGPPEARSGAPVGGG RWQLSDRVEGGSPTLGLLGGSPSAQPGTGNVEAGIPSGRMLEP LPCWDAAKDLKEPQCPGDRVGVQPGNSRVWQGTMEKAGLAWT RGTGVQSEGTWESQRQSDALPSPELLPQDQDKPFLRKACSPS NIPAVIITDMGTQEDGALEETQGS PRGNLPLRKLSSSSASSTG FSSSYEDSEEDISSDPERTLDPNSAFLHTLDQQKPRVVERSV TQAGVQWHDIGSLQPLPP/WIQAIL/HASAFRIAGTTGACHHA RIIFGFLVERGFHHVQDGLYLLIL
662	1401	232	3	KICSSYFLRIICILQKEAQEASNLTYSCDFFSPAIFYFVIYRLY NFKIHWP GAVAH TYSPSTLGGGRGWVT*GREFM
663	1402	250	556	LILSLPLLYGHLKSYTFPSEHYLHLLQTFATFNKYLNVCLIF IHHPVVPPIQGTNVGGSLEPRRLRLQQAMIVPLHFLGNRVR PCLKKQQQQQQQQKK
664	1403	1	373	RMETKPVITCLKTLIIYSFVFWITGVILLAAGVWGLTLGSY ISLIAENSTYAPYVLIVTGTITVAYPLV*FFFSYSSGFSYILA VRLIAGIALVYNIIPRSSRALVRLVLLRFLLSRHPS
665	1404	3	413	NAEHPGMDRDLCCQAKLAHAERDDDMAACMKTVTDQGAELS NEERNLLSDAHTNAV*ARRSSWMGA*RIEQKTEGADTQQQMAP DCREIFATELRDICCVDLSLLEKLLIPNASHA*SLVYYLHMIG DYRYRWL
666	1405	2	334	GGGPLGKMPRAQLADPWQMMAVESPSDCADNGQQIMDEPMGED EISPQTE*VSIKEVAVTHCVKEGHDKADPSQIELLRVLRQGS L GKVYLGGKVGSGDAKQLYAMKVL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
667	1406	2	332	DAAGIRHEAHFGKLECLVQLVRAGA\SLFVSTTRYAQTPA\HIAAFGGHPQCLVWLIQAGANINKPDCEGETPIHKAARSGSLECI SALVANGAHVDNPKKGIRVLEWLFE
668	1407	242	1157	LLKLMFIAELGDYDLAEHSPELVSEFRFVPIQTEEMELAI FEK WKEYRGQTPAQAEETNYLNKAKWLEMYGVDMHVVKARDGNDYSL GLTPTGVLVFEEDTKIGLFFWPKITRLDFKKNKLTLLVVEDDD QGKEQEHTFVFRDLHPKACKHLWKCAVEHHAFFRLRGPVQKSS HRSGFIRLGSFRYSKGTEYQTTKTNKARRSTSFERRPSKRY RRTLQMKACATKPEELSVHNNVSTQSNQSQAQWGMRSALPVSP SISSAPVPVEIENLPQSPGTDQHDRKWL SAASDCCQGGNQWN TRAL
669	1408	278	1	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNF AEF SKKCSGRWK TMSSKEKFKFGEMAKADEVCYDREM KDYGP AKGGKKDPNAPK RPPSGF
670	1409	139	646	AELGSGWAVWAGLGWAGRMEAGGATGALGVGSKLP S AFCFP SSVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDL *VLGRPLSYPPWATTWALPDPFPLSWSPRLTPLGAAQQLPLV LSPVHCLLTSLCRGPDCGVWMTCCQAQVS IAGALVILWG
671	1410	3	442	LCVSVLCFSYSYLNQGWASDPVHGYWFR\AGDHVSRNIPVATN NPVRAVQEETRDRFHLLGDPQNKDCTLSIRD TRES DAGTYVFC VERGNMKWNYKYDQLSVNVTASQDLLSRYRLEVPE SVTVQ EGL CVSVP/WQCPLPLQLDCL
672	1411	84	836	QLQLCQNCTKRGECHCVPDFDYIKTKKEKKRLSVLPPTRLMEA RFSPINQILPWCQRDLAISKAINTQEAPVKEKHARRIILGT HHEKGATTFWSYAIGLPLPSSSILSWKFCHVLHKVLRDGHNV LHDCQRYRSNIREIGDLWGHLH DRYGQLVNVYTKLLTKISFH LKHPQFPAGLEVTDVLEKAAGTDVNNM*VTLHGYMASSPRLP HSFLPRLTPRRPHGAVGLNESVALLVDAHAPDRG
673	1412	307	664	AAPHRMPRAPHFMPLLLLLLLLLSLPHQTAAFPQDPLPLLI QGTSPLSWLPSLEDDAVAA*LGLDFQRFLLNRTLLVAARDHV FSFDLQAE EGEGLVPNKYLTWRSQDVENCAVR*KLT LNRTLL VAARDHVFSFDLQAE EGEGLVPNKYLTWRSQDVENCAVR
674	1413	24	420	HLVPKTRGRGTPSGDQSPVLTLP*GDPPTILGPQTNQPK EHL TNFKSGKRSFHSLLQPLLLLLLHPSISPFLNFGSFPFLVETEET CFIHKLKT PALVTPDSLPLVFNHCGDACLI IHPHFRDVEFHHT GN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Aspartic Acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N = Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
675	1414	1	1101	CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLK PAKGLMSYRIITDFPSLTRNLPSQELPQEDSLHGFQFSQAVTP LAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDASAQL LAYKEKGHSQSSQFSSDQETIAHLLPENVSALPATVAVASPHTT SATPKPATLL\PTNASVTPSGTSQPQLA\TTAPPVTTVTSQPP TTLISTVFTRAAATLQAMATTAVLTTTTFQAPTDSKGSLETIPF TEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPG SSSQGSVPENQYGLPFKEWLLIGSLLFGVLFLVIGLVLLGRIL SESLRRKRYRLDYLINGIYVDI
676	1415	178	621	IFAGSGVMRLKISLLKEPKHQELVSCVGWTTAEELYSCSDDHH IVKWNLLTSETTQIVKLDDIYPIDFWFPKSLGVKKQTHAES FVLTSDDGKFHLISKLRVEKSV EAHCGAVLAGRWNYEGTALV TVGEDGQI*IWSKTGMLIS
677	1416	1258	944	ARATTKRHFILLFLFLRRC\LFLSPRMECNGAILAHCNLHLP GSSSSSASAS*VAGITDVRHHAQLILFVFLVETGFHRVQGAGL KLLTSGDLLTSASQSAGIIMGISHCAQPKKAF*TKTF
678	1417	876	1291	EAGSNDLAT*KTCGRARPSSRSRQFGSRVWNHRQGVRRSSPGE GAGSRSPCRRRHRRKHRRNVQSP*RRRSRSCSRSGRCSVALL GACPVAGHSRGKVVCRAHAITQRRRCGCFDPMVHPKEHRG*R ERSRKWSRS
679	1418	262	539	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNFAEFSKKCSGRWK TMSSKEKFKFGEMAKADEVCYDREMKDYGPAGKGKKKDPNAPK RPPSGF
680	1419	104	236	LTVNYVLVFSRDSGLRAIENLMQKKGKFDYILLETTGLADPGK K
681	1420	3	277	HEAALCRTRAVAAERHFLRVFLFRPFRGVGTESGSESGSSKA KEPRTPSSSYGTAQYRRWPIAQEYKHCTAHNDTGTLCELREP WRRPQ
682	1421	3	576	EGSSQANTLRSRKENRNLLACLESHVLR*QFTESHLCSLMGD NPFQPKSNSKMAELFMECEEELEPWQKKVKEVEDDDDEPIF VGEISSSKPAISNILNRVNPSSYSRGLKNGALSRGITAAFKPT SQHYTNPTSNPVPASPINFHPESRSSDSSVIGQPFSPKPVSVSK TIRPAQSGIGCCLSI
683	1422	6	627	CFSLEDILNFFLQGFSAFLAFYHDKDGNPLTSRFADGLPPFN YSLGLYQWSDKVVRKVERLWDVRDNKIVRHTVYLLVTPRVVEE ARKHFDPCVLEGMELNQGQGVGTENLHWEKRLLENEAMTGSHT QNRVLSRITLALMEDTGRQMLSPYCDTLRSNPLQLTCRQDQRA VAV\CNLQKFKPLPQEYQYFDELSGIPAEDLPYYG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
684	1423	1	1272	AARRRRQLVSRRTAE\YPRRRSSPSARPPDVPGQQPKAAKS PSPVQGGKSPRLLCIEKVTTDKDPKEEKEEEDDSALPQEV SIA ASRPSRGWRSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPN TDQLDYDVGEEHQSPGGISSEEEEEEEEEEMLISEEEIPFKDDP RDETYKPHLERETPKPRRKSGKVKEEKEKKEIKVEVEVEVKEE ENEIREDEEPPRKRGRRRKDDKS PRLPKRRKKPPIQYVRCME GCGTVLAHPRYLQHHIKYQHLLKKKYVCPHPSCGRFLRLQKQL LRHAKHHTDQRDYICEYCARAFKSSHNLAVHRMIHTGEKPLQC EICGFTCRQKASLNWHMCKHDADS FYQFSCNICGKKFEKKDSV VAHKAKSHPEVLIAEALANAGALITSTD ILGTNPES
685	1424	56	526	MTANRLAESLLALSQQEELADLPKDYLLSESEDEGDNDGERKH QKLLAEISSLDGKNRRKLAERSEASLKVSEFNVSSSEGSGEKLV LADLLEPVKTSSSLATVKKQLSRVSKSKTVELPLNKEEIERIH REVAFNKTAQVLSKWDPVVLKNRQAEQL*
686	1425	132	344	RIDFMFHSSAMVNSHRKPMFNIHRGFYCLTAILPQICICSQFS VPSSYHFTEDPGAFPVATNGERFPWQELRLPSVVIPLHYDLFV HPNLTSLDFVASEKIEVLVSNAQTQLIILHSDKLEITNATLQSE EDSRYMKPGKELKVLSPAEQIALLVPEKLTPLHKYVAMDF QAKLGDGFEGFYKSTYRTLGGETRILAVTDFEPTQARMAFP CF DEPLFKANFSIKIRRESRHIALSNMPKVKTIELEGGLEDHFE TTVKMSTYLVAI/DL*FPLMGNDFLGRS
687	1426	3	678	RSKIPRSDPRVRTPAPAEAEQGKSQCPSGSTAQSWSAM DILVP LLQLLVLLLTPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNR KMESKKRELFSQIKGLTGASGKVALLELGC GTGANFQFYPPGC RVTCLDPNPHFEKFLTKSMAENRHLQYERFVVPAGEDMRQLAD GSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAE PYGSAFW
688	1427	240	641	RLQNSSLMDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALL EKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMM AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGSD PTKG
689	1428	1	116	FFFFEMESCSVTQAGVPWHDLSLQPPPPRFKRFSCLS
690	1429	75	511	DPKAQLPEPLRVLWTAHLVAMAPGSRSTSLLA FALLCLPWLQE AGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFEEITYIPKDQ KYSFLHDSQTSFCFSDSIPTPSNMEETQQKSNLELLLRISLLLI ESWLEPVRILMSIVN



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
691	1430	2	1364	FVKLIKHHQAAMEKEAKVMSNEEKKFQQHTQAQKKELNSFLE SQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQ AEEENALLRRQRQYLELEECRRFKRRMLLGRHNLEQDLVREELN KRQTKQDLEHAMLLRQHESMQELEFRHLNTIQMRCELIRLQH QTELTNQLEYNKRRELERRRKHVMEVRQQPKSLKSKELQIKKQ FQDTCKIQTRQYKALRNHLLLETPKSEHKAVLKRLKEEQTRKL AILAEQYDHSINEMLSQALRLDEAQEAECQVLKMQLOQEELEL LNAYQSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEML ALQNERTERIRSLERQAREIEAFDSESMRLGFSNMVLSNLSP EAFSHSYPGASGWSHNPTGGPGPHWGHMPGPPQAWGHPMQGG PQPWGHPS\GPMQ\GVPR/GSSMGVR
692	1431	50	504	LAHGSFGVSDFPAPAAAPAHLTLSFSGSLSPQFRKPLGRAPAM PLVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYS KIVTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSV TSLHSFQVIESLYQKLHEGHGK
693	1432	130	1671	SSPSRELCFYGFWFIASSWWSRWVGSGLPGILPSPARGRTFAS VSRLPPWSAGITLTPFLICQSGSVCPGLGAGFGVRSFHHFVA RSVALLPLAPAAQDSTQASTPGSPLSPTEYERFFALLTPTW KAETTCRLRATHGCRNPTLVQLDQYENHGLVPDGAVCNSLPYA SWFESFCQFTHYRCSNHVYAKRVLCSQPVSILSPNTLKEIEA SAEVSPITMTSPISPHTVTERQTFQPWPERLSNNVEELLQSS LSLGGQEQAPEHKQEQGVHRQEPTEHKQEEGQKQEEQEEQ EEEGKQEEGQGTKEGREAVSQLQTDSEPKFHSESLSSNPSSFA PRVREVESTPMIMENIQELIRSAQIDEMNEIYDENS YWRNQN PGSLLQLPHTTEALLVLCYSIVENTCIITPTAKAWYMEEEILG FGKSVCDSLGRRHMSTCALCDFCSLKLEQCHSEASLQRQCDT SHKTPFVSPLLASQSLSIGNQVGSPEGRFYGLDLYGGLHM
694	1433	517	578	VSWVPSKGDVEGARRPFTRLNTSLGPGLEGRRTWLVPPIPG AVLPGRTQEQRASPLY*PGAPPCQPQGLVAGPWAQ*AGLRSD GFGPPW\RLVGTAGPREKKVQKSKCWHFRCCRHPARRSGWAG RHASLLATGRPCSSAPSQQPLGTAGDSRQELLRPPLV*VNGAQ SSAAGDWGSSPRTAQALARPHRLGHHPAAVAPAAARLTQSGHS PRGPLCRSPGSPRRMGTWGPAGHSHD
695	1434	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG INLSGFGSEQLDTNDESDVSSALS YILPYLSLRNLGAESILLP FTEQLFSNVQDGRLLSILKNNRKS PSQSSLLGNKFKNKIF
696	1435	333	881	GECFIMAADVQNDLVFEFASNMEDERQLGDPATFPVAVIVEH VPGADILNSYAGLACVEEPNDMITESSLDVAEEI IDDDDDDI TLTVEASCHDGETIETIEAAEALLNMDS PGPMLEKRIINNI FSSPEDDMVAVPVTHVSVTLTGIPVEMETQQVQEKYADSPGAS SPEQPKRKKK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
697	1436	3	466	HEASGVSRALLQSAPGTPATVGISVGELWPFARCCSHSYVRS RGLSVSTHLLCFTIYIMNPSMKQKQEEIKENIKTSSVPRRTLK MIQPSASGSLVGRENELSAGLSKRKHRNDHLTSTTSSPGVIVP ESSENKNLGGVTQESFDLMIKGMKK
698	1437	50	241	PLPARGKSTLPATFCSPSAPELASMSVVPNRSQTGWPRGVTQ FGNKYIQQTKPLTLERTINL
699	1438	1	422	AEGEDVPPPLPTSSGDGWEKDLEEAL EAGGCDLETLRNI IQGRP LPADLRKAVWKIALNVAGKGDLSLWDGILDLEPQNTIHKDCL QFIDQLSVPEEKAAELLLDIESVITFYCKSRNIKYSTSLSWIH LLKPLVHLQLP
700	1439	161	413	ALPKFLTHGVKSNERVVWLFPPSFRAATMVHNMVLPDALKSI NNAERRGKQPQVLIRLCSKIIIWFLTMVKYGYIGKFEPTRP
701	1440	211	977	AMAYGHPSPLGMAAREELYSKVTPRNRQQRPGTIKHGSALD VLLSMGFPARRAQKALASTGGRSVQAACDWLFSHVGDPLDDP LPREYVLYLRPTGPLAQKLSDFWQQSKQICGKNKAHNI FPHIT LCQFFMCEDSKVDALGEALQTTVSRWKCKFSAPLPLELYTSSN FIGLFVKEDSAEVLKKFAADF AEAASKTEVHVEPHKKQLHVT LAYHFQASHLPTLEKLAQNIDVKLGCDWVATIFSRDIRFA
702	1441	3	408	QTRPASPTARESVLGVSONMSFNLQSSKKLFI FLGKSLFSL EAMIFALLPKPRKNVAGEIVLITGAGSGLGRLLALQFARLGSV LVLWDINKEGNEETCKMAREAGATRVHAYTCDSCQKEGVYRVA DQVKK
703	1442	708	244	MVARKGQKSPRFRVTCFLRLGRSTLLELEPAGRPCSGRTRHR ALHRRLVACVTVSSRRHRKEAGRRAESFI AVGMAAPSMKERQ VCWGARDEYWKCLDENLEDASQCKKLRSSESSCPQQWIKYFD KRDYLLKFKEKFEAGQFEPSETTAKS
704	1443	3	475	PAPAARSRELLKELRNGQDMDTVVFEDVVVDFLEEWALLNPA QRKLYRDVMLETFKHLASVDNEAQLKASGIS SQQDTSGEKLSL KQKIEKFTRKNIWASLLGKNWEEHSVKDKHNTKERHLSRNPV ERPCKSSKGNKRGRTFRKTRNCNRHLRR
705	1444	276	437	CVCGFFVCFETKSCFVAQAGVQWHNLSLQALPPGFKQFSCLS LLSSWHYRRV
706	1445	2	322	GTRLRRRREAVWFEVVMDFSRMHMYSPPQCV PENTGYTYALS SSYSSDALDFETEHKLDPVFDSPRMSRSLRLATTACTLGDGE AVGADSGTSSAVSLKNRAAR
707	1446	123	410	DTMQAVVPLNKMTAISPEPOTLASTEQNEVPRVVTSGEQEAIL RGNAADAESFRQFRWFCYSEVAGPRKALSQWL CNQWLRPD IHTKE\QILE
708	1447	2	384	PICLFSRPTLRPSRSKVSLEGRGANMAARWRFWCVSVTMVVA LLIVCDVPSASAQRKKEMVLSEKVSQLMEWNTKRFVIRMNGDK FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKYELQLRFFKIK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
709	1448	104	535	QMRVKDPTKALPEKAKRSKRPTVPHDESSDDIAVGLTCQHVS HAISVNHVKRAIAENLWSVCSECLKERRFYDQQLVLTSDIWL LKCQFQCGKNSQHSCLKHFKSSRTEPHCIIINLSTWIIWWY EWDEKIFTPLNKKG
710	1449	116	479	AKERGEERQEGGGWLSGSRWPLVRSAPVAPSSLIISMCLSP GIPEAAPDSPLTASATP*VMLLGDVGKTCFLIQFKDGAFL SGTFIATVGIDFRVRLQALASSREPGLWLRHGGV
711	1450	2	232	FYPRSSADLPFQTRCEFTQSMELAHSLLLNEEALAQITEAK RPVFIFEWLRFLLDKVLAANKVWYCSFFPVALT
712	1451	105	393	MNMKQKSVYQQTKALLCKNFLKKWRMKRESLLEWGLSILLGLC IALFSSSMRNQVFPGMAPQNLGRVDKFNSSSLMVVYTPISNLT QQIMNKTAL
713	1452	2	525	SPQNGCPCDVTGDSVIRVPLTLLVHNLAGLTGLLHHCLSGPLP APSPPPAMSSSRKDLGASSSEPLPVIIVGNGPSGICLSYLLS GYTPYTKPDAIHHPPLLQKRLTEAPGVSILDQDLDYLSEGLEG RSQSPVALLFDALLRPDTEFGGNMKSVLTKHRKEHAIPHVVL GR
714	1453	2	1557	NRRTAQRQGRSCGAREEEVEPGTARPPPAASAMDASLEKI ADPTLAEMGNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPL QSGSQDMVSIQLVQNLMHGDEDEEPQSPRIQNIQEGHMALL GHS LGAYISTLDEKLRKLTTIRILSDTLWLCRIFRYENGCA YFHEEEREGLAKICRLAIHSRYEDFVVDGFNVLYNKKPVYLSA AARPLGQYLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEK LIKDDIERGRPLLLVANAGTAAVGHTDKIGRLKELCEQYGIW LHVEGVNLTALGYVSSSVLAAKCDSTMTGPGWLGLPAVP AVTLYKHDDPALTLVAGLTSNKPTDKLRALPLWLSLQYLGLDG FVERIKHACQLSQRLOESLKKVNYIKILVEDELSSPVVFRFF QELPGSDPVFKAVPVPNMTPSGVGRERHSCDALNRWLGEQLKQ LVPASGLTVMDLEAGTCLRFSPMLTAAGKPLVDIPCFCSGA AG
715	1454	319	873	LCIMDTKEKKERKQSYFARLKKKKQAKQNAETASAVATRHT GKEDNNTVLEPDKCNIAVEEEYMTDEKKRKSQNLKEIRRT LKRYYSIDNQNKTHTDKKEKMMVVQKPHGTMEYTAGNQDTLNS IALKFNITPNKLVELNKLFTHTITVPGQVLFVPDANSPPSTLRL SSSSPGATVSPSS
716	1455	60	681	SAGGDS CRAVPMLRFPTCFPSFRVVGKQLPQEIIFLVWSPKR DLIALANTAGEVLLHRLASFHRVWSFPNENTGKEVTCIAWRP DGKLLAFALADTKIVLCDVEKPESLHFSVEAPVSCMHWMEV TVESSVLTSFYNAEDSNLLLPKLPTLPKNYSNTSKIFSEENS DEI IKLLGDVRLNIVLGGSSGFIELYAYGMFKI
717	1456	357	658	PRDPVTD RARAMPRRLVAGPDLEYFQRHYFTPAEVAQHNRP DLWVSYLGRVYDLTSLAQEYKGNLLKPIVEVAGQDISHWFD KTRDVS YAGTWDCG

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
718	1457	2	481	RIPGRRFRAAFVLGSANVASSVRLRCSFPLSLGGPSGPAAASV ALGPAGPGRSLGRTPDPTGDWEMDSVSFEDVAVAFQTQEEWALLD PSQKNLYRDVMQEI FRNLASVGNKSEDQNIQDDFKNPGRNLSS HVVERLFEIKEGSQYGETFSQDSNLNLNKI
719	1458	6	469	SLSLSVSPFLRLSLGRVGGMAEEMESSLEASFSSSGAVSGASG FLPPARSRIFKIIVIGDSNVGKTCLTYRFCAGRFPDRTEATIG VDFRERAVEIDGERIKIQLWDTAGQERFRKSMVQHYRNVHAV VFVYDMTNMAASFHSLPSWIEECKQH
720	1459	82	490	RRPSGSIIVIMAAESDVLHFQFEQQGDVVLQKMNLLRQONLFC DVSIIYINDTEFQGHKVLAAACSTFMRDQFLLTQSKHVRITILQ SAEVGRKLLLSCTYGALEVKRKELLKYLTAASYLQMVHIAEKR TEAFVKF
721	1460	48	708	AEGLQSAAGIRIDTKAGPPEMLKPLWKA AVAPTWPSCMPRRP WDRQAGTLQVLGALAVLWLGSAVICLLWQVPRPPTWGQVQPK DVPRSWEHGSSPAWEPLAEAEARQORDSCQLVLVESIPQDLPSA AGSPSAQPLGQAWLQLLDTAQESVHVASYWVSLTGPDIGVND SSQLGEALLQKLQQLGRNISLAVATSSPTLARTSTDLQVLAA RGAH
722	1461	436	677	RKKKMLPFPGLKLRTRRYTVSSKSCLVARIQLLNNEFVEFTL SVESTQGESLEAVAQRLELREVITYFSLWYYNKQNR
723	1462	45	569	LQPLSSWESASEVTRSPVSPEDVKQATSNFENLQKQLARKMKL PIFIADAFTARA FRGNPAAVCLLENELDEDMHQKIAREMNLSE TAFIRKLHPTDNFAQSSCFGLRWFTPASEVPLCGHATLASAAV LFHKIKNMNSTLTFTVLSGELRARRAEDGIVLDLPLYPHPQD FHE*
724	1463	79	530	AADTMQSDDVIVDTLGNKQFCSEFKIRTKTQSFRCRNEYSLTGLC NRSSCPLANSQYATIKKEKGQCYLYMKVIERAAPPRRLWERVR LSKNYEKALEQIDENLIYWPRFIRHKCKQRFTKITQYLIRIK LTLKRQRKLVLPLSKKVERREK
725	1464	2	261	FVERGLGDPALPTLMFEPEWAEAAAPVAAGLGPVISRPPPAAS SQNKVSDSREQWELFQAAKRTLVDPSAVCIAGRDTCGTVKGES
726	1465	1	860	VVEFLWSRRPSGSSDPRPRRPASKCQMMEERANLMHMMKLSIK VLLQSALSLGRSLDADHAPLQOFFVVMHCLKHGLKVKKSFIG QNKSFPGPLELVEKLCPEASDIATSVRNLPKLTAVGRGRWL YLALMQKKLADYLVLDNKHLLSEFYEPALMMEEGMVIVG LLVGLNVLDANL\CLKGEDLDSQVGVIDFSLYLKDQDLGGK EHERITDVLQKNYVEELNRHLSCTVGDLDQTKIDGLEKTNSKL QERVSAATDRICSLQEEQQQLREQNELIR
727	1466	69	452	GCYAPSPHLGGSLTPRFFPENGVFHRRLLPRPRFPQPPSVSSAPT LRPLCAHFSGLKRLRLVRKSAEVAPPRTKEGWGSAEPRHSRAP LGLQGLRMAASAQVSVTFEDVAVTFTQEEWGQLDAAQRTLY

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
728	1467	1	439	FRGSLSSPSSLRGRRLVTGQTS PRGTWCCLYPGFCRSVACAMPC CSHRSCREDPGTSESREMDPVVFEDVAVNFTQEEWTLDDISQK NLFREVMLETFRNLTSIGKKWSDQNIYEYQNPRESSFRSLIEE KVNEIKEDSHCGETFTQ
729	1468	103	236	LNFANSAAFAVTMPQNEYIELHRKRYGFRLDYHEKKRKKQSRE A
730	1469	213	809	SGDLSPAELMMLTIGDVIKQLIEAHEQGKDIDLNKVTKTKAAK YGLSAQPRLLVDIIAAVPPQYRKVLMPKPKAKPIRTASGIAVVA VMCKPHRCPHISFTGNICVYCPGGPDSDFEYSTQSYTGYEPTS MRAIRARYDPFLQTRHRIQLKQLGHSVDKVEFIEMGGTFMAL PEEYRDYFRNLHDLALSGHTSNNIYE
731	1470	264	799	WESDVGEGLRPPPPPPPPGRRRTQEPRARDAATVIFACPAALL ETLIAYGSSSPSFCKHRAARPLIFLLHRLTAEATARCPICAL EARNPGRWGICASWPGMKTPFGKAAAGQSRSTGAGHGSVSVTMI KRKAHKKHRSRPTSQPRGNIVGCI IQHGWKDGDDEPLTQWKGT VLDQLL
732	1471	2	763	RDLGVALEAFQWARAGDCGSGAGRAGGEGVDAGRVRPERQHRG RGGGGEPGRRQRGRRQ\RSSRRSGDGGDEVEGSGVGAGEG ETVQHFPFLARPKSLMQKLQCSFQTSWLKDFPWLRYSKDTGLMS CGWCQKTPADGGSVLDLPPVGHDELRSRTRNYKKTLLLRHHVST EHKLEHANAQESEIPSEEGYCDFNSRPNENSICYQLLRQLNEQ RKKGILCDVSVVSGKIFKAHNILVAGSRFFKTLTYCFS
733	1472	82	523	SLRAAAMADVNTARSLQYFYKANSNLVLQADRSLIDRTRRDEP TGEVLSLVGKLEGTRMGDKAQRTPQMQUEERRAKRRKRDEDRH DINKMKGYTLLSEGIDEMVGIIYKPKTKETRETVEVLLSFIQA ALGDQPRDILCGAADEVL
734	1473	536	110	CNSAESRMDVLFVAIFAVPLILGQEYEDERLGEDEYQVYYY YTVTPSYDDFSADFTIDYSIFESEDRNLRLDKDITEAETTIS LETARADHPKPVTVKPVTTPEQSP\DL\NDAVSS\LRSPIPL\ LLS\CAFVQVGMVFM
735	1474	2	557	FVRGPGEQAPAFRKPAPGAMGAQVRLPPGEPCREGYVLSLVC PNSSQAWCEITNVSQLLASPVLYTDLNYSINNLSISANVENKY SLYVGLVLAVSSSIFIGSSFILKKKGLLQLASKGFTRAGQGGH SYLKEWLWWVGLLSILSWNAREKVDL*NITF*PQTSCIFFTIT IEKSTFLSYFPTS
736	1475	127	401	ARGSCPTRPRPANGRMAETKDAAQMLVTFKDVAVTFTREEWRQ LDLAQRTLYREVMLETGCLLVSLGHRVPKPELVHLLKHGQELW IVKRG
737	1476	311	790	YTMLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTQ PASTVQKPGGTVILGCVVEPPRMNVTVRLNGKELNGSDDALGV LITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLASE SAPLPPCHGAVPPHLSHPEAPTIHAASCYS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
738	1477	2	421	WGRRRQLVSEARAQGDVPCSTMSEEEAAQIPRSSVWEQDQON VVQRVVALPLVRATCTAVCDVYSAKDRHPLLGSACRLAENCV CGLTTRALDHAQPLLEHLQPQLATMNSLACRGLDKLEEKLPFL QQPSETVVTS
739	1478	256	1250	AKAFTMAESPGCCSVWARCLHCLYSCHWRKCPRRERMQTSKDC IWFGLLFLTFLLSLSWLYIGLVLLNDLHNFNEFLFRRWGHWMD WSLAFLLVISLLGTYSLLLVLALLRLCRQPLHLHSLHKVLL LLIMLLVAAGLVGLDIQWQQRHSLRVSL/QDCR*L*TPAVRP *EESGEGHWRAHLTSSCPQATAPFLHIGAAAGIALLAWPVAD TFYRIHRREPKILLLLFFGVVLVIYLAPLCISSPCTIMEPRDL PPKPGLVGHRGAPMLAPENTLMSLRKTAECGATVFETDVMVSS DGPVFLMHDEHLSRTTNVASVFPTRITAHSS

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO: 1-739, an active domain of SEQ ID NO: 1-739, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-739.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
  - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:



- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO: 1-739, an active domain of SEQ ID NO: 1-739, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-739, under conditions sufficient to express the polypeptide in said cell; and
- b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 740-1478, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-739.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

## SEQUENCE LISTING

<110> Hyseq Inc  
 <120> Novel Nucleic Acids and Polypeptides  
 <130> 784PCT  
 <140> To be assigned  
 <150> US09/488,725  
 <151> 2000-01-21  
 <150> US09/552,317  
 <151> 2000-04-25  
 <160> 739  
 <170> Pt\_CT\_1  
 <210> 1  
 <211> 556  
 <212> DNA  
 <213> Homo sapiens

<400> 1  
 ttctcgtgggc cgggttgctaa gacttggcga agcgcctgcgc ttgcgcccgg atccctcagg 60  
 cggtctgcagg cttcagcctg cgctgggttg tgaaacagag atgtcagaaa aggagaacaa 120  
 cttcccgcga ctgcccgaagt tcatccctgt gaagccctgc ttctaccaga acttctccga 180  
 cgagatccca gtggagcacc aggtcctggt gaagaggatc taccggctgt ggatgtttta 240  
 ctgcgccacc ctgcgcgtca acctcattgc ctgcctggcc tgggtggatcg gcggaggctc 300  
 ggggaccaac ttgcgcctgg ccttcgtgtg gctgctcctg ttcacgcctt gcggctacgt 360  
 gtgctggttc cggcctgtct acaaggcctt ccgagccgac agctccttta atttcatggc 420  
 gtttttcttc atctttcgga gccagtttg tcctgaccgt catccaggcg attggcttct 480  
 ccggctgggg cgcgtgcggc tggctgtcgg caattggatt cttccagtac agcccgggcg 540  
 ctgcgcgtggt catgct 556

<210> 2  
 <211> 837  
 <212> DNA  
 <213> Homo sapiens

<400> 2  
 gagatgagtc ccaggagagta cggagtcagc tctgagccga ggtcaccgca gaagggagct 60  
 cggctcttcgg ccaggaccgg agcagttgga acaaagggaa tgtggaaatg aaagagagag 120  
 ggagagagag gctggcagat gtaatgagac gcggtgaagg tgtacgcaga ctggcactcc 180  
 cactcctccc ttctgtcttc actgcagccc tgggtaactc gcaggctaac acaaacagct 240  
 tttctcccgc agcctgcctt ctgtcactgt cactttcatg aattcaaagg caatttacca 300  
 gtgatttctg ggtgctgggg ctgatatttt ttgtgcataa ttaagaatgt cttccaagca 360  
 agccacctct ccatttgcct gtgcagctga tggagaggat gcaatgaccc aggatttaac 420  
 ctcaagggaa aaggaagagg gcagtgatca acatgtggcc tcccatctgc ctctgcaccc 480  
 cataatgcac aacaaacctc actctgagga gctaccaaca cttgtcagta ccattcaaca 540

agatgctgac	tgggacagcg	ttctgtcatc	tcagcaaaga	atggaatcag	agaataataa	600
gttatgttcc	ctatatccct	tccgaaatac	ctctacctca	ccacataagc	ctgacgaagg	660
gagtcgggac	cgtgagataa	tgaccagtgt	tactttttgga	accccagagc	gccgcaaagg	720
gagtccttgc	gatgtggtgg	acacactgaa	acagaagaag	cttgaggaaa	tgactcggac	780
tgaacaagag	gattcctcct	gcatggaaaa	actactttca	aaagattgga	aggaaac	837

<210> 3  
 <211> 1562  
 <212> DNA  
 <213> Homo sapiens

<400> 3						
cggaaaccgta	ggaggggtac	ttaaccggac	ggcctaccag	gcctgtggcc	gtgcgcggga	60
agagcactgc	agatctcagg	atgatggggc	gcagccctgg	gtttgccatg	cagcacatcg	120
tgggtgtgcc	ccacgtactg	gttcggaggg	gcctccttgg	aagggacctc	ttcatgacca	180
ggactctctg	cagcccaggc	ccaagccagc	cgggagagaa	aagacctgag	gaggtggccc	240
tggggctgca	ccaccgcctc	ccagcactgg	gaagagccct	ggggcacagc	attcagcaac	300
gagcgcacctc	cacagccaag	acttggtggg	acagatatga	agagtttgtt	ggactcaacg	360
aggttcgaga	ggcccaggga	aaggtgacag	aggctgagaa	agtgttcacg	gtggctcgag	420
ggcttgtccg	agaggctcgg	gaggacttgg	aagttcacca	ggccaagctg	aaggagggtga	480
gggaccgctt	ggaccgtgtc	tccaggaggg	acagtcagta	cttggaactg	gctactctcg	540
agcacaggat	gctgcaggag	gagaagaggc	ttcgcacagc	ctatctgcgt	gcagaagact	600
ctgagcgaga	gaagttctcc	ctcttctctg	cagctgtgcg	ggaaagtcat	gagaaggagc	660
gcacaagggc	tgagaggacc	aagaactggg	ccctcattgg	ctcagtcctg	ggggccctga	720
ttggtgtggc	tggctccacc	tatgtgaacc	gtgtgcgact	acaggagctg	aaggctttac	780
tcctggaggc	gcagaagggg	cctgtgagtc	tccaagaggc	cattcgagaa	caggcgtcta	840
gctactcccc	ccagcagagg	gacctccaca	atctcatggg	ggacttgagg	ggcctggtac	900
atgctgctgg	cccagggcag	gactctgggt	cacaggcagg	tagtcccccg	accagagaca	960
gagatgtaga	tgtcctttca	gctgccttga	aagagcagct	tagtcattcc	aggcaagtcc	1020
attcatgtct	agaaggctta	cgagagcagc	ttgatggcct	agaaaagact	tgtagccaaa	1080
tggctggggg	ggttcagctt	gtaaagtctg	cagcacaccc	aggcctgggtg	gaaccagcag	1140
acggggctat	gccagcttcc	ttgctggagc	aggggagcat	gatcttggca	ctgtcagaca	1200
cggagcagag	actagaagcc	caagtcaaca	ggaacacccat	ctatagcacc	ctgggtcacct	1260
gtgtgacatt	tgtggccaca	ctgcctgtgc	tctacatgct	attcaaagcc	agctaacccc	1320
tggccctccc	tccagagggg	ctgaggcaat	agctgtgaat	gtggatttaa	gtagagaatc	1380
gtagcaatga	accgagcctt	tgggggcatg	tacaacctca	atctgaagga	gcagtatctg	1440
tgtggctcac	cagcaggcat	gcttcgcttt	gtagacaagg	ttcattttaca	tttaattatca	1500
aaactttgtg	ctaattgtcca	attaaaatat	cctgagtttt	attattttaaa	acaaaaaaaa	1560
aa						1562

<210> 4  
 <211> 745  
 <212> DNA  
 <213> Homo sapiens

<400> 4						
agggcttggtg	gctgggtctc	cgtgacagag	gcctggcttt	tctgtcaggg	cagggcctag	60
ccctgcccc	cataaaagag	gagacatagg	gggcttggtg	agataccctg	aaacctcccc	120

cctctgaccc	cgcagccagg	ccccaggctg	gccgggagtg	ccccctcaca	ctggttctcc	180
ccactttctc	tgctgtggc	atcgaaggcc	ccgggcacca	tgccccaggc	cctgggggag	240
gacctgggtg	agcctcccga	gctgcaggat	gactccagct	ccttgggggc	cgactcagag	300
ctcagcgggc	ctggcccata	tcgccaggcc	gaccgctatg	gattcatttg	gggcagctca	360
gcagagccag	ggccgggcca	cccacctgca	gacctcatcc	gccaacggga	gatgaagtgg	420
gtggagatga	cctcgactg	ggagaaaacc	atgtcccggc	ggtacaagaa	ggtaaagatg	480
cagtgcggga	aaggcatccc	gtctgccctg	cgcgcccgat	gctggcccct	gttgtgtggg	540
gccccatgtg	gccagaagaa	cagccctggc	acctatcagg	agctggcaga	ggcccctgga	600
gaccacagtg	ggatggagac	cattggcagg	gacctgcacc	gtcaattccc	tctgcacgag	660
atgtttgtgt	cgctcaagg	ccacgggcag	caggggctcc	tgcagggtgt	caaggcctac	720
acctgtatc	gaccggagca	aggct				745

<210> 5  
 <211> 536  
 <212> DNA  
 <213> Homo sapiens

<400> 5	
acggaagctc	ggttgatgtt tctgcagaag ttttccccct tggtcgggtgg cggagctgct 60
gagcgcgata	gtagcagctc cggcggcagc aacattgact acgaggaatg gcggcggctg 120
ccgcaggacc	tgacgcatcc cagaggtttt tccagagctt ctcagatgct ctaatcgacc 180
aggaccccc	ggcggcggtta gaggtgggag agccttttct gcttccctca cccccgctg 240
accgcctcc	ttccagcacc gcctgattag gactcaggct ctagtgatgc tgcgtctcag 300
cccagtgatt	gagattctcg gtctccttct tctctctcac ggtagccgcg ttacctcaga 360
ctctgtctt	gccctttcca cttccagact cttgcattcc tgaagcttct gagaaaaact 420
tcctctatct	attgggagca tgggtggcat ctgcagttgg gctgaaagga tttttttttt 480
ttaatgacta	aaaaagaaaa ggggactctg ggctcgatga aaattaattt tttctt 536

<210> 6  
 <211> 780  
 <212> DNA  
 <213> Homo sapiens

<400> 6	
atattatcga	ctattccgtc agacgccttc ttgccttttag tgaactgcgg ggacctggcc 60
tttgccggta	ggggccagcg cagaaaagcc tgggagatgc gcgtccaggg ccgcgagtg 120
ggggaagctg	cgggaccgca gagtccgtc ggagccgggt agtcagggcg ccggggcggtt 180
aggcttcaga	tttacttcaa tgttccctaat gggcttgctt cagaagtgtc cactgttctc 240
gccacctgag	gaaccgcatt ttcatgtatt tgtattggga caagacgcgg agtccggtgt 300
gtaaagggcc	tgctttgagg gaagaaaggc cgcagcccag gctcaaaactg gaggattata 360
aggatcgct	gaaaagtggg gagcatctta atccagacca gttggaagct gtagagaaat 420
atgaagaagt	gctacataat ttggaatttg ccaaggagct tcaaaaaacc ttttctgggt 480
tgagcctaga	tctactaaaa gcgcaaaaga agggccagag aaggagcac atgctaaaa 540
ttgaggctga	gaagaaaaag cttcgaaacta tacttcaagt tcagtatgta ttgcagaact 600
tgacacagga	gcacgtacaa aaagacttca aagggggttt gaatggtgca gtgtatttgc 660
cttcaaaaga	acttgactac ctcattaagt tttcaaaact gacctgccct gaaagaaatg 720
aaagtctgag	acaaacactt gaaggatcta ctgtctaaat tgctgaactc aggtattttt 780

<210> 7  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(654)  
 <223> n = a,t,c or g

<400> 7

ctccccgtct	cttccctggc	cttgccctct	ctctttctgc	cctgtagccg	cgggcgtcca	60
aatgaagctg	gaattcctcc	agcgcaaatt	ctgggcggca	acgcggcagt	gcagcactgt	120
ggatgggccc	tgacacacaga	gctgcgagga	cagtgatctg	gactgcttcg	tcatcgacaa	180
caacgggttc	attctgatct	ccaagaggtc	ccgagagacg	ggaagatttc	tgggggaggt	240
ggatgggtgct	gtcctgacct	agctgctcag	catgggggtg	ttcagccaag	tgactatgta	300
tgactatcag	gccatgtgca	aaccctcgag	tcaccaccac	agtgcagccc	agcccctggt	360
cagcccaatt	tctgccttct	tgacggcgac	caggtggctg	ctgcaggagc	tgggtgctgtt	420
cctgctggag	tggagtgtct	ggggctcctg	gtacgacaga	ggggccgagg	ccaaaagtgt	480
tcttccatca	ctcccacaaa	cacaagaagc	aggacccgct	gcagccctgc	gacacggagt	540
accccggtgt	cgtgtaccag	cccggccatc	cgggaggcca	acggggattc	gtggagtgcg	600
ggcccttnc	agaaagggtg	ttgtttggtg	cangcagatt	ccnaacatta	aact	654

<210> 8  
 <211> 469  
 <212> DNA  
 <213> Homo sapiens

<400> 8

tgccgtgggc	ggctggccca	gctggaggaa	gcggcggtgg	cggccacgat	gagtgcgggc	60
gacgcagtgt	gcaccggctg	gctcgttaag	tcgccccccg	agagggaagct	acagcgctac	120
gcctggcgca	agcgtgggtt	tgtcctccgg	cgaggccgca	tgagcggcaa	ccccgatgtc	180
ttggagtact	acaggaacaa	gcactccagc	aagcccatcc	gggtgataga	cctcagcgag	240
tgtgcagtgt	ggaagcatgt	gggccccagc	tttgttcgga	aggaatttca	gaataatttc	300
gtgttcattg	tcaagactac	ttcccgtaga	ttctacctgg	tggccaaaac	tgagcaagaa	360
atgcagggtgt	gggtgcacag	catcagtcag	gtctgcaacc	ttggccacct	ggaggatggt	420
gcagcagatt	ccatggagag	cctctcttac	acgcgctcct	acctgcagc		469

<210> 9  
 <211> 409  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> misc\_feature  
 <222> (1) ... (409)  
 <223> n = a,t,c or g

<400> 9  
 agaaaccnaa cagatctgtg gggcaggaaa atgtttcttt tccagctttc acagctctct 60  
 gagaaggggc atggtgggaa ttttagccga ttttaataaaa gctgcagcat gagacctgtg 120  
 aatcccaccc tgctgcttcc tggatcctgc cacaccccat ccagcagcaa ccaagccagt 180  
 ctgccccctg actgggacag agtggctgag aggggctctg gagccagctg cctggatttg 240  
 aatcccagct gtgccactta ccagctgtgt gactgtagga agctactctt tgtccgtgcg 300  
 agactacgac cctcggcagg gagataccgt gaaacattac aagatccgga cccttgaaca 360  
 aacgggggctt ctacatatcc cccccgaagc accttcagca ctctgcagg 409

<210> 10  
 <211> 1145  
 <212> DNA  
 <213> Homo sapiens

<400> 10  
 aaagattctg ttttgaatat agccagagga aaaaagtatg gagaaaaaac taagagagtg 60  
 tcttctcgga aaaaaccagc cttgaagtgt cttctcagaa acaaccagca ttgaaggcta 120  
 tctgtgacaa ggaagattct gtccgaata cggccacgga aaaaaaggat gaacaaatat 180  
 ctgggacagt gtcttctcag aaacaaccag ccttgaaggc tacaagtgc aagaaagatt 240  
 ctgtttcgaa tatacccaca gaaataaagg atggacaaca atctggaaca gtgtcttctc 300  
 agaaacaacc ggcctggaag gctacaagtg tcaagaaaga ttctgtttcg aatatagcca 360  
 cagaaataaa ggatggacaa ataccgtggg acagtgtctt ctcagagaca accagccttg 420  
 aaggcttaca ggtgatgaga aagattctgt ttcgaatata gccagagaaa taaaggatgg 480  
 agaaaaatct gggacagtgt ctctcagaa acaatcggcc cagaagggtta tatttaaaaa 540  
 gaaagtcttct cttttgaata ttgccacaag aataacgggc ggttggaaat ctggaacaga 600  
 gtatcctgag aatctgccca ccttgaaggc tacaattgaa aataaaaatt ctgttctgaa 660  
 tacagccacc aaaatgaaag atgtacaaac atccacacca gaacaagact tagaaatggc 720  
 atcagaggga gagcaaaaga ggcttgaaga atatgaaaat aaccagccac aggtgaaaaa 780  
 ccaaatacat tctagggatg accttgatga cataattcag tcatctcaaa cagtctcaga 840  
 ggacggtgac tcgctttgct gtaattgtaa gaatgtcata ttactcattg atcaacatga 900  
 aatgaagtgt aaagattgtg ttcacctatt gaaaattaaa aagacatttt gtttatgtaa 960  
 aagattaaca gaacttaaag ataatcactg tgagcaactt agagtaaaaa ttcgaaaact 1020  
 gaaaaataag gctagtgtac taaaaagag actatctgaa aaagaagaaa taaaatcgca 1080  
 gttaaagcat gaaacacttg aattggaaaa agaactctgt agtttgagat ttgccatata 1140  
 gcaag 1145

<210> 11  
 <211> 890  
 <212> DNA  
 <213> Homo sapiens

```

<400> 11
gtagtccgct gcggtaccgg gccggacaat ctgggtcgac gatttcgagc tcgtcatgcg      60
caatgtggcg ctgcggcggg cggcagggcc tgtgtgtgct gaggcggctg agcggcgagc      120
atgcacacca cagagcgtgg cgatggaaca gtaaccgggc ttgtgagagg gctctgcagt      180
ataaactagg agacaagatc catggattca ccgtaaacca ggtgacatct gttcccagc      240
tgttcttgac tgcagtgaag ctaccccatg atgacacagg agccagggtat ttacacctgg      300
ccagagaaga cacgaataat ctgttcagcg tgcagttccg taccactccc atggacagta      360
ctggtgttcc tcacattctt gagcataccg tcctttgtgg gtctcagaaa tatccgtgca      420
gagacccttt cttcaaaatg ttgaaccggg cctctccac gttcatgaac gccttcacag      480
ctagtgatta tactctgtat ccattttcca cacaaaatcc caaggacttt cagaatctcc      540
tctcgggtga tttggatgcc acctttttcc catgtttacg cgagctggat ttctggcagg      600
aaggatggcg gctggaacat gagaatccga gcgaccccca gacgcccttg gtctttaaag      660
gagtcgtctt taatgagatg aaggggagcg ttacagacaa tgagaggata ttctcccagc      720
accttcagaa cagacttctt cctgaccaca cgtactcagt ggtctccggg ggtgaccac      780
tgtgcatccc ggagcttaca tgggagcagc ttaagcagtt tcatgccact cactatcacc      840
caagcaatgc taggttcttc acgtacggta attttccctt agaccagcat      890

```

```

<210> 12
<211> 982
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(982)
<223> n = a,t,c or g

```

```

<400> 12
tttcgtcaca cacgcacacg caccctgcc a ctgcagccgc catggatata agctaacaac      60
acacacccag gcgcgcgcgc gcgttcccac tcgcaccacg caggagtggc ccccgccatc      120
cctaccctcc ttcccacccc ccaccacacc cgctcaccag ctccggtact gctcgtccg      180
gctgccgcgc ccgcgcgcgc cgacgccacc accactgctt cctctgctgc ggggccacag      240
ccttgagtgt cattcaaggg acagcacaac ctcatccaag ctctcctacc tctgccagc      300
cgtgcctctc atcctcccca ttctctgtcc a cactccatc caaagaagag ggaaagcacc      360
gaatagaggg gggcgaaggc aaagtctgct gttcttcccc ctgggcccc ttgctcctcc      420
atcctcatte tctcaccacc agcccccta accccaagga gccaggaac tgaggcgact      480
cgccccactg ccatgtccaa aagcttgaaa aagaaaagcc actggactag caaagtccat      540
gagagtgtca ttggcaggaa cccggagggc cagctgggct ttgaactgaa ggggggcgc      600
gagaatggac agttccccta cctgggggag gtgaagccc gcaaggtggc ctatgagagc      660
ggcagcaa at tgggtgcgga ggagctgctg ctggaggtga acgagacccc cgtggcgggg      720
ctcaccatca gggacgtgct ggcggtgatc aaacactgca aggacccct cgggtcaag      780
tgtgtcaagc aaggtgagag cagcggcttg ctacgtgttt tgccgggcgg tgggaccgct      840
cggggcgcag ggcaatgaaa ggggtggcgc gcatgttgaa gggggtgtgt tgccgatga      900
tggggtgggg gccagagagc accgcagtg caagtgagtt tcgccgggga ttccagcaaa      960
tcgtnncccg ggaattccgg ac

```

```

<210> 13
<211> 440
<212> DNA
<213> Homo sapiens

```



<400> 13  
 ccgtgccgga attcccgcgt cgacgatttc gtggctaagg cggcaggcac gggcaccacc 60  
 agggcgccca ggagccgccc gccgcgggca tggaccagct gtactgcca cggagcgct 120  
 gccagtcttt tggtaagaac tagtcacaca gacctcaacc tgatgcgtgg agacaaggaa 180  
 atgcttttca gtgtgtccag aaagagaaaa tgcagggtgc ttctgcggag gtgcgcatcg 240  
 ggcccatgag actgacgcag gacctatttc aggttttgcg gatctttgca aaggaagata 300  
 gtcagagcga tggcttctgg tgggcctgcg acagagctgg ttatagatgc aatattgctc 360  
 ggactccaga gtcagccctt gaatgctttc ttgataagca tcatgaaatt attgtaattg 420  
 atcatagaca aactcagaac 440

<210> 14  
 <211> 581  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
 tttcgtttgg ccggctgcgg gcacctcctg gtctcgtgc tggggctgct gctgctgctg 60  
 gcgcgctccg gcacccgggc gctggtctgc ctgccctgtg acgagtccaa gtgcgaggag 120  
 cccaggaact gcccggggag catcgtgcag gccgtctgcg gctgctgcta cacgtgcgcc 180  
 agccagagga acgagagctg cggcgggcacc ttccgggattt acggaacctg cgaccggggg 240  
 ctgcgttctg tcatccgccc cccgctcaat gccgactccc tcaccgagta cgaagcgggc 300  
 gtttgcaag atgagaactg gactgatgac caactgcttg gttttaaac atgcaatgaa 360  
 aaccttattg ctggctgcaa tataatcaat gggaaatgtg aatgtaacac cattcgaacc 420  
 tgcagcaatc cctttgagtt tccaagtcag gatatgtgcc tttcagcttt aaagagaatt 480  
 gaagaagaga agccagattg ctccaaggcc cgtgtggaag tccagttctc tccacgttgt 540  
 cctgaagatt ctgttctgat cgagggttat gctcctcctg g 581

<210> 15  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 tttcgatatg cggccaatgt gggatcgatg tttcaatatt ggaagcgctt tgatttacag 60  
 cagctgcaga gagaactcga tgccaccgca acggtatttg cgaaccggca ggatgaaagt 120  
 gagcagtcca gaaagcggct tatcgaacag agccgggagt tcaagaagaa cactccagag 180  
 gtgaggcgcg tgaccatcgt gttcgctttg aagggtatctt agaatgctgg tgcatgttca 240  
 ggcgacgctc cgtgagcgtt tcattttcat cagatgaacg cacggcgggc aaacaaccgc 300  
 tttctttccc cagatgtctt cagccccatt tccagcagaa cgcagccat cctgcaggct 360  
 gtggggatgt ggaaattgat aggttgtctg gaaatatgaa agtcagagcc aattccagggt 420  
 gcagatactg gacaagcttg gtctgtaaga acacgtgggc aggtgtgtgg gtgtctcaaa 480  
 ccctcgagct catccagac cctgtcccat gtcagtttagc aagccacca agtcataag 540  
 ggatcctgtg ggggtggaagg tccgcggggc ctgcttcctt gttgctgggt caggcggagt 600  
 gtctgaaggc tgcacgcata tgggcatagc agtgcgccta acgcttcttg taaaacagac 660

atttcgcctg ctaagccttt taaatgcctc tct

693

<210> 16  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<400> 16  
 tttcgtggaa agagagaaac caccgctgcg ggtgggtaga gaagcacttg gcgcctcggg 60  
 gaggggaccg cgcccgcctc atttgcgcct tgcagcactg ctggaccagg ttacaagatg 120  
 ttcacctaa agtgagacct agtgactaca tttcctacgg gaacaaataa atgggttttc 180  
 atctcccga gatacattac aaacaaatat ggtgctaaaa gaactcctta cctttctctg 240  
 actacaattt atttggacat acttttgtat tgaagagagg tatacatact gaagctactt 300  
 gctgtactat aggagactct gtccctgtagg atcatggacc atcctagtag ggaaaaggat 360  
 gaaagacaac ggacaactaa acccatggca caaaggagtg cacactgctc tcgaccatct 420  
 ggctcctcat cgctcctctg ggttcttatg gtgggaccca acttcagggt tggcaagaag 480  
 ataggatgtg ggaacttcgg agagctcaga ttaggtgaag gtctcccaca ggtgtattac 540  
 tttggaccat gtgggaaata ta 562

<210> 17  
 <211> 899  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 tttcgtgcgt ccccggccca accatggcgt cctccgcggc eggctgcgtg gtgatcgttg 60  
 gcaggaagtc tgaacagca gttggagtgt agtggttaag aggaaaggact caggagtcag 120  
 attgcttggc ttcattctcat agatccataa cttatcacc ttgtggactt aattcctcca 180  
 tgctcagtt tatcacttat gtaggcttaa ttcctccatg cctcagtttc cctacatata 240  
 aaatggaaat actaataaca cttatcttgt agggttgttg taaagattaa catagtggag 300  
 tcattgggcg aagctgggcc atgctgtttg ccagtggagg cttccagggtg aaactctatg 360  
 acattgagca acagcagata aggaatgcc tggaaaacat cagggtgggcc agccggcgct 420  
 ctccagaagg aatggaagtg ggtctgtttc tctcagtttg tcttgtttgt catatcctca 480  
 aggctatgag gatctgtgat gtcacatttt cgtctgatgg ctactgcagt gcctctgagt 540  
 tggtaaaggc caggcctaca gtggctggaa tgtgaattca cactggggaa gggctcccat 600  
 gggggaggaa acgacccttc ttgctaagag gatctgcac aagcgtgagt gactttgcag 660  
 gcttctccag ctgtttgccc cggggctgga gggctggggt ttctgcttc catctaggca 720  
 ggaggaactc gcttccagca tgtgacagcc atagctgcag gggcattaca gtttaagaac 780  
 agaggtcctg cagcttgttt tgacctgttg atctagtaat ggtaggacct aaatgaaaac 840  
 atcttgaatt ttagttagag gtttagcact catgtgagag gacagaactg gagctgttt 899

<210> 18  
 <211> 519  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

ggaattcccg	ggtcgacgat	tctgtctccg	cccgcccgaa	gccgcgcca	ctgcccagag	60
ccagagggat	ggtggtagtc	acggggcg	agccagacag	ccgtcgtcag	gacggtgcca	120
tgtccagctc	tgacgccgaa	gacgactttc	tggagccggc	cacgccgacg	gccacgcagg	180
cggggcacgc	gctgccctcg	ctgccacagg	agtttcctga	ggttggtccc	cttaacatcg	240
gaggggctca	cttactaca	cgctgtcca	cactgcggtg	ctacgaagac	accatggttg	300
cagccatggt	cagtggcg	cactacatcc	ccacggactc	cgagggccgg	tacttcacgc	360
accgagatgg	cacacacttt	ggagatgtgc	tgaatttcct	gcgctcagg	gacctccac	420
ccagggagcg	tgttcgagct	gtgtacaaag	aggcccagta	ctatgccatc	gggcccctcc	480
tggagcagct	ggagaacatg	ccgccactga	aaggcgaga			519

&lt;210&gt; 19

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

tttcgtgcag	gggccaggcc	tctctaggct	ctccggctga	gccgggttg	ggcccgggtt	60
gggcccgcgc	gggactctgg	agcattggga	tttgtagcgc	gccctctggg	taggcggctg	120
tagcggagag	gcgtgcggga	tcgggatgtc	ggggctgctc	acggaccggg	agcagagagc	180
gcaggagccg	cggtaccccg	gcttcgtgct	ggggctggat	gtgggcagtt	ctgtgatccg	240
ctgccacgtc	tatgaccggg	cggcgcggtt	ctgcggctcc	agcgtgcaga	aggtagaaaa	300
tctttatcct	caaattggct	gggtagaaat	tgatcctgat	gttctttgga	ttcaatttgt	360
tgccgtaata	aaagaagcag	tcaaagctgc	aggaatacag	atgaatcaaa	ttgttggtct	420
tggcatttca	acacagagag	caacttttat	tacgtggaac			460

&lt;210&gt; 20

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

gagatcaagg	agggtcaga	agaggcgatg	tctgatctgt	cctccaggca	gcaaaggaaa	60
gggaggtgtg	ttcctggcag	aaggcacagc	ttgtactgag	gcctggcagc	agaacagagt	120
atgcaatttg	tgaagctgtg	gtgtggctgc	agtggagagt	tcccaacaag	gctacgcaga	180
agaacccct	tgactgaagc	aatggagggg	ggtccagctg	tctgctgcca	ggatcctcgg	240
gcagagctgg	tagaacgggt	ggcagccatc	gatgtgactc	acttgaggga	ggcagatggt	300
ggcccagagc	ctactagaaa	cgggtgtggac	ccccaccac	gggccagagc	tgccctctgtg	360
atccctggca	gtacttcaag	actgctccca	gcccggccta	gcctctcagc	caggaagctt	420
tccctacagg	agcggccagc	aggaagctat	ctggaggcgc	aggctgggccc	ttatgccacg	480
gggcctgcca	gccacatctc	ccccggggcc	tggcggaggc	ccaccatcga	gtcccaccac	540
gtggccatct	cagatgcaga	ggactgcgtg	cagctgaacc	agtacaagct	gcagagttag	600

attggcaagg	gtgcctacgg	tgtggtgagg	ctggcctaca	acgaaagtga	agacagacac	660
tatgcaatga	aagtcctttc	caaaaagaag	ttactgaagc	agtatggctt	tccacgtgc	720
cctccccga	a					731

<210> 21  
 <211> 519  
 <212> DNA  
 <213> Homo sapiens

<400> 21						
tttcgtttat	gggaagccag	taacactgtg	gcctactatc	tcttccgtgg	tgccatctac	60
atTTTTggga	ctcgggaatt	atgaggtaga	ggtggaggcg	gagccggatg	tcagagggtcc	120
tgaaatagtc	accatggggg	aaaatgatcc	gcctgctgtt	gaagccccct	tctcattccg	180
atcgcttttt	ggccttgatg	atttgaaaat	aagtccgtgt	gcaccagatg	cagatgctgt	240
tgctgcacag	atcctgtcac	tgctgccatt	gaagtTTTT	ccaatcatcg	tcattgggat	300
cattgcattg	atattagcac	tggccattgg	tctgggcata	cacttcgact	gctcagggaa	360
gtacagatgt	cgctcatcct	ttaagtgtat	cgagctgata	gctcgatgtg	acggagtctc	420
ggattgcaaa	gacggggagg	acgagtaccg	ctgtgtccgg	gtgggtgggc	agaatgccgc	480
gctccagggt	ttcacagctg	cttcgcggaa	gacctgtg			519

<210> 22  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<400> 22						
tttcgtgctg	gaggttcgct	agccgaagcg	gctgcatactg	gagccgcgtc	tgccccgcgt	60
gctcggagcg	gattctgccc	gccgtccccg	gagccctcgg	cgccccgctg	agccccgcgat	120
cacttcctcc	ctgtgaccaa	ccggcgctgc	aggtttagagc	ctggcaatgc	cgtttgggtg	180
tgtgactctg	ggcgacaaga	agaactataa	ccagccatcg	gaggtgactg	acagatatga	240
tttgggacag	gtcatcaaga	ctgaggagtt	ttgtgaaatc	ttccggggcca	aggacaagac	300
gacaggcaag	ctgcacacct	gcaagaagtt	ccagaagcgg	gacggccgca	aggtgcggaa	360
agctgccaa	aacgagatag	gcatcctcaa	gatggtgaag	catcccaaca	tcctacagct	420
ggtggatgtg	tttgtgaccc	gcaaggagta	ctttatcttc	ctggagctgt	gagtgtgggt	480
ctggggaccc	aaaattcccc	agcggccagg	gctttcacct	gtcccaccct	ctgcagctaa	540
ggag						544

<210> 23  
 <211> 749  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
 caacgtcgac gatttcgtgc ggggctgtgg ggagggcacg gactgacaga cggactccgg 60  
 cggaatgggg ggtgtggctg ctccgccagg gtcccagg tgggagagcg gctccgccc 120  
 caccgatgcc cggacccct ctgtcttctg ctagacatgc tcttctctc gtttcacgca 180  
 ggctcttggg aaagctggtg ctgctgctgc ctgattccc cgcacagacc ttgggaccgg 240  
 ggccaacact ggcagctgga gatggcggac acgagatccg tgcacgagac taggtttgag 300  
 gcggccgtga aggtgatcca gagtttgccg aagaatggtt cattccagcc aacaaatgaa 360  
 atgatgctta aattttatag cttctataag caggcaactg aaggacctg taaactttca 420  
 aggcctggat tttgggatcc tattggaaga tataaatggg atgcttggag ttcactgggt 480  
 gatatgacca aagaggaagc catgattgca tatgttgaag aaatgaaaaa gattattgaa 540  
 actatgccaa tgactgagaa agttgaagaa ttgctgcgtg tcataggctc attttatgaa 600  
 attgtcgagg acaaaaagag tggcaggagt tctgatataa cctcagatct tggtaatggt 660  
 ctactttcta ctccaaacgc caaaaccgtt aatggtaaag ctgaaagcag tgacagtgga 720  
 gccgagctcg aggaagaaga ggctgtgtg 749

<210> 24  
 <211> 556  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
 tttcgtgctt taaggggcgg acgggcggga ggtcggggtc ctccggggat tcgagccggg 60  
 gggctcggtg tgggcgccat ttctcggcgt ctaccgagga gccgcccctt tctcagcctt 120  
 gctcggctct tccccgctct ggtcgccggg gctcgccgt cccagctca gtgacaaaaa 180  
 tgctgagttt cttccgtaga acactaggc gtcggctctat gcgtaaacat gcagagaagg 240  
 aacgactccg agaagcacia cgcgcgccca cacatattcc tgcagctgga gattctaagt 300  
 ccatcatcac gtgtcgggtg tcccttctgg atggtactga tgttagtgtg gacttgccaa 360  
 aaaaagccaa aggacaagag ttgtttgatc agattatgta ccacctggac ctgattgaaa 420  
 gcgactattt tggctctgaga tttatggatt cagcacaagt agcacattgg ttggatggta 480  
 caaaaagcat caaaaagcaa gtaaaaattg gttcacccta ttgtctgcat cttogagtta 540  
 agttttattc ctcaga 556

<210> 25  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
 gtcggtgaga atccagggag aggagcggaa acagaagagg ggcagaagac cggggcactt 60  
 gtgggttgca gatcccctca gccatgttgg gagccaagcc acactggcta ccagggtccc 120  
 tacacagtc cgggctgccc ttggttctgg tgettctggc cctgggggcc ggggtggccc 180  
 aggaggggtc agagcccgct ctgctggagg gggagtgcct ggtggtctgt gagcctggcc 240  
 gagctgctgc aggggggcc gggggagcag ccctgggaga ggcacccctt gggcgagtgg 300  
 catttgctgc ggtccgaagc caccaccatg agccagcagg ggaaaccggc aatggcacca 360  
 gtggggccat ctacttcgac caggtcctgg tgaacgaggg cgggtggctt gaccgggcct 420  
 ct 422

<210> 26  
 <211> 506  
 <212> DNA  
 <213> Homo sapiens

<400> 26  
 agaagatgtg aagtcgtatt atacagtaca tctaccacaa ttagaaaata tcaatagtgg 60  
 tgaaaccaga acaatatctc actttcatta tactacttgg ccagattttg gagtccctca 120  
 atcaccagct tcatttctca atttcttggt taaagtgaga gaatctggct ccttgaaccc 180  
 tgaccatgga cctgtggtga tccaccgtag tgcaggcact ggacgctcca gcaccttctc 240  
 tgtggtacac acttgtcttg ttttgatgga aaaaggagat gatattaaca ttaaacaagt 300  
 gttactgaac ataagaaaat tccaaatggg tcttatctca gacccagat caactgagat 360  
 tctcatacat ggctataaca gaaggagcaa aatgtgtaaa gggagattct agtatacaga 420  
 aacgatggaa agaactttct aaggaagact cctcctgct tttgatcatt caccaacaa 480  
 aataatgact gaaaaataca atagga 506

<210> 27  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 caggcctttg tgtaaggcca gaggaggatc acgggtgcc aaaaccttca cggggccaag 60  
 ggctggtgtc ccggggtctg tgacttaaca ggcagagatg tggagaccag gtgcttgtgc 120  
 ccgggacggg cctggtctgc atcctgagga cactgcccat gttccatgac gaggagcacg 180  
 cccgagcccg cggcctctct gaggacaccc tgggtgctacc cccggccagc cgcaaccaga 240  
 ggattctcta caccgtgctg gagtgccagc ccctcttcta ctccagtgc atgaccatcg 300  
 ctgagtgggt ttgccttgcc cagaccatca agaggcacta cgagcagtac cacggctttg 360  
 tggatcatcca cggcaccgac accatggcct ttgctgcctc gatgctgtcc ttcattgtgg 420  
 agaacctgca gaagactgtc atcctcaactg gggcccaggt gccatccat gccctgtgga 480  
 gcgacggccg tgagaacctg ctgggggcac tgctcatggc tggccagtat gtgatcccag 540  
 aggtctgcct tttcttcag aatcagctgt ttccgggcaa ccgggcaacc aaggtagacg 600  
 ctccgagggt cgcagctttc tgctcccgga acctgctgcc tctggccaca gtgggtgctg 660  
 acatcacaat caacagggag ctggtgcgga aggtggacgg gaaggctggg ctggtggtgc 720  
 acagcagcat ggagcaggac gtgggcctgc tgcgcctcta ccctgggac cctgcgccc 780  
 tggttcgggc cttcttgag cctcccctga agggcgtggg catggagacc ttcggttcag 840  
 ggaacggacc 850

<210> 28  
 <211> 990  
 <212> DNA  
 <213> Homo sapiens

```

<400> 28
tttttttttt ttacttgtaa tacgtatttt aatttttggt tcatatgagt ttaagtgttg      60
tctaggtgac atcaaaatct aaggcaaaaca gacttgacca tcttcagacc cactgcattc      120
tcaagctgaa gtggtctgct catagtttgt gtgccagggt gctcatcagt attgatactg      180
tcccagaaca ggttgtaggt ataattcaga gactgtcctt tgcaaaggaa atgaccagca      240
tttcaactgt atgtcttcct ggaagggtag attctgctat atcttctttg tctgcatcaa      300
aagactcaag aggaatgtgg acacatttca tatcccattt gtagagtaaa gcttcaagtg      360
accagtcagc actcctaact tgataagtag accacaattg gaccttgga ttcttgtgca      420
tcaaaaaata tattgtagcc aaaatgtctt caaaatcttc tggttcaaag aacacatcag      480
atgcaaggat aatatcttgt ggtggttagag ccagaagatc ccaagatata tgaccccatg      540
ttagtcctac cacctgcaga tgtggcagggt tattcatttg gcagctttgc cgacagactt      600
ccagacagtg aggcagttct gagctgtctg acagtattac ttctgcacca catttggcag      660
ccaaaattcc tggaaaggctc actccagctc caatctgcgg gacgtggacc tccaggacag      720
ccccgtcggc ccccggaacc ggctcctccg agaatcgaaa gcgctgggcc cggaaccctt      780
gtcctcggaa atcgtgctcg cccagtaggg cgtcgttggg cccggggcgg gcgggggacc      840
gcggaaggct ccgggctgcc agactgcgcg agcgggaagc cgcgggccac gtggccgtag      900
cacctgacgg caagaagggg aaagcccaga tctggtgata accctgccgc gctagcgagc      960
gaagaaagcc cggagcaagg cgaaagagac

```

```

<210> 29
<211> 622
<212> DNA
<213> Homo sapiens

```

```

<400> 29
tttttttttt ttgtgttgat aaagctttat ttataaacac actcacaggg ccagatttgg      60
gccacggggc atagttgcc a gcccggcttt aactgctggt cctcacgtta gtctcactgc      120
ctcctgcagg gtgggcatgt ggggtgctgtg ttcacccagc ccttcctcc accccacaaa      180
caccctgggt gctgtcctgg agcgcgacac actgggcata cgtgagggtg ggctgttcaa      240
tgccgttgtc cgctggctcg aggcagagtg tcagcggcag cagctgcagg tgacgccaga      300
gaacaggcgg aaggttctgg gcaaggccct gggcctcatt cgcttccgc tcatgacct      360
cgaggagtgc gctgcaggta acagagctcg ggctcagggg ctggtttggg aggggagtgg      420
cacacagggt ggcatactggg taccgaggat agtgcccccg agttcactgc ggaaagcctg      480
gcagatgcct ggcataataca gataggaaga aacctggctt gtgaggacgc gtccacaggg      540
ccatctgtta gcccgggcc ggctctgtcc ccaccgtgca cactgccaga cccgcctct      600
cgtgtctgtc cagctgtttt gg

```

```

<210> 30
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(181)
<223> n = a,t,c or g

```

<400> 30  
 tttttttttt ttgagacgga gntgngetct gtnaccacagg ntagagtga atggcacgnt 60  
 ctcggtcac tgcaagctct gcgtcctggg ttgacgccat tctcctgcct cagcctcccg 120  
 agtagctggg actacaggag cttcgccacc aattccagcc tggggtggac agagtataa 180  
 g 181

<210> 31  
 <211> 1956  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 aaactccgaa cacatccaaa catcagaagg aacaaactcc agacacaccg cctttaagaa 60  
 ctgttacgct caccgcgagg gtccacggct tcattctcca agtcagacca agaaccaccc 120  
 aattccggac acaaaaggcg tagcgtgcct cctgtgattg ttgaagagct gtggtgtgct 180  
 gctgagtggc gtgtgtattc catgtgaggg gaaggggtcca acagtcttgg tcattcagac 240  
 tgcagttccc caggacagac ccacgaagtc aagcatgcgg agtcagacca agcctggaa 300  
 ccagccatc agagcagggg gccacggccc agaccgggtg cggcctctgc ctgcagcctc 360  
 ttccggcatg aagagttcta agtcttcaac ttcttggct ttgagttcc gactcagcag 420  
 gctcaagagg gccagcagtg aggacacgct caacaagcca ggaagtaccg ctgcatcggg 480  
 ggtggttcgc ctgaagaaga ccgccactgc cggagccatc tcggagctca cggagagccg 540  
 cctgaggagc ggcacagggg cctttacaac aactaaacgg acaggcattc cagccccacg 600  
 ggaattttca gtaactgtct caagagagag gtctgtgcca cgtggtccct ccaacccag 660  
 gaaatcagtg tccagtccaa ctctctccaa cactcccact cctacgaaac acctgaggac 720  
 cccttcaca aagcccaagc aagagaatga aggtggagaa aaggctgcgc ttgagtccca 780  
 agttcgggaa cttttggcag aagccaaagc aaaagatagt gaaattaaca ggcttcgaag 840  
 tgaactaaag aaatacaaaag agaaaaggac tctgaacgct gaggggactg atgctttggg 900  
 cccaatgtc gatggaacat cagtctcccc aggtgacacg gaacctatga taagagctct 960  
 tgaggagaag aacaagaact ttcagaaaga gctttccgat cttagaggaag aaaaccgggt 1020  
 cctgaaggag aaactgatct atcttgagca ctcccaaat tcagaagggg cagcaagtca 1080  
 cactggcgac agcagctgcc caacatccat aactcaagag tcaagcttcg gaagcccaac 1140  
 tggaaatcag ttgtccagtg acattgatga gtataaaaaa aacatacatg gaaatgcatt 1200  
 acggacatca ggctcctcaa gttagcagtg taccaaagct tctttgtcgc cagatgcttc 1260  
 cgactttgag cacttacag cagagacacc ctcaaggccc ctgtcctcca ccagtaaccc 1320  
 ctttaagagt tcaaaagtgt ctactgctgg gaggttccca aacagcgtaa gtgaattgtc 1380  
 cctggcttcc ctacagaga agatacaaaa gatggaagaa aaccaccata gactgcaga 1440  
 agaactacag gctactctac aagaattatc agaccagcaa caaatggtac aggaattgac 1500  
 agctgaaaat gagaagctgg tggatgaaaa gacgatttta gagacatcct ttcacagca 1560  
 tcgagagagg gcagagcagc taagtcaaga aaatgagaag ctgatgaatc ttttacaaga 1620  
 gcgagtaaag aatgaagagc ccaccactca ggaaggaaaa attattgaac tggagcagaa 1680  
 gtgcacaggt attcttgaa agggccgctt tgaaagagag aagctactca acattcagca 1740  
 gcagttgacc tgtagcttgc ggaaggttga ggaagaaaac caaggagctt tagaaatgat 1800  
 taacagctcg aaggaagaaa atgaaaaact gaatgagttt ctagaactgg aacggcataa 1860  
 taataacatg atggccaaaa ctttgggaaga gtgtagagtt accttgggaag ggctaaaaat 1920  
 ggagaatgga tctttgaagt ctcatattgca ggggtga 1956

<210> 32  
 <211> 513  
 <212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 32

ctcagcacca	caaggaagtg	cgggacccac	acgcgctcgg	aaagttcagc	atgcatgaag	60
tttggggaga	gctcggcgat	taacacagcg	acccgggcca	gcgcagggcg	agcgcaggcg	120
gcgagagcgc	agggcgggcg	ggcgtcggtc	ccgggagcag	aaccgggctt	tttcttggag	180
cgacgctgtc	tctagtcgct	gatcccaaat	gcaccggctc	atctttgtct	acactctaata	240
ctgcgcaaac	ttttgcagct	gtcggggacac	ttctgcaacc	ccgcagagcg	catccatcaa	300
agctttgcgc	aacgccaacc	tcaggcgaga	tgagagcaat	cacctcacag	acttgtaccg	360
aagagatgag	accatccagg	tgaaaggaaa	cggctacgtg	cagagtccta	gattcccgaa	420
cagctacccc	aggaacctgc	tcctgacatg	gcggcttcac	tctcaggaga	atacacggat	480
acagctagtg	tttgacaatc	agtttggatt	aac			513

&lt;210&gt; 33

&lt;211&gt; 712

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

acagacatgg	ttccagctct	gtagaactga	gagaaagaat	aaacaagtca	cacattagcc	60
cttcaaaaag	atgaccgacc	tcttgagaag	tgttgtcacc	gtaattgatg	ttttctacaa	120
atacaccaag	caagatgggg	agtgtggcac	actgagcaag	ggtgaactaa	aggaacttct	180
ggagaaaagag	cttcattccag	ttctgaagaa	cccagatgat	ccagacacag	tggatgtcat	240
catgcatatg	ctggatcgag	atcatgacag	aagattggac	tttactgagt	ttcttttgat	300
gatattcaag	ctgactatgg	cctgcaacaa	ggtcctcagc	aaagaatact	gcaaagcttc	360
aggggtcaaag	aagcataggc	gtgggtcaccg	acaccaagaa	gaagaaagtg	aaacagaaga	420
ggatgaagag	gataaccag	gacataaatc	aggttacaga	cattcaagtt	ggagtggagg	480
agaggagcat	ggatatagtt	ctgggcactc	aaggggaact	gtgaaatgta	gacatggggtc	540
caactccagg	aggctaggaa	gacaaggtaa	tttatccagc	tctgggaacc	aagaggggatc	600
tcagaaaaga	taccacaggt	ccagctgtgg	tcattcatgg	agtgggtggca	aagacagaca	660
tggttccagc	tctgtagaac	tgagagaaa	aataaacaag	tcacacatta	aa	712

&lt;210&gt; 34

&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

cagattttctc	aggtagctc	agatagcaat	ccactgtgtt	cctttatctc	cagcagatat	60
atatcaatat	cttgaagcag	ttttctactc	aatttagaag	aacttctggt	ttaaatttaca	120
attctttttt	ctctcccatg	cttgttgttt	ctcattcaaa	caagactggc	atagctactt	180
tatgagggtg	ggtctccctg	aattttaagt	tccaaagatc	tctggacctg	atcatattga	240
ctttattccg	tgggatcaac	tcttcattggc	cagttcttcc	tctgtcactg	agttcttagt	300
gctgggcttc	tctagccttg	gggaattgca	gcttgccttc	tttgagctct	ttctctgcct	360

ctatttgatt	atcttgagtg	gaaacatcat	catcatctca	gtcattcatt	tggatcacag	420
cctccacaca	cccatgtact	tctttctagg	tattctttct	atctctgaaa	tcttctacac	480
aactgttatt	ctgccaaga	tgtttatcaa	cttattctct	gtattcagga	cactctcctt	540
tgtgagttgt	gccacccaaa	tgttctacga	aatcgtcggc	cggggaactc	aggaacggtc	600

<210> 35  
 <211> 985  
 <212> DNA  
 <213> Homo sapiens

<400> 35						
tttcgtccta	ctgtccctgt	cctgcccttg	cagacatgtg	tcctgccctt	gcagacagcc	60
gcaggcaggc	agggaccacc	atgagcaacc	cctgtctctcc	tcctgagggg	cagcacagag	120
cctggaggag	gcctgagtgg	ggttgaggcc	tggggcgagc	tgggggtggag	gggcactggc	180
tgccgggctc	cagggatctt	ctccccctcc	tgccccggag	ggtgctggca	caggggtggg	240
gtcactccc	actccgtaga	cacaatgatc	agaggctcctg	ggtgtctggg	gaagctgggc	300
tgtgcgtgta	tgcgtctacc	atgtgggggt	gcctgtgagt	gtgctggggc	gtctgcagtg	360
aaggcctcct	gagaccactc	cacggaaaaca	ccgggaatcc	ctgcagctga	gcctgtctct	420
cacgggaccg	ggaagctgga	gagagcccca	accctgcccg	ctggggccga	gctccctgct	480
cctgcagcag	tcctgtgccc	cacactctga	gtctgcccta	tcacacagctg	ctgggcctct	540
ctgtggccac	catggtgact	cttacctact	tgggggcccc	ctttgctgtc	atccgccgag	600
cgtccctgga	gaagaacccg	taccaggctg	tgcaccaatg	ggggactcag	cagcgactta	660
tccaacatcc	agagagcggg	agcgagggcc	agagcctgct	ggggccactc	agggccttct	720
ctgcgggggt	gagcctggtg	ggcctcctga	ctctggggagc	cgtgctgagc	gctgcagcca	780
ccgtgagggg	ggcccagggc	ctcatggcag	ggggcttctc	gtgcttctcc	ctggcgcttct	840
gcgcacaggt	gcagggtggtg	ttctggagac	tccacagccc	caccaggtg	gaggacgcca	900
tgtctggacac	ctacgacctg	gtatatgagc	aggcgatgaa	aggtacgtcc	cacgtccggc	960
ggcaggagct	ggcgccatc	cagga				985

<210> 36  
 <211> 464  
 <212> DNA  
 <213> Homo sapiens

<400> 36						
ccgtatcggc	gtttatatac	tgaagataag	cctgatgagt	aacaggcttg	ctcgtcatac	60
tttcgtgagt	attggcggtt	tacaggcaag	tcgtaaaata	acagcctggc	tattcagagt	120
atgataaaaa	cagggggcaa	gggatgttgc	ttaatatgat	gtgtggtcgt	cagctgtcgg	180
caatcagttt	gtgcctggcc	gtaacattcg	ctccactgtt	caatgcgcag	gccgatgagc	240
ctgaagtaat	ccctggcgac	agcccggttg	ctgtcagtga	acagggcgag	gcactgccgc	300
aggcgcaagc	cacggcaata	atggcgggga	tccagccatt	gcctgaaggt	gcggcagaaa	360
aagcccgcac	gcaaactgaa	tctcaattac	ccgcagggtta	caagccgggt	tatcttaacc	420
agcttcaact	gttgtatgcc	gcacgcggta	tttcctgcag	cgtg		464

<210> 37  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
 tcgcacaaga gctgctgatg tctatgtctt ttcgctcacg ggaaaatctc gaaacgtgag 60  
 ttccctcaacc gtgcggcgaa gtgcggtagg cgggatgtcg gcattagcgt tgtttgattt 120  
 gctcaagcca aattatgcgc tggcgactca ggtagagttt accgaccgga aaattgttgc 180  
 tgagtaacac acgtatcctt cgccaaatgg tcacggcgag gtgcgggggt atctgggtgaa 240  
 gcccgcaaag atgagcggca aaacgccagc cgtagtgggt gtgcatgaga atcgtggact 300  
 gaatccgtat atcgaagatg tggcacggcg agtggcgaag gcgggggtata tcgccctggc 360  
 acctgacggc ttaagttccg ttggagggtta tccgggaaat gatataaagg tggatatccg 420  
 agcggcccc 429

<210> 38  
 <211> 556  
 <212> DNA  
 <213> Homo sapiens

<400> 38  
 gagaataacc tagacgttat tgacttgatg ccccgcgctg gtaaggcgct ggataccacg 60  
 cagcgcgcg tgctgtttta tgcagtaacc cgatggggca attaatgaa acagagacat 120  
 ggcaattcct tgctgacaac agaaacgaaa tgtatatcat gccgcttagg tgtgccgttg 180  
 tcacctcaac ggcgattcca ggctataagg atagaagaag tgaaattgag atggtttgcc 240  
 tttttgattg tgttattagc gggttgttca tcaaagcatg actatacgaa cccgccgtgg 300  
 aacgcgaaa gtccgggtgca acgtgcgatg cagtggatgc caataagcca gaaagccggt 360  
 gcagcctggg gcgtcgatcc acaattgatc acggcgatta tcgctatcga atcgggtggg 420  
 aatccgaacg cggtagtaaa atcgaatgcc attgggtttg tgcagttaaa agcttcaacc 480  
 tccggacgtg atgtttatcg ccgtatgggc tggagtgggt agccgacgac cagcgagctg 540  
 aagaattcct caagac 556

<210> 39  
 <211> 890  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 accacgctgc aggaattcgg cagcaggcca aaccaagag aagtttttat gctgccaggg 60  
 atttgtaaca gtaccgacac cagtacccaa acttcaaaga tatccgatat caaaatgact 120  
 tgagcaatct tcgtttttat aagaataaaa ttccattcaa gccagatggt gtttacattg 180  
 aagaagttct aagtaaatgg aaaggagatt atgaaaaact ggagcacaac cacacttaca 240  
 ttcaatggct tttccccctg agagaacaag gcttgaactt ctatgccaaa gaactaacta 300  
 catatgaaat tgaggaattc aaaaaaaca aagaagcaat tagaagattc ctccctggctt 360

ataaaatgat	gctagaat	tttgaataa	aactgactga	taaaactgga	aatgttgctc	420
gggctgttaa	ctggcaggaa	agatttcagc	atctgaatga	gtcccagcac	aactat	480
gaatcactcg	tattctttaa	agccttggtg	agcttggata	tgaaagtttt	aaatctcctc	540
ttgtaaaatt	tattcttcat	gaagctcttg	tggagaatac	tattcccaat	attaagcaga	600
gtgctctaga	gtattttgtt	tatacaatta	gagacagaag	agaaaggaga	aagctcctgc	660
ggttcgccca	gaaacactac	acgccttcag	agaactttat	ctggggaccg	cctcgaaaag	720
aacagtcgga	gggaagcaaa	gccagaaaa	tgtcttcccc	tctcgctcc	agtcataaca	780
gtcaaaacttc	tatgcacaaa	aaagccaagg	actccaaaaa	ttcctcctca	gctgttcatt	840
taaatagcaa	aacagctgaa	gacaaaaaag	tggcaccaaa	agagcctgtg		890

<210> 40  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 40	
accggctgcc	atcttagtct agggactgag gagtcgccgc cgccccgagt cccggtacca 60
tgcatttcac	gggtggccttg tggagacaac gccttaaccc aaggaagtga ctcaaactgt 120
gagaacttca	gggttttccaa cctattggtg gtatgtctga cagtggatca caacttggtt 180
caatgggtag	cctcaccatg aaatcacagc ttcagatcac tgcatctca gcaaaactta 240
aggaaaataa	gaagaattgg tttggaccaa gtccttacgt agaggtcaca gtagatggac 300
agtcaaagaa	gacagaaaaa tgcaacaaca caaacagtcc caagtggaag caaccctta 360
cagttatcgt	taccctgtg agtaaattac att 393

<210> 41  
 <211> 437  
 <212> DNA  
 <213> Homo sapiens

<400> 41	
gcattccttg	aaagaaatgt tacagccaga tcacagcgca gaacgataaa atggcacaat 60
ccaacaacaa	ttttacattt tcgcgaccgc tttggctgct ttcagggtccg tttcaatgat 120
atactgccag	tcgttaattc aaaaatagtt gataattaca acaatctatt gaattgaaac 180
gctttccttc	gtaattcgca actggaacac gcacgctatg agtaaaccga ttgtgatgga 240
acgcggtggt	aaatacccgcg atgccgataa gatggccctt atcccgggta aaaacgtggc 300
aacagagcgc	gaagccctgc tgcgcaagcc ggaatggatg aaaatcaagc ttccagcgga 360
ctctacacgt	atccagggca tcaaagccgc aatgcgcaaa aatggcctgc attctgtctg 420
cgaggaagcc	tcctgcc 437

<210> 42  
 <211> 392  
 <212> DNA  
 <213> Homo sapiens

```

<400> 42
tcccctgCGT caattttcct gacagagtac gcgtaataac caaatcgCGc aacggaaggc      60
gacctgggtc atgctgaagc gagccaccag gagacacaaa gcgaaagcta tgctaaaaca      120
gtcaggatgc tacagtaata cattgatgta ctgcatgtat gcaaaggacg tcacattacc      180
gtgcagtaca gttgatagcc ccttoccagg tagcgggaag cataatttcg caatccagag      240
acagcggCGt tatctggctc tggagaaagc ttataacaga ggataaccgc gcatgggtgct      300
tggcaaaccg caaacagacc cgactctcga atggttcttg tctcattgcc acattcataa      360
gtaccatcc aagagcacgc ttattcccca gg                                392

```

```

<210> 43
<211> 555
<212> DNA
<213> Homo sapiens

```

```

<400> 43
tggtcgcgc tcataatgg gagttttgat actgtggatt gccggttcga tgtggtagcc      60
ttcacgggga atgaggttga gtggattaag gatgccttta atggccactc ataattaagg      120
tttaaggatt agcgtgcaag aaagaattaa agcttgcttc actgaaagca ttcaaactca      180
aattgcggcg gcagaggcgc ttccggatgc catctcccgt gcagccatga cgctgggttca      240
gtctctgctc aatggcaaca aaatcctctg ttgtggtaat ggaacttcg ctgccaatgc      300
acagcatttt gctgccagca tgatcaaccg tttcgaaacg gagcggccca gcttacctgc      360
cattgcacta aatactgata atgttgtctt aacggcgatt gccaacgata gcttacatga      420
tgaagtgtat gcaaaacagg tgcgggcgct gggatcatgc ggagatgtat tgtagccat      480
ttccaccggt ggcaacagcc gcgatattgt taaagcagtt gaagccgcgc ttacgcgtga      540
tacgaccatt gtggc                                555

```

```

<210> 44
<211> 553
<212> DNA
<213> Homo sapiens

```

```

<400> 44
ctatgacctg attacaattc aggtccgacc cgagatctcc aaaatgccag gacgctgtgg      60
ctacacaagc taaccatgct gattaatgaa aagaaactca acatgatgaa tgccgagcac      120
cgcaagctgc ttgagcagga gatgggtcaac ttccgtgttc agggtaaaga ggtgcatatc      180
gagggctata cgccggaaga taaaaaataa aaacagtgcc ggagcacgcc tccggcaact      240
tgcataaaaa caaacacaac acgcaccgCG aatgatgaaa aaatatctcg cgctggcttt      300
gattgcgCG ttgctcatct cctgttcgac gaccaaaaaa ggcgatacct ataacgaagc      360
ctggggtcaaa gataccaacg gttttgatat tctgatggcg caatttgccc acaatattga      420
gaacatctgg ggcttcaaag aggtggtgat cgctggctcct aaggactacg tgaaatacac      480
cgatcaatat cagaccCGca gccacatcaa cttcgatgac ggtacgatta ctatcgaacc      540
catccccggg aca                                553

```

<210> 45  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

<400> 45  
 tctcgttacg acttcgagcg ttggaccgag ggatctctct actatcgctg caagcgagcc 60  
 agaaaaaact ggatgaactg atcgaacagc actaaaccca ggacaggaat cgcgaatgaa 120  
 caggctttttt tcaggctcgtt ccgatatgcc ctttgcgctg ctgcttctcg cgcgcagctt 180  
 attactgctg ggcggtctgg ttgcgtggcc gatggtgtcg aatatcgaaa tcagtttttt 240  
 acgtctgcgc ctcaatccca acatcgagtc aacgtttgtt ggggtgagca actatgtgcg 300  
 taccctctcc 310

<210> 46  
 <211> 627  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
 ctgcgtgact cgcttcgctt ccccgacgag ctgggttccc ggagcgcaga gccagcgtt 60  
 agcgggtggg ctccccgagg cccctgccc tcgccgggct gctccagggt gtcgctcctc 120  
 tggctgctcc cgaaggggct tctggccctg aggacggtgg tgccaagcga acttcatttt 180  
 taaaaagaac tgggtggatga gaagagcgag cgagggcgag ctatggaccc tgtgagtcag 240  
 ctggcctctg cgggcacctt ccgggtgctg aaggagcccc ttgccttcct gcgagccctg 300  
 gaattgcttt ttgcaatctt tgcatttgca acatgcggtg gctattctgg aggcctgcgg 360  
 ctgagtgctg actgcgtcaa caagacagaa agtaacctca gcatcgacat agcgtttgcc 420  
 taccatttca ggttgaccca ggtgacgttt gaggtgcccc cctgcgaggg aaaggaacgg 480  
 cagaagctgg cattgattgg tgactcctcg tcttcagcag agttcttcgt cactgttgct 540  
 gtcttcgctt tcctctactc tttggctgcc actggtcgtt acattttctt tcacaacaaa 600  
 aaccgggaaa acaaccgggg ccactg 627

<210> 47  
 <211> 998  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 acctgggcac cgtgtcctat ggcgccgaca cgatggatga gatccagagc catgtcaggg 60  
 actcctactc acagatgcag tctcaagctg gtggaaacaa tactgggttca actccactaa 120  
 gaaaagccca atcttcagct cccaaagtta ggaaaagtgt cagtagtcga atccatgaag 180  
 ccgtgaaagc catcgtgctg tgcacaaacg tgacccccgt gtatgagtct cgggcgcggcg 240

```

ttactgagga gactgagttc gcagaggctg accaagactt cagtgatgag aatcgcacct 300
accaggcttc cagcccggat gaggtcgctc tgggtcagtg gacagagagt gtgggcctca 360
cgctggctcag cagggacctc acctccatgc agctgaagac cccagtggc caggtcctca 420
gcttctgcat tctgcagctg tttcccttca cctccgagag caagcggatg ggcgtcatcg 480
tcagggatga atccacggca gaaatcacat tctacatgaa gggcgctgac gtggccatgt 540
ctcctatcgt gcagtataat gactggctgg aagaggagtg cggaaacatg gctcgcgaag 600
gactgcggac cctcgtgggt gcaaagaagg cgttgacaga ggagcagtac caggactttg 660
aggtgagccg actcccaggc atccccatcct cctacgacgg tgccttcctt acgctgaaat 720
tagttcttcc tgtctttgta tgaaattaga gctgggatcg ctatagtcta ggagtgaagg 780
cagcttcgct cagcaggagc atggggggat cctgtctgca tttctgttcc caccatttct 840
ccagcttgct ggggaaggag ggttacagaa gcaaagaagt gccagtttcc ttagaattgt 900
gcttgataac tcctcaatga tcacacgcca gccgagctga gtacacataa gagtatgtgc 960
acataggcgc ctccccctct gtccccagag cccatgcg 998

```

&lt;210&gt; 48

&lt;211&gt; 864

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(864)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 48

```

tttttttttt ttgagacaca gtctggctat gtcaccagc ctgagtacag tagcatgac 60
ctggttcgct gcaacctcca cctcccaggc tcaagtgatc ctccacctc agcctcctga 120
gtagctagga ctacaggtac gtgccacaac acctggctaa tttttttatt tttttagag 180
acaagggtct ccctacgttg tccaggctgg acttgaactc ctgggttcaa gcgacccac 240
caccttggcc tcccacagca ctggggttac aggaggagc cactgcacct ggccctgtct 300
ttactgatgg tccctgcccc tgccctccac acctaacctt gggcaccac tcccgaagct 360
ctcctactgg ctgcagggtc tgcctctgtg aggacagtga agccgatgac acgggaggtg 420
aagtcgaagg ccgtctgctg gccatcgtgg atcactgaga tgcagtggcg gtccccgtag 480
ctggcccgct gcatgccacc ctggaagatg gtgaagggca acccctgcct agtggtcagc 540
cagaggattc tggtaatcgc tttgcaagga aagggaacct aaggcacgag gctgcggagg 600
ggctctgggt gctgggcttc gctggacacg ggccactgg cagtagctgc cgtcagagtg 660
acagctgacg agcaggcggc cgtcccgtg ccaccagatg ttctccagtt gctggctgct 720
gaggaagtgg tagagcacgc ggctgccctg taggtcccag atgacaacga ggccctcggc 780
gtagccgatc aggatctggg tggggtcttc aggtgcttcc tgcattgctt caccatttng 840
aacaacacgc cgtggggggc cctc 864

```

&lt;210&gt; 49

&lt;211&gt; 1327

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

```

tttcgtgagc atttgagggc tgtttatgat ctatggggta aaactctctg actgactgga 60

```

tgaggaaaat	gaaatgcgag	aggggtgagc	ccaaggttca	ttcatctgct	caatcgaggc	120
cactcattct	ggccactgtg	tgccagatgc	tggggattct	gtcctcttgg	gagctgacgt	180
agcccagggtg	gtggctgtgg	gctgctggag	gtggggatcc	aggtggagga	gcaagtctag	240
ggaagtgtgc	tggggaggcc	ctctctgagg	aggtgacatg	ccagctgaga	tctgaatggc	300
aggaaggagt	ggccatgagg	acatgggtga	tgacagtctg	ggtagaaaga	tgaaggaggg	360
gaagcaggta	aggagtgtgt	atctaattct	gggagccact	ggagggtgaa	agcagggtt	420
agaagtcagg	gatttacatt	ttaaagagat	cacctctggc	agggctttgt	taagagtggc	480
ctgcaagagg	ccaagcatgg	ttccaggggg	ccagttgcag	agggctgggtg	caggagccca	540
ggcaaggatt	acggggctca	gtcctgcccct	gtggggagca	agagtacacg	gctggattcc	600
agagctgcca	gcaggcctac	ccccctggggc	ctgcctgtgg	cctctcatcc	ctgcctgtcc	660
cagtagacac	tgggggtggg	taagtgtccc	cgtgaagggg	gggcccaggc	gattctgggt	720
ctggccctgt	gtctacaggg	gagcaccgtg	gcctggggcg	tggcgtctcc	aagggtcgga	780
gcctgaagat	ggacaggaag	gtgtggacag	aaacacttat	cgagggtggg	atgccctgc	840
ttgccaccga	tacttgggg	ctgccccatt	caacagctgt	ctgggtctcc	cagccccctc	900
cctatctcag	tgaccacagc	accttgagc	tggaaagaga	ccctttgtga	taatatagtg	960
ggtggggatt	tcggaaaagc	aatttttggc	aaagtcagca	aactggccag	tgagctaaga	1020
atgtttttat	agttgtaaag	tgttattttt	ttttaagaa	aaaaaaagga	agaaaatgca	1080
gcagagactg	tatgtgttct	gtaaagccga	aaataattac	tatttcgccc	tttagagaaa	1140
gaatttgcta	acttctgatc	taatttcact	gtcatccatt	gaatagatgt	gtaaactgag	1200
gtctggggca	gggctgtaat	ctgcctgaga	ttaccctgta	aatgcatatt	gaccaccatc	1260
cctgcctctt	tctgtcccac	ttctgaatga	cccagggcct	tctcccctac	cttgcacagc	1320
ctgtatt						1327

<210> 50  
 <211> 436  
 <212> DNA  
 <213> Homo sapiens

<400> 50						
ctgtcgtgca	attccgagca	ggcactgctc	agtctggtgc	ctgtgcagag	ggagctactt	60
cgaaggcgct	atcagtcacg	ccctgccaaag	ccagactcca	gcttctacaa	gggcctaggt	120
acctgcccct	cccagctgag	gctttctgag	ccccaccga	ccccagaca	cctcagcgta	180
gcctctgtct	cccatcacat	gttcccctct	catcgctccc	tttgcccaca	tcttccagac	240
ttcttgcgcg	cccattccc	atcagacaat	ctcccctaca	ccctccagtc	ccctttcccc	300
tcacctctctc	cagctactcc	ctctgaccat	gctcttatcc	tccaccacag	acttaaatgg	360
gggcccagat	gaccctctgc	agcagacagg	ccagctcttc	gggggcctgg	tgcgatgat	420
ccggcgccgc	tacccc					436

<210> 51  
 <211> 481  
 <212> DNA  
 <213> Homo sapiens

<400> 51						
tgcctagca	gtaagttggt	tggcatgtgg	tgggcaggca	gggctggcag	tagtcggacc	60
acttcagtct	ccctgctctg	ccttccccag	caccattcgg	tgcctcgaac	ctcctggtga	120
accccctgga	gccccaaaat	gcagataaga	tcaagatcaa	gacgcagac	ctgggcaacg	180
cctgctgggt	ggtatgagca	agtgtgggag	agcagagtgg	ggggccctgc	tccaagggtg	240



gaggcacagg	gccgctcttg	gggagcccta	ccccagtctg	cagtgcacgt	gaaccgtcgg	300
ctgggtgggc	actggtcctg	cccagtcaac	agcactgggg	ccatggccaa	gggcaggggc	360
cactaggaag	ggatcagcct	cagcctcaga	tcactggggc	tgtccctctt	ggaggacctg	420
gggaccccg	ggctcacagc	aaacccact	gagcttctcg	ggtaggcgga	tccgggtggg	480
g						481

<210> 52  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<400> 52						
cccgggtcga	cccacgcgtc	cgagctcctc	gttgtggaga	caagatcaaa	aatcatatgt	60
atagaatgtg	actgtggctc	ccttaaagat	tgtgccagtg	atagatgttg	tgagacctct	120
tgtacccttt	ctcttggcag	tgtttgcaat	acaggacttt	gctgccataa	gtgtaaataat	180
gctgcccctg	gagtggtttg	cagagacttg	ggtggtatat	gtgatctacc	ggaatactgt	240
gatgggaaaa	aggaagagtg	tccaaatgac	atctacatcc	aggatggaac	cccatgttca	300
gcagtatctg	tttgtataag	aggaaactgc	agtgaccgtg	atatgcagtg	tcaagccctt	360
tttggctacc	aagtgaaga	cggttcccca	gcgtgctatc	gaaaattgaa	taggattggt	420
aaccgatttg	gaacg					435

<210> 53  
 <211> 728  
 <212> DNA  
 <213> Homo sapiens

<400> 53						
ccgggtcgac	ccaacgcgtc	ggacgccagt	ttagcccagg	tccacggact	acaatgtttc	60
gtattcctga	gtttaaatgg	tctccaatgc	accagcggct	tctcactgat	ttactatttg	120
cattagaaac	tgatgtacat	gtttggagga	gccattctca	caaagtctgt	aatggatttt	180
gtcaatagca	atgaaaatat	tatttttgta	cataacacaa	ttcacctcat	ttcccaaatg	240
gtagacaaca	tcatcattgc	ttgtggagga	attttacctt	tgctctctgc	tgctacatca	300
ccaactgggt	ctaagacgga	attggaaaat	attgaagtga	cacaaggcat	gtcagctgag	360
acagcagtaa	ctttcctcag	ccggctgatg	gctatggttg	atgtacttgt	gtttgcaagc	420
tctctaaatt	ttagtgagat	tgaagctgag	aaaaacatgt	cttctggagg	tttaatgcga	480
cagtgcctaa	aattagtttg	ttgtgttgct	gtgagaaact	gtttagaatg	tccgcaaaga	540
cagagagaca	ggggaaataa	atcttcccat	ggaagcagta	aacctcagga	agttcctcaa	600
agtgtgactg	ctacagcagc	ttcgaagact	ccattggaaa	atgttccagg	taacctttct	660
cctattaagg	atccggatag	acttcttcag	gatgttgata	tcaatgcct	tcgtgctggt	720
gtctttctg						728

<210> 54  
 <211> 2228  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

tttttttttt	ttcctgaaat	gtaaattggt	tttaatatat	ttaagagcac	acagaagtct	60
tgatttataa	aaaaataaat	atataacatg	acaaatttac	tgatgatcct	ggagctctga	120
ggtcaaactc	tttaaagtat	cagtgtaaaac	ataaaacatc	catgatctgt	taacacacac	180
aggagcatat	tccagttgta	aaaaacaaat	tccttgaagg	ctcagaacga	acaaaaatca	240
gtcttttatg	cagaaagcac	atccaaagct	aggcaatgaa	gttcagcctg	ggccacgtga	300
accttttcacc	agccagccta	taacctatgg	agccaggaca	ggaaagcatg	atccttcagc	360
tcagacgccc	accagggctt	ccagacaact	gcagaatgaa	agagtcacct	agaggctccc	420
cagcccctgc	tgccatcata	aagcacggga	gggattgttt	tgtccttagc	ggctctgtcc	480
taaatttgag	agcaggagac	tgagaagggt	atgctcatta	aatattgtca	ttgtaacacg	540
gaatggaaat	catgatcctt	gcccattggg	actgagctga	aagaaagagg	aacctcacat	600
gaggctttcc	tagagaccag	gatgttgggt	gagtgggctg	gcacttctca	agtgggcaag	660
gaagaactgc	ttttctccag	ctgacatgct	ctcaggggtg	aagaagttta	gcttaaaata	720
ctgatggcgc	ctgcataaac	tggggatttg	ggaactgagt	ttttagctct	gtgacacaca	780
acataaaaaa	caaaaatcca	gtctcttagt	ctaaattcgg	attaaaatct	gaaatgtttt	840
tatggagttg	ccaacaggct	ggaatgtacc	tgatacaatt	taatctgctt	ttatttcttt	900
ggctgtcttc	caaaccactt	tcttcttgta	attcttaagt	tggttagttc	tccttctcca	960
gaaaaattac	ccctaagaat	cttccctaata	gtgagggtgt	acttccgaat	agaagagtcc	1020
ttcggtgaa	atggcatctc	caaggcctac	agttcgaatg	gggtctttac	acaccaatac	1080
tggtgtgaag	tggaaggata	ttccctctct	gtgccattct	actactggct	tgtttgggtt	1140
taataacaat	ctggagcctg	cctccgaatg	ggaagtcatg	aactcttggg	gtgccctcag	1200
agacactcgg	ctggtgtcta	tggtttctgt	ggcgagggcc	tgtgtcccag	ccacacgagc	1260
tcctgcagcc	acggctgcca	gctgggtggc	ccagtgtcca	tccacagttg	ccaggatgtg	1320
gtagaccagc	gtgtggaaat	ggatcctggt	gagatccgag	gctctgcttt	tactcctccc	1380
atgttctttc	aagatccaga	agaggatgtc	actgaccatg	cccacatcag	gaacaccgtt	1440
ccaggaaagag	agagaagagt	gagggtccaga	ggctgactgg	gtgagaaata	acagctcctg	1500
ttcattcagc	ccaagggaag	tcaccgcggg	aaagacctgc	tgaagggaaca	atgctgtctca	1560
tgagctccct	gttagtcata	ctggcccagc	tctaggtgaa	actggaatac	cagtggggat	1620
gtcagaaatg	gaggttacaa	cctccaagag	tctcttctc	tggagctcct	tgctttgtcc	1680
ctccatcatg	tgcaatccag	agaggcccc	caggtctggc	tgaaactcct	ccaggctaga	1740
cacaaacacc	tccagcatat	tcatggcccc	gttggagagg	tcgtgagaga	agatgaatcg	1800
gttggcatgg	ggagctttta	actggcccca	ctcctccct	gcttgatact	ctaaaatgag	1860
gtggaaactca	tccacttcct	gcaatgactc	tgggtggaaca	aagacattgt	catcaagaag	1920
ctcatgtagc	tttggacca	ctggaccgca	aagaagaacc	tttaaactctg	agttggctgc	1980
aaattttctgt	ccaattaaag	ctgcatttcc	tcctacatag	tgtctgggctc	ctgggaactc	2040
tgacgcaccc	tgggcaatgt	cgtgaaaagt	ttccttatca	ctgaagaagc	gctcagcagc	2100
tgtcccttc	cccataagct	gaatgaaggc	ttcttcaga	tcattccttg	aatgcagaat	2160
gctgtgatct	ttcccatctc	caggactaag	gccaaagtgc	tgcaagagct	tcacccctga	2220
ggaattca						2228

&lt;210&gt; 55

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

gcaggagttc	aagaccaacg	tggccaacat	ggggaaagcc	catcactact	aaaaatacaa	60
aaactagcca	ggcgtggtga	cacacatctg	taatcccagc	tactcgaggc	gctgaggcag	120
gagaatcact	tgaaccagga	ggcagaggtt	gcagtgaacc	gagatcatgc	cactgcactc	180
cagcctgggc	cacagagcaa	gactccatct	gacaactagc	tgttccagcc	cccagccact	240

tgagtcacat	cagctgaggc	cccacacacc	aagaagcaga	ggtgagtccta	atccacagag	300
ccctggctcag	acatgatgac	ggtggcttca	cccgggggtc	tccgcacagc	agcggcctcg	360
ggtaagcaga	acctcgctcc	ggggtttaca	aatccttcct	cgtgc		405

<210> 56  
 <211> 1652  
 <212> DNA  
 <213> Homo sapiens

<400> 56

actaggggag	gtgctcaagt	gccagcaggg	cgtatccagt	ctggcctttg	ccctggcctt	60
cttgacgcgc	atggacatga	agccgctggg	ggtcctgggg	ctgccggccc	ctacggctcc	120
ctcgggctgt	ctttccttct	gggaggccaa	ggcgcagctg	gccaaagagct	gcaaggtgct	180
ggtagacgcg	cttcgacaca	acgccgccgc	tgctgtgcc	ttttttggcg	gcgggtctgt	240
gctacgcgct	gccgagccgg	ctccccatgc	cagctacggc	ggcatcgtct	cgggtggagac	300
agacctgctg	cagtgggtgcc	tggagtccgg	cagcatcccc	atcctgtgcc	ccatcgggga	360
gacggccgcg	cgccgctccg	tgcttctcga	ctccctggag	gtgaccgcgt	cgtgggcaa	420
ggcgtgcggg	cccacaaaa	tcattcttct	caataacaca	ggcggcctgc	gcgacagcag	480
tcataaggtc	ctgagtaacg	tgaacctgcc	cgccgacctg	gacctgggtg	gcaacgccga	540
gtgggtgagc	acaaaagaac	ggcagcagat	gcggtctatc	gtggacgtgc	tcagccgcct	600
gccccaccac	tcctcggccg	tcataccgcg	cgctagcacg	ctgctcactg	agctctttag	660
caacaagggg	tccgggaccc	tgttcaagaa	cgccgagcga	atgctacggg	tgccgcagcct	720
ggacaagctg	gaccagggcc	gtctagtggg	cctgggtcaac	gccagcttcg	gcaagaagct	780
cagggacgac	tacctggcct	cgctgcgccc	gcggtgcac	tccatctacg	tctccgaggg	840
gtacaacgcc	gcgcgcattc	tgacctgga	gcccgtcctg	gggggcaccc	cgtacctgga	900
caaatttgtg	gtgagctcca	gccgccaggg	ccaaggctcc	ggccagatgc	tgtgggagtg	960
cctgcggcgg	gaccttcaga	cacttttctg	gcgctcccgg	gtcaccaacc	ccatcaatcc	1020
ctgggtacttc	aaacacagtg	atggcagctt	ctccaacaag	cagtggatct	tcttctgggt	1080
tggcctggct	gatatccggg	actcctatga	gttgggtcaac	cacgccaaag	gactgccaga	1140
ctcctttcac	aagccagctt	ctgaccaggg	cagctgacct	tcacctgga	cactacaggc	1200
cctggaatgg	ccaggggtgga	ccaaaagcca	tgcccagctg	ggcatgacct	caggcagcca	1260
gccacaggct	gaagggggct	tgttggctga	gtgatctgca	gaggagaaag	cagccccag	1320
ctctgcccc	gaggaggcgc	tgaagtggga	caagcacagg	aaagaagggg	accagtctag	1380
gaccccaact	tgactcactc	taaagctaca	accaaaatggc	cttcgatttt	caacctgggg	1440
attaggggag	gggagggtgc	cttcaggggc	tcttactcag	gacttaacct	ttaagggtga	1500
gcttagtttc	tgctctcttg	tgcttatgtt	ttgaggctcc	cttaccctaaa	ataatacccc	1560
tgctgcgctg	atattctacc	attcatttta	attccttttg	gtcttgagct	ttttcaggag	1620
gccttgatta	aaatgcaaat	acttgtctga	ga			1652

<210> 57  
 <211> 1129  
 <212> DNA  
 <213> Homo sapiens

<400> 57

tttttttttt	ttgagacgga	gtctcgtctt	gtggcccagg	ctggagtgc	gtggcgcgat	60
ctcggctcac	tgcaagctcc	gctccccggg	ttcacgccat	tctcctgcct	cagcctcccg	120
agtagctggg	actacaggcg	cccgtacca	cgccccgcta	attttttgta	tttttagtag	180

agacgggggtt	tcaccgtgtt	agccaggatg	gtctcgatct	cctgacctcg	tgatccgccc	240
gcctcggcct	cccaaagtgc	tgggattaca	ggcgtgagcc	accgcgccc	gcccatttac	300
taaatgttaa	gttccttata	attccatctc	tttcagcacc	caatacaggg	gtttacatag	360
aggaagtact	caatatttcc	tttctttttt	tctttttttt	ctggagatag	tctcgctctg	420
tcaccaggct	ggagtgccagt	ggcgtaatct	cggctcactg	caacctccac	ctcctgggtt	480
cacgccattc	tctgcctca	gcctcccag	tagctgggac	tacaggcgcc	caccatcacg	540
cccggctaata	tttttttgta	tttttagtag	agatgggggtt	tcaccgtgtt	agccaggatg	600
gtctcgatct	cctgaccttg	tgatccgccc	gcctcggcct	cccaaagtgc	tgggattaca	660
ggtgtgagcc	accgcgccc	gcctaaaaaa	atTTTTTTTT	tcttgagaca	aagtcttgct	720
ctgttgccca	ggctgaagtg	caggggcatg	atatcagctc	attgcaacct	ccacctccc	780
ggttcaagcg	attctcctgc	ctcagcctcc	cgagtagctg	ggattacagg	tgcctccgc	840
cacgtccagc	taattttctg	tttttagta	gagacggggt	ttcaccgtgt	tagccaggat	900
ggtctcgatc	tctgacctc	gtgatccacc	tgcctcagcc	tcccaaagtg	ctgggattac	960
aggcgtgagc	cactgagccc	agccccattt	tatttcattt	ctctaacagc	aatgatatat	1020
atacatccca	tagtatatcc	tactgatata	atagccccct	tccccattca	acacctgtgt	1080
aatcaggaaa	taaaaccctc	gtgcagcatt	ggcgtctgga	tagtctctg		1129

<210> 58  
 <211> 475  
 <212> DNA  
 <213> Homo sapiens

<400> 58						
gttccgccc	attggcataa	tacgccaagc	cctgtgctct	gcagacggcc	accagagaag	60
gatccttact	ctgcgcctgg	gattgctcgt	tatccccgtt	ctccccgcaa	gtaacctgtt	120
cttccgagtg	ggcttctgtg	tcccagagct	ggggtgctgt	gtgatgctgc	tttttggatt	180
cggagcctgc	gcaaacacac	cgagaaaaag	aagctcatcg	ctgccgtggg	gctgggaatc	240
ctactcagca	agatgctgag	aggctgagat	gcgcggtgcg	cggcggcgag	tggcgagcgc	300
aggggcggtt	ttcagaggcg	ctgtgtctgt	gtgtccccctc	agtgtgagg	ttcgctgcaa	360
catcggcaga	aacctggctg	ctaaaggcaa	ccaaacgggc	gccatcagat	accaccggga	420
agctgtaagc	ttaaatccca	agacgaaatc	gtcgacacgg	gaattccggc	cttgc	475

<210> 59  
 <211> 711  
 <212> DNA  
 <213> Homo sapiens

<400> 59						
ggaaaatagc	agatttttggg	ttcagtaacc	tcttctactcc	tgggcagctg	ctgaagacct	60
ggtgtggcag	ccctccctat	gctgcacctg	aactctttga	aggaaaagaa	tatgatgggc	120
ccaaagtgga	catctggagc	cttggagttg	tcctctacgt	gcttgtgtgc	ggtgccctgc	180
catttgatgg	aagcacactg	cagaatctgc	gggcccgcgt	gctgagtggg	aagttccgca	240
tcccattttt	tatgtccaca	gaatgtgagc	atttgatccg	ccatatgttg	gtgttagatc	300
ccaataagcg	cctctccatg	gagcagatct	gcaagcacia	gtggatgaag	ctaggggacg	360
cogatcccaa	ctttgacagg	ttaatagctg	aatgccaaac	actaaaggaa	gaaagacagg	420
tggacccccct	gaatgaggat	gtcctcttgg	ccatggaggga	catgggactg	gacaaagaac	480
agacactgca	gtcattaaga	tcagatgcct	atgatcacta	tagtgcaatc	tacagcctgc	540
tgtgtgatcg	acataagaga	cataaaaacc	tgcgtctcgg	agcacttcct	agcatgcccc	600

```

gagccctggg cctttcaagc accagtcaat atccaggcgg agcaggcagg tactgctatg 660
aacatcagcg tccccaggt gcagctgata aaccagaga accaaattgt g 711

```

```

<210> 60
<211> 344
<212> DNA
<213> Homo sapiens

```

```

<400> 60
ggcacgagaa tttttaggcc accgagcttc tataacatgg tcatgagctc gggcgcacca 60
tagatttccc aaagctgagg ttgcataacc cctctgctga ggacagatct taccgaagat 120
cgcacgaagt gctgccatgg agatctgctt gaatgcgctg atgacagggc agaccttgctc 180
gaggatatct gggaaaatca agattcaatc tccactatac tgattgaatg ctgtgaaaaa 240
cctctgttgg aaaaatccca ctgcattgcc gaagtggaaa atgatgagat gcctgctgac 300
ttgccttcat tagctgctga ttttgttgaa agtaaggatg ttgt 344

```

```

<210> 61
<211> 594
<212> DNA
<213> Homo sapiens

```

```

<400> 61
gcttgagctc gagegacggc gctggcggag acgcgggctg ctctcccct ccccgccgct 60
tttcctaaaa ggattgtaca ccttagaagt gcttaaggaa gaggatgaa gctctgaatc 120
gtgtcctgca gcagattctg agtgccaccc aagatgaaga gagggacaag cttgcatagt 180
aggcggggca agccagaggc cccaaaggga agtcccaaaa tcaacaggaa gtctggtcag 240
gagatgacag ctgttatgca gtcaggccga cccaggctct catccacaac tgatgcacct 300
accggtctct ctatgatgga aatagcttgt gctgctgctg ctgctgctgc tgcattgcta 360
ccaggagagg agggaactgc ggagcggatc gaacgggttg aagtaagcag ccttgcccaa 420
acatccagtg cagtggcctc cagtaccgat ggcagcatcc acacagactc tgtggatgga 480
acaccagacc ctgagcgac aaaggtgcc attgctcacc tgcagcagaa gatcctgaag 540
ctcacagaac aaatcaagat tgcacaaaca gcccgacgaa atcgctgacc cggg 594

```

```

<210> 62
<211> 1609
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(1609)
<223> n = a,t,c or g

```

&lt;400&gt; 62

cgaagttatg	gccttcctta	taaggaaaag	gggtggattg	gaggaatcgc	caattgaagt	60
ttogaaggat	cgcttttagct	gaatatcaga	gaaccttggtg	aagatcttaa	agagcaacta	120
aagcataaag	aattttcttct	ggctgctaata	acttgtaacc	gtgttggtgg	tctttgtttg	180
aaatgtgtctc	agcatgaagc	tgttctttcc	caaaccata	ctaattgttca	tatgcagacc	240
atcgaaagac	tggttaaaga	aagagatgac	ttgatgtctg	cactagtttc	cgtaaggagc	300
agcttggcag	atacgagca	aagagaagca	agtgccttatg	aacaggtgaa	acaagttttg	360
caaatactctg	aggaagccaa	ttttgaaaaa	accaaggett	taatccagt	tgaccagttg	420
aggaaggagc	tggagaggca	ggcggagcga	cttgaaaaag	aacttgcac	tcagcaagag	480
aaaagggcca	ttgagaaaga	catgatgaaa	aaggaaataa	cgaaagaaag	ggagtacatg	540
ggatcaaaga	tgttgatctt	gtctcagaat	attgcccaac	tggaggccca	ggtggaaaag	600
gttacaaaagg	aaaagatttc	agctattaat	caactggagg	aaattcagag	ccagctggct	660
tctcgggaaa	tggatgtcac	aaaggtgtgt	ggagaaatgc	gctatcagct	gaataaaacc	720
aacatggaga	aggatgaggc	agaaaaggag	cacagagagt	tcagagcaaa	aactaacagg	780
gatcttga	ttaaagatca	ggaaatagag	aaattgagaa	tagaactgga	tgaaagcaaa	840
caacacttgg	aacaggagca	gcagaaggca	gccctggcca	gagaggagt	cctgagacta	900
acagaactgc	tgggcgaatc	tgagcaccaa	ctgcacctca	ccagacagga	aaaagatagc	960
attcagcaga	gcttttagca	ggaagcaaag	gcccaagccc	ttcaggccca	gcaaagagag	1020
caggagctga	cacagaagat	acagcaaatg	gaggcccagc	atgacaaaac	tgaaaatgaa	1080
cagtatttgt	tgctgacctc	ccagaataca	tttttgacaa	agttaaagga	agaatgctgt	1140
acattagcca	agaaactgga	acaaatctct	caaaaaacca	gatctgaaat	agctcaactc	1200
agtcaagaaa	aaaggtatac	atatgataaa	ttgggaaagt	tacagagaag	aatgaagaa	1260
ttggaggaac	agtgtgtcca	gcatgggagg	agtacatgag	acgatgaagc	aaaggctaag	1320
gcaggtggat	aagcacaggc	aggccacagc	ccaggagggtg	gtgcagggtcc	ccagaagcag	1380
gaccngcttc	ttccnggaga	gggaggggnc	gtcggaagag	gtgggnccgn	cttgggggnc	1440
nngttaccga	gnatnncnaa	tcttttttgg	ttgaccgggt	tggacagggg	ggacttnant	1500
gttttncaaa	ggngnttttt	cattccanct	tgttttngct	taatttngcn	caacgnaccc	1560
acggcctncc	cggnttgaaa	ccccccnccc	tgaggggggg	ttntcccc		1609

&lt;210&gt; 63

&lt;211&gt; 615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

catcctatcc	cgtgtgggtg	aattcgccgc	tgactgctga	ggtgccaccc	gagctgctgg	60
ctgctgccgg	cttcttccac	acaggccatc	aggacaaggt	gaggtgcttc	ttctgctatg	120
ggggcctgca	gagctggaag	cgcggggacg	acccctggac	ggagcatgcc	aagtggttcc	180
ccagctgtca	gttctctgtc	cggtcaaaaag	gaagagactt	tgtccacagt	gtgcaggaga	240
ctcactccca	gctgctgggc	tcttgggacc	cgtgggaaga	accggaagac	gcagcccctg	300
tggccccctc	cgtccctgcc	tctgggtacc	ctgagctgcc	cacacccagg	agagagggtcc	360
agtctgaaag	tgcccaggag	ccaggagggg	tcagtccagc	cgaggccacg	agggcgtggg	420
gggttcttga	gccccagga	gccagggatg	tggaggcgca	gctgcggcgg	ctgcaggagg	480
agaggacgtg	caaggtgtgc	ctggaccgcg	ccgtgtccat	cgtctttgtg	ccgtgcggcc	540
acctggtctg	tggctgagtg	tgcccccggc	ctgcagctgt	gccccatctg	gcagaagccc	600
ccgtcccgca	gccgg					615

&lt;210&gt; 64

&lt;211&gt; 839

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(839)  
 <223> n = a,t,c or g

<400> 64

aagaatgtct	ggaagagatg	gaagaaaagg	ttttttgtat	tgggtgcaggt	cattcagtag	60
acgtttgcca	tgtgcagtta	tcgggagaag	aaagcggagc	ctcagggaact	tctacaattg	120
gatggctaca	ctgtggatta	caccgacccc	cagccagggt	tggagggtgg	ccgagccttc	180
ttcaatgctg	tcaaggaggg	agacaccgtg	atatttgcca	gtgacgatga	acaagaccgc	240
atcctgtggg	tccaggccat	gtatcggggc	acggggcagt	cacacaagcc	tgtgcccccg	300
acccaagtcc	agaaaactcaa	cgccaaggga	ggaaatgtac	ctcagctgga	tgcccctatc	360
tctcaatttt	acgcagatag	agctcaaaaa	catggcatgg	atgaatttat	ctcttccaac	420
ccctgtaact	ttgaccacgc	ttccctcttt	gagatggtag	aacgccttac	tttggatcac	480
agacttaatg	attcctattc	ttgcctgggc	tggttcagtc	ctggccagggt	gtttgtacta	540
gacgagtatt	gcgcccgaag	tggagtcagg	gggtgtcacc	gacatctctg	ctacctcaga	600
gacttgcttg	aacgggcaga	aaatggcgcc	atgatcgacc	ccacccttnt	tcactacagc	660
tttgcccttc	gtgcatccca	tgtccatggg	aacaggccctg	atggaattgg	gaactgttga	720
ctgttgaaga	aaaggaacgt	tttttgaagg	aaatcaaaaag	aggaggnttc	cgnagtctctg	780
ctaagaaaaa	tcagggttaca	acatttttagg	naattgcttt	tcccatttgg	gtcgaacct	839

<210> 65  
 <211> 1678  
 <212> DNA  
 <213> Homo sapiens

<400> 65

caagcagctg	atcgtgctgg	gaaacaaagt	ggacctcctg	ccccaggatg	ctcctggcta	60
ccggcagagg	ctgcgggagc	gactgtggga	ggactgtgcc	cgcgccgggc	tcctgtctggc	120
ccctggccaac	caagggccac	agcgccccgt	caaggacgag	ccacaggacg	gggagaatcc	180
gaatccgccg	aactgggtccc	gcacagtggg	cagggacgtg	cggctgatca	gcgccaagac	240
cggctatgga	gtggaagagt	tgatctctgc	ccttcagcgc	tcctggcgct	accgtgggga	300
cgtctactta	gtgggcgcca	ccaacgcggg	caaatccact	ctctttaaca	cgctcctgga	360
gtccgattac	tgcaactgcca	agggctccga	ggccatcgac	agagccacca	tctccccttg	420
gccaggtagt	acattaaacc	ttctgaagtt	tcctatttgc	aacccaactc	cttacagaat	480
gtttaaaagg	catcaaagac	ttaaaaaaga	ttcaactcaa	gctgaagaag	atcttagtga	540
gcaagaacaa	aatcagctta	atgtcctcaa	aaagcatggg	tatgtcgtag	gaagagttgg	600
aaggacattc	ttgtattcag	aagaacagaa	ggataacatt	ccctttgagt	ttgatgctga	660
ttcacttgcc	tttgacatgg	aaaatgaccc	tgttatgggt	acacacaaat	ccaccaaaca	720
agtagaattg	actgcacaag	atgtgaaaga	tgccactggg	ttttatgaca	cccctggaat	780
tacaaaagaa	aattgtattt	taaatcttct	aacagaaaaa	gaagtaaata	ttgttttgcc	840
aacacagtcc	attgttccaa	gaacttttgt	gcttaaacca	ggaatgggtc	tgtttttggg	900
tgctataggc	cgcatagatt	tcctgcaggg	aaatcagtc	gcttggttta	cagtcgtggc	960
ttccaacatc	ctccctgtgc	atatcacctc	cttggacagg	gcagacgctc	tgtatcagaa	1020
gcatgcagggt	catacgttac	tccagattcc	aatgggtgga	aaagaacgaa	tggcaggatt	1080
tcctcctctt	gttgctgaag	acattatgtt	aaaagaagga	ctgggggcat	ctgaagcagt	1140
ggccgacatc	aagttttcct	ctgcagggtg	ggtttcagta	acacctaat	ttaaggacag	1200
actgcatctc	cgaggctata	cacctgaagg	aacagttttg	accgtccggc	cccctctctt	1260
gccatatatt	gttaacatca	aaggacagcg	catcaagaaa	agtgtggcct	ataaaaccaa	1320

gaagcctcct	tcctttatgt	acaacgtgag	gaagaagaaa	ggaaagataa	atgtatgaga	1380
ccgaccttgt	tactccaga	tattaactgt	attgaacaca	acaaaatata	ttgaatttgt	1440
attaaacata	taacgcataa	ataaagctcc	cattcttacc	cttaaaaaata	aaaggagaa	1500
gaaaaaaaaa	gatgccataa	ggcatatacg	tggttttggg	tattccgggg	tcttcccgtg	1560
gtctgttcac	tttgcggtgg	tggtgatata	ttaggcagtc	ggggcgctg	atgtacgcct	1620
tcttatagag	gtacatggtt	ggatgcagcg	tcttgacgtg	ggattcgctt	tattcgcc	1678

<210> 66  
 <211> 1888  
 <212> DNA  
 <213> Homo sapiens

<400> 66

tccacgggtg	catccatgat	gcctcgtcag	gagactgtgg	agtgtttg	caagttcaat	60
gccccgagaa	aactgaaggg	tgccatcctc	acgaccatgc	ttgtctccag	gaacttctca	120
gctgccaaaa	gcctattgaa	caagaagtcg	gatggcggtg	tcaagccaca	gagcaacaac	180
aaaaacagtc	tcgtaagccc	agcccaagag	cccgcgccct	tgacagcggc	catggagcca	240
caaaccactg	tggtagacaa	cgctacagat	gggatcaagg	gctccacaga	gagctgcaac	300
accaccacag	aagatgagga	cctcaaagct	gccccgctcc	gcactgggaa	tggcagctcg	360
gtgcctgaag	gacggagctc	ccgggacaga	acagccccct	ctgcaggcat	gcagccccag	420
ccttctctct	gtccttcagc	catgcgaaaa	caggagatca	ttaagattac	agaacagctg	480
attgaagcca	tcaacaatgg	ggactttgag	gcctacacga	agatttgtga	tccaggcctc	540
acttctcttg	agcctgaggg	ccttggtaac	ctcgtggagg	ggatggattt	ccataagttt	600
tactttgaga	atctctgtgc	caagaacagc	aagcctatcc	ataccaccab	cctaaaccca	660
cacgtccacg	tgattgggga	ggacgcagcg	tgcatcgcc	acatccgcct	caccagctac	720
atcgacgggc	agggctgggc	ttcgaaccca	gccaaagtcag	aagaagaccc	gggtctggca	780
cccgctggga	atggcaagtg	gctcaatgtc	cactatcact	gctcaggggc	ccccctgccg	840
caccgctgca	gtgagctcag	ccacaggggc	ttttaggaga	ttccagccgg	aggtccgaac	900
cttcgcagcc	agtggctctg	gagggcctga	gtgacagcgg	ccagtcctgt	ttgtttgaag	960
gtttaaaaa	attcaattac	aaaagcggca	agcagccaat	gcacgcccc	gcatgcagcc	1020
ctcccgcccc	cccttctgtg	ctgtctctgc	tgtaccgagg	tgttttttac	atttaagaaa	1080
aaaaaaaaa	aaaaaaagat	tgtttaaaaa	aaaaaggaat	ccataccatg	atgcgtttta	1140
aaaccaccga	cagcccttgg	gttggcaaga	aggcaggagt	atgtatgagg	tccatcctgg	1200
catgagcagt	ggctcaccga	ccggccttga	agaggtgagc	ttggcctctc	tggtccccat	1260
ggacttaggg	ggaccaggca	agaactctga	cagagctttg	ggggccgtga	tgtgattgca	1320
gctcctgagg	tggtcctgct	acccaggtgc	taggaatgaa	cttctttgga	acttgcatag	1380
gcgcctagaa	tggggctgat	gagaacatcg	tgaccatcag	acctaacttg	gagagaacgc	1440
agagctccca	gcctgctgtg	gaggcagctg	agaagtgggt	gcctcaggac	tgagagcccg	1500
gacgttgctg	tactgtcttg	tttagtgtag	aagggaagag	aattggtgct	gcagaagtgt	1560
acccgccatg	aagccgatga	gaaacctcgt	gttagtgtga	catgcaactc	ctcatccatt	1620
tctataggat	gcacaatgca	tgtgggccct	aatattgagg	ccttatccct	gcagctagga	1680
gggggagggg	ttgttgctgc	tttgcttctg	gttttcttct	aacctgggca	aggagagagc	1740
caggccctgg	gcaaggctcc	cgtgcgcctc	ttgggttcc	tggtttcttg	ttgcttgatc	1800
tggaccatct	ttgtctttgc	cttttcacgg	taggggtccc	atgctgaccc	tcactctggg	1860
cctgggcctc	ttgccaagt	tgccccctg				1888

<210> 67  
 <211> 1712  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 67

ctttacccaa	gaatgtggta	ttcgtgcttg	acagcagtg	ttctatggtg	ggaaccaa	60
tccggcagac	caaggatgcc	ctcttcacaa	ttctccatga	cctccgaccc	caggaccgtt	120
tcagtatcat	tggattttcc	aaccggatca	aagtatggaa	ggaccacttg	atatcagtca	180
ctccagacag	catcagggat	gggaaagtgt	acattcacca	tatgtcacc	actggaggca	240
cagacatcaa	cggggccctg	cagagggcca	tcaggctcct	caacaagtac	gtggcccaca	300
gtggcattgg	agaccggaga	gtgtccctca	tcgtcttct	gacggatggg	aagcccacgg	360
tcggggagac	gcacaccctc	aagatccctca	acaacaccg	agaggccgcc	cgaggccaag	420
tctgcatctt	caccattggc	atcggcaacg	acgtggactt	caggctgctg	gagaaactgt	480
cgctggagaa	ctgtggcctc	acacggcgcg	tgacagagga	ggaggacgca	ggctcgcagc	540
tcacggtgtt	ctacgatgaa	atcaggaccc	cgctcctctc	tgacatccgc	atcgattatc	600
ccccagctc	agtgtgtcag	gccaccaaga	ccctgttccc	caactacttc	aacggctcgg	660
agatcatcat	tgcggggaag	ctggtggaca	ggaagctgga	tcacctgcac	gtggagggtca	720
cgcagcagaa	cagtaagaaa	ttcatcatcc	tgaagacaga	tgtgctgtg	cggcctcaga	780
aggcagggaa	agatgtcaca	ggaagcccca	ggcctggagg	cgatggagag	ggggacacca	840
accacatcga	gcgtctctgg	agctacctca	ccacaaagga	gctgctgagc	tcctggctgc	900
aaagtgcaga	tgaaccggag	aaggagcggc	tgcggcagcg	ggcccaggcc	ctggctgtga	960
gctaccgctt	cctcactccc	ttcacctcca	tgaagctgag	ggggccgggtc	ccacgcattg	1020
atggcctgga	ggaggccac	ggcatgtcgg	ctgccatggg	acccgaaccg	gtggtgcaga	1080
gcgtgcgagg	agctggcacg	cagccaggac	ctttgctcaa	gaagccatac	cagccaagaa	1140
ttaaaatctc	taaaacatca	gtggatggtg	atccccactt	tggtgtggat	ttccccctga	1200
gcagactcac	cgtgtgcttc	aacattgatg	ggcagcccg	ggacatcctc	aggctggtct	1260
ctgatcacag	ggactctggt	gtcacagtga	acggagagtt	aattggggca	cccggccctc	1320
caaattggcca	caagaaacag	cgcacttact	tgcgactat	caccatcctc	atcaacaagc	1380
cagagagatc	ttatctcgag	atcacaccga	gcagagtcac	cttggtggtg	ggggacagac	1440
tggtgctccc	ctgcaaccag	agtgtggtgg	tgaggagctg	ggggctggag	gtgtccgtgt	1500
ctgccaacgc	caatgtcacc	gtcaccatcc	agggctccat	agcctttgtc	atcctcatcc	1560
acctctacaa	aaagccggcg	cccttccagc	gacaccacct	gggtttctac	attgccaaca	1620
gcgagggcct	ttccagcaac	tgagggtct	tctgtgagtc	tggcatcctg	attcaggaac	1680
tgaccacagca	gtccgtggca	gttgctggtc	ga			1712

&lt;210&gt; 68

&lt;211&gt; 839

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

gttttttctc	gagcaggtta	gccaatatac	ctttgctatg	tgagttata	gagaaaagaa	60
gtctgaacca	caagaattaa	tgagcttga	aggctatact	gtggattata	ccgatcccca	120
cccaggcctt	cagggtggtt	gtatgttctt	taatgctgtt	aaagaaggag	atactgtaat	180
ctttgccagt	gatgatgaac	aggacagaat	attatgggtt	caagccatgt	atagggccac	240
aggatcaatca	tataaaccag	ttcctgcaat	tcaaaccag	aaactgaatc	ctaaaggagg	300
aactctccat	gcagatgctc	agctttatgc	agatcgtttt	cagaaacatg	gtatggatga	360
gtttattttct	gcaaaccctt	gcaagcttga	tcatgccttc	cttttttagaa	tactccagag	420
gcagactttg	gatcacagac	tgaatgattc	ctattcttgc	ttgggatggt	ttagccctgg	480
ccaagtcttt	gtgttagatg	agtactgtgc	cogttatggt	gtgagaggct	gtcacagaca	540
tctctgctac	cttgacgaac	tgatggaaca	ttcagaaaaat	ggtgctgtca	ttgacccctac	600
cctgctccat	tacagctttg	cattctgtgc	ctctcgatgt	gcacggcaac	aggcctgatg	660
gaattgggac	tgtttcagt	gaagaaaaag	aaagatttga	ggagataaaa	gagagactct	720
cttccctttt	agaaaatcag	ataagccatt	tcagatactg	ttttcccttt	ggacgacctg	780
aagggtgctct	aaaagctaca	ctttcattac	ttgaaagggt	tttaatgaaa	gatattgcc	839

<210> 69  
 <211> 801  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(801)  
 <223> n = a,t,c or g

<400> 69  
 agacgggctg ctccatgagg tgctgaacgg gctcctagat cgccctgact gggaggaagc 60  
 tgtgaagatg cctgtgggca tcctcccctg cggctcgggc aacgcgctgg ccggagcagt 120  
 gaaccagcac gggggatttg agccagccct gggcctcgac ctgttgctca actgctcact 180  
 gttgctgtgc cggggtgggtg gccacccact ggacctgtc tccgtgacgc tggcctcggg 240  
 ctcccgtgtt ttctccttcc tgtctgtggc ctggggcttc gtgtcagatg tggatatcca 300  
 gacgcagcgc ttcagggcct tgggcagtgc ccgcttcaca ctgggcacgg tgctgggcct 360  
 cgccacactg cacacctacc gcggacgcct ctccctacctc ccgcgcactg tggaacctgc 420  
 ctgcccacc cctgcccata gcctgcctcg tgccaagtcg gagctgacct taaccccaga 480  
 ccagccccg cccatggccc actcaccct gcctcgttct gtgtctgacc tgcctcttcc 540  
 cctgccccag cctgccctgg cctctcctgg ctgcgcagaa cccctgcca tctgtccct 600  
 caacggtggg ggcccagagc tggctgggga ctgggggtggg gctggggatg ctccactgtc 660  
 cccggacceca cagctgtctt cacctcctgg ctctcccaag gcagctctac actcacccgt 720  
 ctaaaaaaag gcccccgtaa ttcccccgga catgnnnccc cgctctagag gatcaagcaa 780  
 ctacgcggcg gctcacgacg c 801

<210> 70  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 70  
 agaaggggtg cccaaccttg ctcatggcag ctggcagctt ctatgacatt ctggccatca 60  
 ctggcttcaa cacatgcttg ggcatagcct ttccacagg ctctactgtc tttaatgtcc 120  
 tcagaggagt tttggagggtg gtaattgggtg tggcaactgg atctgttctt ggatttttca 180  
 ttcagtactt tccaagcgt gaccaggaca aacttgtgtg taagagaaca ttccctgtgt 240  
 tgggggtgtc tgtgctagct gtgttcagca gtgtgcattt tggtttccct ggatcaggag 300  
 gactgtgcac gttgggtcatg gctttccttg caggcatggg atggaccagc gaaaaggcag 360  
 aggttgaaaa gataattgca gttgcctggg acatttttca gcccttctt tttggactaa 420  
 ttgggagcag aggtatctat ttgcattctt cagaccagaa actgtaggcc tttgtgttgc 480  
 caccgtaggc atttgcagta ttgatacgaa tttttgacta cattttctga a 531

<210> 71  
 <211> 540  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

tgtgcgagga	attcgaatca	ggtaatggag	aggactggca	tgaagggggc	acaggactgt	60
gaaaacctga	gtgattctgt	ccttcctca	tcctctatcc	ctgaaccagg	gcagacatag	120
atggaatcag	agcaggagtt	gggtttgatg	tggtttcagg	tcacacctatc	agagtttgag	180
agatttaggc	catgaaccat	tatgaatata	gatgagaacc	tttgtaattg	ctgaaggagg	240
tagtagtgca	ggcaagtcct	gtgtgcaaga	cctgctgctc	ccagttagta	cggaccctg	300
tgacattcac	agaagttcag	aatgtctgag	atgctctgca	ggctacctta	tctccgtctg	360
cagctacacc	tccagtgatc	acaatcagtg	ctacgctggc	acagccagcc	tggccctgct	420
ctggattgga	ggcatcctca	agggctgctt	gctgtggaag	cagtttcgct	ggaccgagag	480
gagccactgg	aattttgggt	actgggcctt	atggtcaccc	gggaatggga	atggctgctg	540

&lt;210&gt; 72

&lt;211&gt; 428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

cggacgcgtc	cgcccacg	tccgcccacg	cgctccgctag	aaattttctgt	ggaactccat	60
ttgactttct	atctgtgaaa	tccaaactgt	ctctgaagaa	ataagaaaaa	tagtgttttg	120
acttttagga	gacaactatg	tttattat	tgccttgcaa	attaatgtct	aaatttgtac	180
aagcacctat	ctacagattt	ttccaggtaa	accatcatgt	tttatgtgta	aaggtagatt	240
gatgtgcatt	tactttatac	tttggtactt	aggccattac	acatctttgc	actggaattg	300
gtgcagatat	ataagtgatc	ctaagtgtga	tgctgcccag	accccaggaa	tgcagagggtg	360
agcatgacac	acacagtc	tgccctgatg	gagctcatag	actagtgaag	gaatagggct	420
ctatgacc						428

&lt;210&gt; 73

&lt;211&gt; 584

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

gctggagtca	ttgcctgggt	tcaaagagat	tgtgagcagg	ggagtaaaag	tggattactt	60
gactccagac	ttccctagtc	tctcgtatcc	caattattat	accctaata	ctggccgcca	120
ttgtgaagtc	catcagatga	tcgggaacta	catgtgggac	cccaccacca	acaagtcctt	180
tgacattggc	gtcaacaaa	acagccta	gcctctctgg	tggaatggat	cagaacctct	240
gtgggtcact	ctgaccaagg	ccaaaaggaa	ggtctacatg	tactactggc	caggctgtga	300
ggttgagatt	ctgggtgtca	gaccaccta	ctgcctagaa	tataaaaatg	tcccaacgga	360
tatcaatttt	gccaatgcag	tcagcgatgc	tcttgactcc	ttcaagagt	gccgggcca	420
cctggcagcc	atataccatg	agcgattga	cgtggaaggc	caccactacg	ggcctgcac	480
tccgcagagg	aaagatgcc	tcaaggctgg	tagacactgt	cctgaagtac	atgaccaagt	540
ggatccagga	gcggggcctg	caggaccgcc	tgaacgtcat	tatt		584

<210> 74  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
 ggcacgagat tttcatccaa aacaaacact ggacttcctg cggagtgaca tggctaattc 60  
 gaaaatcaca gaagaggtga aaaggagtat agcacaacag tatctagatt tgacagtagc 120  
 ccggaacaag tggaccctga tgccgaagtc gatgcagccc catctaccac atcttcatgt 180  
 ggacattgag attcacacgc tggctcctga aggggtgctca gtctccttgg tgattaaggt 240  
 cctgcttgaa ctggtgccaa ctccatggca gggaagttgc ttttggttgc ctggtctggg 300  
 ttcccagatc ctttctgggg caaggagcta tcagaccctg ctttcaag 348

<210> 75  
 <211> 365  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
 caagcaaagt ggggatgtca cctgcaactg cactgatggg cgcttgggcc ccagctgcct 60  
 gacctgcgtc ggccactgca tttttggcgg ctactgtacc atgaacagca aaatgatgcc 120  
 tgaatgccag agcccacccc acatgacagg gcccgggtgt gaggagcacg tcttcagcca 180  
 gcatcagcca ggacatataa cctccatcct aatccctatg ctgtagctgc tgctgctggg 240  
 tctggtggcc ggagtgatat tctgccataa acggcgagtc caaggggcta agggcttcca 300  
 gcaccaacgg atgaccaacg gggccatgaa cgcgcagatt gcaaacccca cctacaagat 360  
 gtacc 365

<210> 76  
 <211> 700  
 <212> DNA  
 <213> Homo sapiens

<400> 76  
 caagaacct cagcaccaac acaaatgtat ctttgcagac cgaaggaatc agctaaacaa 60  
 tttacagtca tctcaatctc tactaaaaca aaaatcacat ccaacatgcc acctgacacc 120  
 atttctttct ctctctctct tttgctcctt gcgatgagga attcatctct ccttgagcct 180  
 cgttcttgaa gagataacag tatagcaaca actctgccac tgaaatcctg ttctctgacc 240  
 gatattggca cctgcaaaga gaaacaacca gtaacaggca gcagcagcat cagtattaat 300  
 cttccatgat gaaatcttta caggtcaaga acaagtacac agctcttttc tcactccttc 360

acagtggacc	atgcaactag	ttgaggtgga	agacaatgga	ttgtctacaa	gccttttgaa	420
cagtggagaa	tgcagggcgt	tggctttagg	aagaggcaga	aatccaggca	gaacttgaac	480
gtttggaaaag	agtcagaaat	cttcacatac	gtgagctgaa	aagaataaac	aatgaagata	540
attcacagtt	caaagatcac	ccaacattaa	atgaaagata	tttattactt	catctgcttg	600
gtagaggtgg	ctttagttaa	gtgtataagg	taatgtatgg	tttattcttg	tttttttaca	660
ctaattgtagc	aaggatatag	gagtatgtgg	ttaagaagtg			700

<210> 77  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens

<400> 77						
ttgcctagca	catggcaggg	tgcagcgct	gtctgaatgt	gtgaagagtt	cttagtgatg	60
ggtaaagggt	gttctgtgt	gttttagatt	ctgctcagca	atcctcagat	gtgggtggtta	120
aatgattcca	atcctgaaac	cgacaaccgt	caagaaagtc	cttcccagga	aaacattgac	180
cgagtgagt	acaggccttt	gtgccctcag	cttggacagc	ctcgggtggg	gttgcctggg	240
gtaacctggg	tgaatcaggc	agcaggactg	ggggagtccg	tgctgaaacc	ttggctccca	300
ggctccaggt	gtaacctgcc	cacctcagag	gccacccacg	cagtaacaga	gggcagggga	360
ggcctccttg	gaaagcagga	aaactgggga	agtgtcagga	agttctcttt	aggtttgctg	420
cctttg						426

<210> 78  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

<400> 78						
tttcgtgcta	tggtcttggc	tggtcaacac	gactgcagac	ccatggacaa	gagcgcaggc	60
agtggccaca	agagcgagga	gaagcgagaa	aagatgaaac	ggaccctttt	aaaagattgg	120
aagaccctgt	tgagctactt	cttacaaaat	tcctctactc	ctgggaagcc	caaaaccggc	180
aaaaaaagca	aacagcaagc	tttcatcaag	taagttgaga	atcctgagct	tgcaaatatc	240
aatagttagc	tgctgaactg	aaaaggggaa	ctctgatgag	cgtaagctaa	catacagaac	300
ctctcttgca	ggccttctcc	tgagggaagca	cagctgtggt	cagaagcatt	tgacgagg	358

<210> 79  
 <211> 322  
 <212> DNA  
 <213> Homo sapiens

<400> 79  
 gggtttttca atttttccag cccaaagtta aaagggttga aaatcaattc ctctttggtc 60  
 ctatgagataa ggaagaacat acttcgtttc ttagatgcag aacgagatgt gtcagtgggtc 120  
 aagagcagtt ttccaagcaa agacgccaga cactccagtg tgcaccggtg gttcacccaa 180  
 ctgcattggg gaccgccctc tcatactcca gccaggccgt gacgtgaccg acctccgact 240  
 tctgcgcaaa ggcagcgcaa gccgttggga tcccctgctc cccctcgctc aacagtcggg 300  
 ccattacacc tttcatactg cg 322

<210> 80  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

<400> 80  
 cgaaagcacg ccagaaaaca aaataaaagc aatacataac cacaaaaata atagcgtata 60  
 gatgatcaac aagaattaaa acgcgtaaca tagtatagtc aaaaagaata cacgaaaaag 120  
 aaactccata aaaaatgcaa tatcatacag gcagatatca agccagacaa taccctggat 180  
 aatgaatcca taactattct aaagcttagc gattttgggt cggcttcaca tgttgccgat 240  
 aatgacataa cacccttcac ttctcagacc acatccgctg catcatcgcc cccgcggacg 300  
 ctacgccgcg 310

<210> 81  
 <211> 134  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
 tcgagtaaac catgggacta aagcttggct ccaaagcatt caggctgaac gaaaaacatg 60  
 gactgctatt gcataatac aacgtgcatt ggacgagaac gatgctatgg aacctgcata 120  
 ggcgacacgg tcgg 134

<210> 82  
 <211> 358  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
 ctctgggaga gaaagactaa tgggcaggat ccattactt cattggtaaa gatagtcgga 60  
 tactctcacc acttttaata ctttttagtat tacagttgat cagattacct ttacttgata 120  
 tgaattattt ctaagttcat tcccctgtgt tgtagcttat ttcaacaatt ccaactagcc 180

gtttaaaatt	cctcaaagaa	actgggtcatg	gaacaccaat	ggaagaaata	cctgaggagg	240
aattatcaga	ggatgttgaa	cagattgatc	acgctgatag	ggagttgcgg	cgtggccaaa	300
acttgagggtg	caaaggaatt	catagattgc	ctactcatat	acaagtaggg	caaaatcg	358

<210> 83  
 <211> 723  
 <212> DNA  
 <213> Homo sapiens

<400> 83						
tacacacaca	cacacacaca	cacacacact	cactctctca	gaggagagaa	aatattaaga	60
atcgtgtatt	ttacacaggt	atccaaacat	aaaaatactt	tagaattgct	tactgtatgg	120
acaggttata	tggatggag	tttgtagtat	ccacattaac	aaagcaagtt	tatatggact	180
ggttatgata	ttagggatat	gaattagaaa	tggatgttgt	tgactcatt	taaaatattt	240
tgctctcac	tttatcccca	gttatagtgt	ccttttgaat	ttttctcaca	cagtgtctact	300
atatttcacg	aactggtata	taaacaaacc	aaaattattt	cttcaaatac	agaacttatc	360
tacgaagggc	gacgcttagt	cttagaacct	ggaaggctgg	cacaacattt	ccctaaaact	420
actgaggaaa	accctatatt	tgtagtaagc	cgggaacctc	tgaataccat	aggattaata	480
tatgaaaaaa	tttcctccc	taaagtacat	ccacgttatg	atttagacgg	ggatgctagc	540
atggctaagg	caataacagg	ggttgtgtgt	tatgcctgca	gaattgccag	taccttactg	600
ctttatcagg	aattaatgcg	aaaggggata	cgatggctga	ttgaattaat	taaagatgat	660
tacaatgaaa	ctgttcacaa	aaagacagaa	gttgtgatca	cattggggatt	tctggtatcc	720
aga						723

<210> 84  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens

<400> 84						
ggcacgagga	aaatgggacc	caccgtctct	cccatctgcc	taccaggcac	ctggggcgac	60
tacaacctca	tggatgggga	cctgggactg	atctcaggct	ggggccgaac	agagaagaga	120
gatogtgctg	atcgccctca	ggcggggagg	tcacccgcag	ctgggtaaag	aaaatgggaa	180
ccggggagag	gggaccctac	gtgggaagaa	tcagaggaag	atgtacataa	gagtaagtgg	240
acaagatgtg	tggatgagaa	gggcgcgtag	tgctaaacag	acaataagag	accgctcagg	300
tgtgggggtga	cctaattggg	agacgtggaa	tatgttttgt	ggcacggagg	aaagtctaata	360
ggatatcgtg	tttaggagga	cgatggagtc	ttacgtgctc	gttgatg		407

<210> 85  
 <211> 342  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 85

ggcacgagct	cgaaaattta	atcaagagtg	cgcactctta	ttccctttac	tgagggtaat	60
atctacacgg	agcctagaca	gccgaaccag	aggcttcctt	ttgtccaaga	agaggatgga	120
atagacaagc	tggagctgct	ggctcccggg	tgaatttcag	acctgggggt	ctcagctcca	180
ggcaacttgg	actcccagga	cctcctgacg	gtcctgacta	tactgtttac	taccggttcc	240
atcgacttgc	catggtgact	gctgcctcac	gattggagcg	tgaacacctt	acgcattctat	300
gacactaggg	atacaatgga	gaggtataga	gcaaccctag	cg		342

&lt;210&gt; 86

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 86

cgctccgcag	gttttagcacc	gactgtagct	ctgatcagca	ggaccgatta	aacggaactg	60
cccctagcgg	ttttaaccgc	tcctgaccag	tcccgttgcc	gcaccccatc	ttggaagtat	120
gccctggcca	gtaggagcca	caaagcgcca	ttagcctcac	tgcatttcag	gtacaggccg	180
gcgccagccg	tgccctacca	ggtccaccgg	ctccgagcag	cagcaagccc	ggtcggaaag	240
cgaaagtggc	ctcgccatgt	ccagaccggc	cagctcccc	gcctacctga	ccccgccccg	300
cagccgcacc	tgggtccgag	tcatcgccgc	ggccgccacg	gccccgcaca	ggaaggcggc	360
agcaaagagc	gcacgctcga	cgcgctgcag	ccaggacagc	gccatggcgc	ccctcgtgcc	420

&lt;210&gt; 87

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

ggcacgaggg	gagaaggcgg	ggctgggcct	cagcttccca	aagggttttg	aggaactggg	60
cttttctgac	accctcaaag	gtcagaaggt	taaaggggca	gaaggcattc	ggaaagctcc	120
cctccacacg	tgacacctct	ctgacttctg	acctagggtt	ccaccaccgc	ttcaatccca	180
atgcctccag	ctccttcaag	cccagtggga	ccaagtttgc	cattcagtat	ggaactgggc	240
gggtagatgg	aatcctgagt	gaggacaagc	tgactgtgag	tggcctttga	ctccaggaag	300
cctcgagcct	gggagaaccc	tgttgtctaa	gatcatctgg	cttagggagg	ggcttgagggt	360
gcaggggctt	cctgagccga	tggtatggggc	tt			392

&lt;210&gt; 88

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



```

<400> 88
gggaggaata taatgcatta cccaaatggt catgccatat gtattgcaaa tggacattgt      60
atcatcttgt gaaatagtca taacattaaa gtttgggtat agtagtttagc atattttcat      120
ggccagtatt gatgctattt tttcccttac ctatcagact ctttcaaaga gaaaagaggg      180
agcagttgga attttatgtt tgttgttcta ttttgtctat tatgaattgt gacaaaacca      240
ttataaaaga tgacaagtgt gtgtgtttct ttttttcttt ttaaactgta gggaacatag      300
tcattagtga tctcaaatac cgaaagacat tt                                     332

```

```

<210> 89
<211> 535
<212> DNA
<213> Homo sapiens

```

```

<400> 89
attaacctag gaaatacatg ttatatgaac agtggtatatt aagccttggt tatggccaca      60
gatttcagga gacaagtatt atctttaaat ctaaatgggt gcaattcatt aatgaaaaaa      120
ttacagcatc tttttgcctt tctggcccat acacagaggg aagcatacgc acctcgata      180
ttctttgagg cttccagacc tccatgggtt actcccagat cacagcaaga ctgttctgaa      240
tacctcagat ttctccttga caggctccat gaagaagaaa agatcttgaa agttcaggcc      300
tcacacaagc cttctgaaat tctggaatgc agtgaaactt ctttacagga agtagctagt      360
aaagcagcag tactaacaga gaccctcgt acaagtgcag gtgagaagac tttaatagaa      420
aaaatgtttg gaggaaaact acgaactcac atacgttggt tgaactgcac gagtacctca      480
caaaaagtgg aagcctttac agatctttcg cttgcctttt ggccttcctc ttctg      535

```

```

<210> 90
<211> 432
<212> DNA
<213> Homo sapiens

```

```

<400> 90
gcccgggacg acccacgcgt acgactcagt ttaagtccaa actttctaata aatttgatgt      60
agcagcgtaa tgggctgcat tactagttag ttccttatgt gagtgtgcga gcatatgctg      120
gatgacttat ctagaataat gtagaagaga attaaacatt gaatgggagc tttaaattagt      180
taattttctga ggttcccttc cattcttaga attctttgat ttttatattg aattgagaga      240
actagtatag tttttatttc agcaaaattat aacaccattg ttctcaaggc atggaaaatg      300
tgcttttcat ctttaagata ctaaaccctt tcaactcatgg caattttttt tagctagcct      360
ctaagcttgg aaagcagtgg accccattaa taatcctggc caactctctt agtggaaacta      420
atatggggaga ag                                     432

```

```

<210> 91

```

<211> 780  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(780)  
 <223> n = a,t,c or g

<400> 91  
 ccatgcatag gattaaactg aatgatcgaa tgacatttcc cgaggaacta gatatgagta 60  
 cttttattga tgttgaagat gagaaatctc ctcagactga aagttgcact gacagtggag 120  
 cagaaaatga aggtagttgt cacagtgatc agatgagcaa cgatttctcc aatgatgatg 180  
 gtgttgatga aggaatctgt cttgaaacca atagtggaaac tgaaaagatc tcaaaatctg 240  
 gacttgaaaa gaattccttg atctatgaac ttttctctgt tatggttcat tctgggagcg 300  
 ctgctgggtg t cattattat gcatgtataa agtcattcag tgatgagcag tggtagcagct 360  
 tcaatgatca acatgtcagc aggataaacac aagaggacat taagaaaaca catgggtggat 420  
 cttcaggaag cagaggatat tattctagtgt ctttcgcaag ttccacaaat gcatatatgc 480  
 tgatctatag actgaaggat ccagccagaa atgcaaaatt tctagaagtg gatgaatacc 540  
 cagaacatat taaaaacttg gtgcagaaag agagagagtt ggaagaacaa gaaaagagac 600  
 aacgagaaat tgagcgcaat acatgcaaga taaaattatt ctgtttgcat cctacaaaac 660  
 aagtaatgat ggaaaantaa attgaggttc ataaggataa gacattaaag gaagcagtag 720  
 aaatggctta taagatgatg gatttagaag aggtaataacc cctggattgc tgcgccttg 780

<210> 92  
 <211> 867  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
 ctcagtcatg ccagtgcctg ctctgtgcct gctctgggccc ctggcaatgg tgaccgggccc 60  
 tgccctcagcg gcccccatgg gggggccaga actggccacag catgaggagc tgaccctgct 120  
 cttccatggg accctgcagc tggggccaggc cctcaacggg gtgtacagga ccacggaggg 180  
 acggctgaca aaggccagga acagcctggg tctctatggc cgcacaatag aactcctggg 240  
 gcaggaggtc agccggggccc gggatgcagc ccaggaaactt cgggcaagcc tgttgagac 300  
 tcagatggag gaggatattc tgcagctgca ggcagaggcc acagctgagg tgctggggga 360  
 ggtggcccag gcacagaagg tgctacggga cagcgtgcag cggctagaag tccagctgag 420  
 gagcgccctg ctgggcccctg cctaccgaga atttgaggtc ttaaaggctc acgctgacaa 480  
 gcagagccac atcctatggg cctcacagg ccacgtgcag cggcagaggc gggagatggg 540  
 ggcacagcag catcggctgc gacagatcca ggagagactc cacacagcgg cgctcccagc 600  
 ctgaatctgc ctggatggaa ctgaggacca atcatgctgc aaggaaact tccacgcccc 660  
 gtgaggcccc tgtgcaggga ggagctgcct gttcactggg atcagccagg gcgcccggcc 720  
 ccacttttga gcacagagca gagacagacg caggcgggga caaaggcaga ggatgtagcc 780  
 ccattgggga ggggtggagg aaggacatgt accctttcat gccacacac ccctcattaa 840  
 agcagagtca aggcattctca aaaaaaa 867

<210> 93  
 <211> 690

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

tcggaaccgc	cctgaattac	ctctgtcgac	ccacgcgtcc	ggggaaacgc	ttctacagga	60
tatggaaaaa	tttggctcga	tgatgtttcc	tgtgatggag	atgagtcaga	tctctggcca	120
tgcaggaaca	gtgggtgggg	aaataatgac	tgcagtcaca	gtgaagatgt	tggagtgatc	180
tgttctgatg	catcgatat	ggagctgagg	cttgtgggtg	gaagcagcag	gtgtgctgga	240
aaagttgagg	tgaatgtcca	gggtgccgtg	ggaattctgt	gtgctaattg	ctgggggaatg	300
aacattgctg	aagttgtttg	caggcaactt	gaatgtgggt	ctgcaatcag	ggctctccaga	360
gagcctcatt	tcacagaaag	aacattacac	atcttaattg	ccaattctgg	ctgcgctgga	420
ggggaagcct	ctctctggga	ttgtatacga	tgggagtggg	aacagactgc	gtgtcattta	480
aatatggaag	caagtttgat	ctgctcagcc	cacaggcagc	ccaggctggg	tggagctgat	540
atgccttgct	ctggacgtgt	tgaagtgaag	catgcacaca	catggcgtgc	tgtctgtgat	600
tctgatttct	ctcttcacgc	tgccaatgtg	ctgtgcagag	aattaaactg	tggagatgcc	660
atatctcttt	ctgtggggaga	tcacttttgg				690

&lt;210&gt; 94

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

cgagtggcga	ggttcatcat	ggaggcagac	ggagtctcgc	tctgttggcc	aggctggagt	60
gcaggggctg	gatctcggct	cactgcaacc	tccgtctccc	ggactaaagc	aattatcctt	120
cctcacgctt	ccgagtagct	ggaattacag	gtgtcaagct	agggatgcgg	tccattccca	180
ttgccactgc	ttgcaccatt	taccataagt	tcttttgcca	gaccaacctg	gacgcctatg	240
acccttacct	gattgccatg	tcttcaattt	acttggccgg	caaagtggaa	gagcagcacc	300
tgcggactcg	tgacatcatc	aatgtgtcca	acaggtactt	taacccaagc	ggtagcccc	360
tgggaattgga	ctcccgttcc	tgggaactcc	gggacagcat	cgtgcagtgt	gagcttctca	420
tgctgagagt	ctgcgccttc	caggtctcct	tccagcatcc	acacaagtac	ctgctccact	480
acctggtttc	cctccagaac	tggctgaacc	gccacagctg	gcagcggacc	cctgttgccg	540
tcaccgcctg	ggccctgctg	cgggacagct	accatggggc	gctgtgcctc	cgcttccagg	600
cccagcacat	cgccgtggcg	gtgctctacc	tggccctgca	ggtctacgga	gttgaggtgc	660
ccgcgcaggt	cgaggctgag	aagccgttgg	gtggcagatt	tatgccatgg	acacagagat	720
cccctaaggt	cctggcccag	gcctgcccac	agagaagcca	catctgcgtt	tgtcctttga	780
gaggactttg	actacaatac	aggcatgaca	tcaatgaaag	gaaagtcatg	aaatcgatga	840
gactgaatcc	ctacggattt	cttaaaagcc	agatttgtag	ggagaatgaa	tgtgcaacgt	900
ggctgaaatc	tattttgtgt	aataaaaggt	gatacaagtc	aaaaaaaa		948

&lt;210&gt; 95

&lt;211&gt; 541

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 95  
 ttagttttata aagaaaagac atttaattgg ctcatagttc tgcaggetgt acaggaagca 60  
 tagtagcttc tgcttctggg gaggcctcag gaaacttaca atcacagcag aaggtgaagg 120  
 ggaagcaggc acgccgtaca tggctgggct ttcggcctcc tcttcatcaa caaggagtgc 180  
 gtgggtcatgg cctatctctt caccaccttc aacgccttcc aggggggtctt catcttcgtc 240  
 tttcactgcg ccttacagaa gaagggtgagg tcgaggcgagg gtccctgggtc acagcctccc 300  
 ttggagacgt ttctgggta cccaggagaa ggcggcgagg gtggagggga ctcaggggct 360  
 ccctcaagcc cccagtgagt gctgcagggc ttctgtgggtc aggtctgcgt ccccgaggag 420  
 gggagcacga gctcagggtt agggagggtt taaccacggg tgaagagggt tctgttgaca 480  
 gacgctgagg ccgcaaacgc tcctcctctc tcttcacact cgccaacacc gcggtggcgc 540  
 t 541

<210> 96  
 <211> 603  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
 cagcccgtaa ggtgatctta cctccaaata tgagattcca tgaggagaag aggctggact 60  
 ttgaatggac actgaaggca ggggtgagaaa aaggctagcc ctggaagtga aataagggct 120  
 gggagggcca agaattgatga tagacggtga gggactgagg gatcagctga tgagttaagc 180  
 ctcaacacct gtccctagggc tttgcagatg gccctcaaac gtgtttacac cctcctgagc 240  
 tcctggaaact gcctagaaga ctttgatcag atcttctggg gccagaagag tgccctggct 300  
 ggtcagtggt tccccgaggt ctccataatc ccttaattggc cctcttgat gactcatcac 360  
 actccacagt cccccgtaac tctttgcaag aagagacctt atcatatctg gtcaactcag 420  
 agaggccttg agaattgaaa cgcagaagct ggggttcaggg aggggttatat acctgaaccc 480  
 ctggggtaga ttttgagaa gggatatgca ggctgtggta catatatcct ctttccaccg 540  
 cccaccaaag agaacgttcg ccagtgcctg caggatgatg agttgttcag cttccctcgt 600  
 gcc 603

<210> 97  
 <211> 1385  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 tctttcagca aggtgggggc aagcagaatg cctcccagga tttcacacct gagccctgcc 60  
 ccaccctgct gagaaaacac tccgccacgt gaagagacag aggaggatgg caggagttac 120  
 ctcgggaaac aaacaggatc ttctctgccc tgctccagtc gagttggcct gaccgccttg 180  
 gatcagtgc cttttgctgg cagacagggg agagcagctt ccagcctggg tcagaagggg 240  
 tggcgagcc cctcgccccc tcaccctcca ggctgctgtg agagtgtcaa gtgtgtaagg 300  
 gcccaaactc aggttcagtg cagaaccagg tcagcaggta tgcccgcctg tacgttaagg 360  
 gggccctcta aacccttgc ctggcctcac ctggccagct caccctttt ggggtgtagg 420  
 gaaaagaatg cctgaccctg ggaaggctcc ctggtagaat acaccacact tttcagggtg 480  
 ttgcaacaca ggtcctgagt tgacctctgg ttcagccaag gaccaaagaa ggtgtgtaag 540  
 tgaagtgggt ctcagtcctc agacatgtgc ccctttgctg ctggctacca ctcttcccca 600  
 gagcagcagg ccccgagccc cttcaggccc agcactgccc cagactcgct ggcactcagt 660

tcctcatct	gtaaaggtga	agggtgatgc	aggatatgcc	tgacaggaac	agtctgtgga	720
tggacatgat	cagtgtctaa	gaaagcagca	gagagagacg	ctccggcgcc	ccagcccccac	780
tatcagtgtc	cagcgtgctg	gttccccaga	gcacagctca	gcacacact	gacactcacc	840
ctgcctgcc	cctggccaga	gggtactgcc	gacggcactt	tgactctga	tgacctcaaa	900
gcactttcat	ggctgccctc	tggcagggca	gggcagggca	gtgacactgt	aggagcatag	960
caagccagga	gatggggtga	agggacacag	tcttgagctg	tccacatgca	tgtgactcct	1020
caaacctctt	ccagatttct	ctaagaatag	cacccccctc	cccattgccc	cagcttagcc	1080
tcttctccca	ggggagctac	tcaggactca	cgtagcatta	aatcagctgt	gaatcgtcag	1140
gggtgtctg	ctagcctcaa	cctcctgggg	caggggacgc	cgagactccg	tgggagaagc	1200
tcattcccac	atcttgccaa	gacagccttt	gtccagctgt	ccacattgag	tcagactgct	1260
cccggggaga	gagccccggc	ccccagcaca	taaagaactg	cagccttggg	actgcagagt	1320
ctgggttgta	gagaactctt	tgtaaagcaat	aaagtttggg	gtgatgacaa	atgttaaaaa	1380
aaaaa						1385

&lt;210&gt; 98

&lt;211&gt; 2191

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

accaccaccc	gtgcgggggg	atatctgagc	catttctctg	tgggcttttg	tttttcaaag	60
actgggcagg	ttgttggtga	ggtgtgtgtg	ggctgccacg	atthttgtgga	agtataatac	120
tttgtcatta	tgagatgtcg	tctctcggtg	cctcctttgt	gcaaattaaa	tttgatgact	180
tgcagttttt	tgaaaactgc	ggtggaggaa	gttttgggag	tgtttatcga	gccaaatgga	240
tatcacagga	caaggagggtg	gctgtaaaga	agctcctcaa	aatagagaaa	gaggcagaaa	300
tactcagtgt	cctcagtcac	agaaacatca	tccagtttta	tggagtaatt	cttgaacctc	360
ccaactatgg	cattgtcaca	gaatatgctt	ctctgggac	actctatgat	tacattaca	420
gtaacagaag	tgaggagatg	gatatggatc	acattatgac	ctgggccact	gatgtagcca	480
aaggaatgca	ttatttacat	atggaggctc	ctgtcaaggt	gattcacaga	gacctcaagt	540
caagaaacgt	tgttatagct	gctgatggag	tattgaagat	ctgtgacttt	ggtgcctctc	600
ggttccataa	ccatacaaca	cacatgtcct	tggttggaac	tttcccatgg	atggctccag	660
aagttatcca	gagtctccct	gtgtcagaaa	cttgtgacac	atattcctat	ggtgtggttc	720
tctgggagat	gctaacaagg	gaggtcccc	ttaaagggtt	ggaaggatta	caagtagctt	780
ggcttgtagt	ggaaaaaac	gagagattaa	ccattccaag	cagttgcccc	agaagttttg	840
ctgaactgtt	acatcagtg	tgggaagctg	atgccaaaga	acggccatca	ttcaagcaaa	900
tcatttcaat	cctggagtc	atgtcaaatg	acacgagcct	tctgacaag	tgtaactcat	960
tcttacacaa	caaggcggag	tggagggtgc	aaattgaggc	aactcttgag	aggctaaaga	1020
aactagagcg	tgatctcagc	tttaaggagc	aggagcttaa	agaacgagaa	agacgtttaa	1080
agatgtggga	gcaaaagctg	acagagcagt	ccaacacccc	gcttctcttg	cctcttgctg	1140
caagaatgtc	tgaggagtc	tactttgaat	ctaaacacaga	ggagtcaaac	agtgcagaga	1200
tgtcatgtca	gatcacagca	acaagtaacg	gggagggcc	tggcatgaac	ccaagtctgc	1260
aggccatgat	gctgatgggc	tttggggata	tcttctcaat	gaacaaagca	ggagctgtga	1320
tgcattctgg	gatgcagata	aacatgcaag	ccaagcagaa	ttcttccaaa	accacatcta	1380
agagaagggg	gaagaaagtc	aacatggctc	tggggttcag	tgattttgac	ttgtcagaag	1440
gtgacgatga	tgatgatgat	gacgggtgag	aggagtataa	tgacatggat	aatagtgaat	1500
gaaagcagaa	agcaaagtaa	taaaatcaca	aatgtttgga	aaacacaaaa	gtaacttgtt	1560
tatctcagtc	tgtacaaaaa	cagtaaggag	gcagaaagcc	aagcactgca	tttttaggcc	1620
aatcacattt	acatgacgt	aatttcttat	caattctact	tttatttttg	cttacagaaa	1680
aacgggggga	gaattaagcc	aaagaagtat	atttatgaat	cagcaaatgt	ggtgcctgat	1740
tatagaaatt	tgtgatccta	tatacaatat	aggactttta	aagttgtgac	attctggctt	1800
tttcttttaa	tgaatacttt	ttagtttgta	tttgacttta	tttcttttat	tcaaatcatt	1860
tttaaaaact	tacattttga	acaaacactc	tttaactcta	attgttcttt	gacacgtagt	1920
aattctgtga	catacttttt	ttttcttata	gcaatacact	gtaatatcag	aaatggttgg	1980
cctgagcaac	ctagtaagac	ctcgtctcta	ctaataatta	aaaaactagc	tggcatggta	2040
gcacacacct	gtagtcccag	atacttggga	ggccaaggca	ggaggattgc	ttgagacct	2100
gcaatcagtc	agggctgcag	tgagccatga	tggcaccact	gcactctagc	ctgggcaaga	2160

gaacaagatc ctgtctcaaa aaacagggaa a

2191

<210> 99  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> (1)...(335)  
 <223> n = a,t,c or g

<400> 99  
 ggacgagggc tgaacttcag gtggatgatg agacaaaata gaccgatagg aatcgtctgg 60  
 ctatatactc cttgttgcca ctgctgagtg actagactgg cccagagatc cgcggtgcac 120  
 atgctggccg ctctccctc agaaaaaggc aatggcctaa atactgttta aatgacctga 180  
 ctcgatgctg tgggaaactg gctgctctgc tgcatgccgt gtgactgtca gtccaaccgt 240  
 tacatttgcc acgttctcca cacgggggat agacgcaatg cgcccaggtc ccagttttct 300  
 ttggaggcag cagctctcgc agggctgaat gttgn 335

<210> 100  
 <211> 348  
 <212> DNA  
 <213> Homo sapiens

<400> 100  
 cctactctgg gggatcaacc agatcttcat tccataactc gtgcttctcg tcctaaatta 60  
 tgtactagaa aaaattgtaa tcctcttact ataactgtcc atgaccctaa ttcaactcag 120  
 tagtattatg gcatgtcatg ggaattaaga ttttatatcc caggatttga tgttgggact 180  
 atgttcacca tccaaaaaat cctggtctca tggagcccac ccaagccaat cgggccttta 240  
 actgatctag gtgaccctat gttccagaaa cccctaaca aagttgattt aactgttcct 300  
 ccaçcattct tagtcataaa agatacactc caaaagtctg agaaaatc 348

<210> 101  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
 agcctcaata atgtaacact gccccaagcg aaaacagaaa aagatttcat ccaactctgc 60

acccctgggg	taattaagca	agagaaactg	ggcacagttt	actgtcaggc	aagctctcct	120
ggagcaaata	tgattggtaa	taaaatgtct	gccatttctg	ttcacggtgt	gagtacctct	180
ggaggacaga	tgtaccacta	tgacatgaat	acagcatccc	tttctcaaca	gtaggatcag	240
aagcctattt	ttaatgtcat	cccaccaatt	cccgttgggt	ctgaaaattg	gaatagggtg	300
caaggatctg	gagatgacaa	cttgacttcc	ttggggactc	tgaatttccc	tggtcgaacg	360
gtttcttttt	cttttgagat	ggagtctcgc	tctgtcgccc	aggctggagt	gcagtg	416

<210> 102  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

<400> 102						
acgcgtccga	caaaaacaac	aacagatggg	gaaactgaaa	gtgcatagca	caaaatgcgg	60
actaattctg	aaatcaccaa	tatgtatctg	tgcttgggaa	atagaggcat	acacaggaat	120
gcagatgccc	acacactcac	attcacactc	acactcactc	tcacactcac	tctcacactc	180
actctcactc	gcactctcac	actacaccga	gatgctcaca	cactcagcct	ccccatgccc	240
aggccctgc	tctttgttaa	tcataagaag	accgtggaca	acccacctgg	aaactatgtg	300
cccacagacc	cagactgaag	gtgataaaaag	agggtggctg	gcttgggggc	tg	352

<210> 103  
 <211> 702  
 <212> DNA  
 <213> Homo sapiens

<400> 103						
aaagcagggtg	cctggaaaag	cctgctgagg	gtgaagggga	accatccagt	gtcctggggt	60
ggggaagcat	tttctcttt	atgagtctgt	ctctggctct	catggaacaa	aagtgggcag	120
tggtggtatg	agaagcagag	gctaattgtc	tacccctgc	ctccaagtag	aattactcct	180
tgtctgtgta	cctggtgagg	cagttgactg	caggaaccct	tctacaaaaa	ctcagagcaa	240
agggtatccg	gaaccagac	cactcgcggg	cactgagtga	gtaacatctt	tcctctcttc	300
cccacctgat	ctggattcaa	gtcttctcgg	ccctccagcc	ttcataatta	aaccataacc	360
tcttttttga	caacttactc	cccttctcac	atgaacccca	accctcccc	tctacccttg	420
accagtcttc	cagtctttat	agttgaagtt	ggaccactcc	caggcaccct	tgaatttcca	480
atcatgtatc	tgctttgcac	ctcacagtcc	ctaactccag	ccctgctaga	atatgggctc	540
tccggactgg	aaagaatctt	aggggtcctc	taatctaacc	ctcacatgat	gcttcaactc	600
ctccagatca	tctctaacat	agccagagtg	tcacgctatg	tttaagcatc	ttcagggatg	660
ggaaaatccc	ccacacccat	gtattgcggc	cgctctagag	ga		702

<210> 104  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 104  
 ggcaacatac attgtggact ttggcttcag tacaacattc agagaggggc agatgctgac 60  
 agctttttgt ggcatgtacc cctacgtggc ccagaaagc tccctgggac aggcattgcca 120  
 gtgacccgcc agggacatac aaagcctcag tgtcactctg tatttcagga atacagtagg 180  
 tagaaggggc aggactttgc ccttttactc agggaaagc ccaaacttca agaaaaaatt 240  
 ctacacaggaa gatatacatg cccaccaactt cttgcccttc aacttgactc attaaaaaat 300  
 tactaatgct gaacgccagg aagtgtcctt cactgtaact gatgaaaaat ccatgggtga 360  
 aaagtagcca gaagatgcca ctgataccat acgaagagcc actcctggac caccctaaac 420  
 aatccagctc atgggtggcca tgggatttca ggccaagaac atctctgtgg caatcataga 480  
 aagaaaattc aactatccca tggccacctt cctcatttta gagcacacaa aacaagagag 540  
 gaagtgtctc accatcagag aactgtccct tcctcccggt gttccacct ctcttcccc 600  
 atccactgaa ctttccacct tccctctctc actgatgcgg gctcataggg agccagcttt 660  
 taacgttcag cctccgaag aaagccagg 689

<210> 105  
 <211> 776  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
 agcaaagcag gagctggcca agctgatgcg gattgaggac cctccctcc tgaacagcag 60  
 agtcttgctg caccacgcca aagctggcac catcattgcc cggcaggag accaggacgt 120  
 gagctgcac ttcgtgctct ggggtgcct gcacgtgtac cagcgcatga tcgacaaggc 180  
 ggaggacgtg tgctgttctg tagcgagcc cggggaactg gtggggcagc tggcgtgct 240  
 cactggcgaa cctctcatct tcacactgcg agcccaagc gactgcacct tcctgcggat 300  
 ctccaagtcc gacttctatg agatcatgcg cgcacagccc agtgtggtgc tgagtgcggc 360  
 gcacacggtg gcagccagga tgcgcctt cgtgcgccag atggacttcg ccatcgactg 420  
 gactgcagtg gaggcgggac gcgcgtgta cagggtgcag tcccaccgct ctgctcaggc 480  
 ccggcctagg ggtggggacc tgggggtggt cagaccttgc tgacctccac gccactcag 540  
 gcaggcgac cgtccgact gcacttacat cgtgtcaat gggcggtgc gtacgtgat 600  
 ccagcgaggc agtggcaaga aggagctggt gggcgagtag ggccgaggc acctcatcgg 660  
 cgtggtgagc gcgacccca cccactgacc tctggcctt tccaggccag tccctcgga 720  
 actcacagc atcatcccg gtaatccagg gtaggtgaa gtttttccg gggctc 776

<210> 106  
 <211> 707  
 <212> DNA  
 <213> Homo sapiens

<400> 106  
 cccacgcgtc cggatggacc ccaggaacca cccagacctt aggcagggg acagcatggg 60  
 acacagttgc ttccactcca ggaaccagc agactacagc ttcagctgag ggaagacgaa 120  
 cccaggagc aaccaggcca gcagctccag ggacaggcag ctgggcagag ggttctgtca 180  
 aagcacctgc tccgattcca gagagtcac cttcaaagag cagaagcatg tccaatacaa 240



cagaaggtgt	ttgggagggc	accagaagct	cggtgacaaa	cagggctaga	gccagcaagg	300
acaggagggg	gatgacaact	accaaggctg	ataggccaag	ggaggacata	gaggggggtca	360
ggatagctct	tgatgcagcc	aaaaaggctc	taggaaccat	tgggccacca	gctctggtct	420
cagaaacttt	ggcctgggaa	atcctcccac	aagcaacgcc	agtttctaag	caacaatctc	480
agggttccat	tggagaaaca	actccagctg	caggcatgtg	gaccttggga	actccagctg	540
cagatgtgtg	gatcttggga	actccagctg	cagatgtgtg	gaccagcatg	gaggcagcat	600
ctggggaagg	aagcgtgca	ggggacctag	atgctgccac	tggagacaga	ggcccccaag	660
caacactgag	ccagaccccg	gcagtatgac	cctggggacc	ccctggg		707

&lt;210&gt; 107

&lt;211&gt; 485

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(485)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 107

ccgctggaac	atcagggtact	ggggacaactg	gccctggtaa	cacagcagtc	tcaggcacac	60
ctgtgggtatc	acctggagca	actcctggag	ctccaggtag	cagcaccct	ggggaagcag	120
acattggaaa	caccagtttt	ggaaaatcag	ggacccaac	agtatctgct	gcctcaacta	180
ccagtagccc	tgtgagtaaa	cacaccgatg	cagcctcagc	cacagcagtg	acaatctctg	240
gaagcaaacc	aggtacacct	ggaacaccag	gtggtgcaac	tagtggaggc	aaaattacac	300
ctggaattgc	atgaccaccc	ctggacaaa	agagccctg	cttctccggg	tatggagggt	360
atttccctgt	aaatcctcac	cagaacccat	gtgctgatte	cctgtaatct	tcccacaata	420
aatttttagc	agctctgnnn	nnnnnnnnnn	nggggcgccc	gttttaaggg	accacacctt	480
actcg						485

&lt;210&gt; 108

&lt;211&gt; 565

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

cgggctcacc	gctgctgtct	cccgtctcca	agtctttctt	gtgaaatcca	aattggattc	60
tcttgatctt	ccatctttcc	agggcagtga	gcttgctcct	gttcctgctg	cagaagttgt	120
agaaggaact	ggcctcagag	cccacgtgt	cctcatcctc	ctcccgacc	ctgctccctg	180
cttctgagct	cctgtctgcc	gcctcctctc	tcttgctctt	ggcgtggtag	ctccgggaag	240
cctccttctc	aatctccagc	agcctctcgt	tccatgcgtc	ccagggtgctc	tccgaggaca	300
tcgagtctgc	gcggcgccctc	ctgccgtggt	ccgggcgggt	cagctccagc	tgctgcttca	360
ggacccagat	gtcgtggctg	ctcacgtctc	cccaggcgct	gctctcgctc	agggtgcgcc	420
gccgcctccc	caaccaggag	ccagcgtcgc	tctcctcctc	tttctcctcc	tcccttcccc	480
acctccggta	cccttctgct	aaaaacctct	cgtttcggct	ctgccactcg	tgaatgatcc	540
tctccacgtc	ctcgtcctcg	acctcg				565

<210> 109  
 <211> 986  
 <212> DNA  
 <213> Homo sapiens

<400> 109  
 ggatgacgtg ccgcccccg ctcctgacct ctacgacgtg cccctggct tgcggcgcc 60  
 tggcccgcc accctgtacg atgtgccccg tgaacgggtg ctctctctg aggtggctga 120  
 tgggtggcgtg gtcgacagtg gtgtgtatgc ggtgcctccc ccagctgaac gtgaagcccc 180  
 ggcagagggc aagcgctgt cgccctccag caccggcagc acacgcagca gccagtctgc 240  
 gtctctcttg gaggtggcag ggccgggccc ggaacccctg gagctggaag ttgctgtgga 300  
 ggccctggca cggctgcagc aggtgtgag cgccaccgtt gccaccttc tggacctggc 360  
 aggcagcgcc ggtgcgactg ggagctggcg tagccctct gagccacagg agccgctggc 420  
 gcaggacctg caggctgctg tggccgccc cagagtgc gtccacgagc tgttgagtt 480  
 tgcccgagc cgggtgggca atgtgcccc cactctgac cgtgccctgc atgccaagct 540  
 tagccggcag ctgcagaaga tggaggacgt gcaccagacg ctggtggcac atggtcaggc 600  
 cctcgacgct ggccggggag gctctggagc cacccttgag gacctggacc ggctggggc 660  
 ctgctcgccg gctgtgccc aggacgcca gcagctggc tccttctgc acggcaatgc 720  
 ctactgctc ttcagacgga ccaaggccac tgcccgggg cctgaggggg gtggcaccct 780  
 gcacccaac cccactgaca agaccagcag catccagtea cgacccctgc cctcaccccc 840  
 taagttcacc tcccaggact cgccagatgg gcagtacgag aacagcgagg ggggctggat 900  
 ggaggactat gactacgtcc acctacagg ggaaggagg agtttttaga agaccagaa 960  
 ggagcttctg ggaaaaagg cagcat 986

<210> 110  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

<400> 110  
 cgaagggaaa gcagcaggtt ggggcttctt gtggccaact tcagagcctg tcaccaggaa 60  
 aggttaagcat gggaggaagg aagatggcga cagatgaaga aaatgtctat ggttttagaa 120  
 agaacgctca gtcccgccag gagtccacgc ggaggctcat ccttgttggg agaacagggg 180  
 ccgggaagag cgccactggg aacagcatcc tgggccagag acggttcttc tccaggctgg 240  
 gggccacgtc tgtgaccagg gcctgcacca cgggcagccg caggtgggac aagtgccacg 300  
 tggaagtcgt ggacactccg gacattttca gctcccaagt gtccaagaca gatcctggct 360  
 gtgaggagag aggtcactgc tacctgctct cggcccccg accccacgcg ctgg 414

<210> 111  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature

&lt;222&gt; (1) ... (419)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 111

gactctcggg	ttacgttcac	taacgaagga	gggcggtggt	gggggtgatg	tggcggcctt	60
tgagggtggc	acaggggctg	cggccagccg	ggcgctgggg	cagtgcgggc	agctccagaa	120
gctcatcgtc	atcttcattg	gcagcctgtg	cgggctgtgc	accaagtgcg	ctgtgtccaa	180
cgacctcacc	cagcaggaga	tacagacccc	ggagatacaa	cagagaaatg	cataatgtcc	240
agtcaattta	ttaaagttcc	aaagtntnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	300
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnatttcaa	tatgattaaa	gcaggagtga	360
ggacacagcg	aaagtgagac	aaggaaaaga	gaacaaaata	aaacaggaga	gacagaata	419

&lt;210&gt; 112

&lt;211&gt; 1191

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

gtgcaagggtg	ctgtcactca	cgtgtgccct	cgacctccc	gttcacccgc	agccttctca	60
gcgcctctcc	ctgggcggga	ggcctcctca	ccagcctacc	tgttgctctg	gaaaaaaaaa	120
ccgtcccccg	actccgtccc	tacccccagt	cttcggccgg	ctctggcccc	tggggagggg	180
gctgcacggg	ggaaggaggc	tggctatggg	cccggctgcc	cgctgcatgt	acctcctcct	240
ccacccatcg	cctcttgcc	gggggttaact	ttgcctgggg	ctcattcttt	ggttaagctg	300
aagctgccgt	gggtggccaa	accgcagatt	ctttgcaaat	tctgagctgg	cagagctcgc	360
agccgggagc	cggccgggga	agaggagact	tgcgcgcgc	aagccgcctg	cctccaccct	420
gctctccatc	tcccgtctca	gaagggtctg	gaagctcgcg	gccgggggtc	cacctggaag	480
ctgcttgcat	ggctgaaccc	agcttaggtc	cctgacgggg	ctgctggtgg	aattctcccc	540
cttcgaagct	ggggagggtt	aggaggggga	aggcttctgt	gaagctctca	aaccactaat	600
agagccccct	ccccaacagt	gacggcgcag	atgctcccc	ttttcttagt	tgacaccacc	660
aggcagcttc	ctggccgttg	gtagggtcct	gcagctggct	gagggaacag	ggaccggcag	720
gggactttgt	taggggagg	ttgggatggg	cagtggggcc	ctgaaagtta	atatattgga	780
acctagctcg	agtgtcgttc	tttccaattc	cgaaagtaga	aagagtaaaa	ataggggtga	840
ttgggggtgg	gttagtagaa	tgcctctctc	aggcgctcc	cccctcccc	accgttttag	900
agagctaggc	ctcagccagt	cttgccactc	ccatctcagt	gcttcttgaa	gaggctgttt	960
tgagtgttga	tgaagagcaa	tgcaattatg	ccaaacagta	ttgagcagaa	taatttattt	1020
cttttttttc	ttttgtctta	aatcatgaat	cccgccaggt	acggtggctc	acgcctgtca	1080
tcccagcact	ttgggaggcc	aaggcggggc	gattacttaa	tacttaaggt	caggagtctg	1140
agaccagcct	ggccgatatg	gtgaaacctc	gtctctacca	aaaaaaaaaa	a	1191

&lt;210&gt; 113

&lt;211&gt; 1240

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (1240)

&lt;223&gt; n = a,t,c or g

```

<400> 113
agaacacgaa ctagtgtctc taagccacta taatagttgc acatacaaca tgagtgtggt      60
gtggtaggat gcttttcctt ttaggtcttt actgaacttt caagggatta aaaccaatgt      120
atgtcaactt tatagcaaaa gattcagatt ctaatcctga ataccaatgc attttagagg      180
gggaaaaaat gagggatgta aaatatatat agtagggtaa gaggttttgcc ttggaacaat      240
gtgcatattc tattttaatt tggaatgttt tatacttgca tttcatgtta ttaggttttt      300
ggactggact gtgtttttcc aaaaaatgaa aaatcaacta ttttgccacc ttattattca      360
acctacctgc ccatagttgt ctatgccagt tactaatcta tttaaattta ataaatcaaa      420
agctgtcctt agggattggc caagagtcgt aagtccttca gcctgaagggt ttttcaattc      480
attcataaac gttgcatggg tttctttcca tccagccttg atagcatagg gcggtctctc      540
gaaagtgacc agcatatacc tgtctcctct gctggcaggg tcccggggcac ggagcttcat      600
gaaggctctt accgcgcctt tggccgtgtc caggtagggt gtgccagat ggctgcgctg      660
gttcatagag gcagacgtgt ctatcaggaa cagtaagatg ggcatagtgc tggccgggga      720
caccggggcc cgagggtggt gagaaagagg agatggtaga ggtggaggcg ccggtggcgg      780
cgaccgccgc tagcggggcg ggggagcacg gccccggga ggaaaacact gtctgggtct      840
ttcctccggc tgcggggaat tectccccg atagttgaga ggaaactccc cagaccaggt      900
gctccccgtc gtaccnccgc ctccgcctcc tctgcctgc ctgccgctg gggcgggcgc      960
ccagccgtct gtctgtcggg tegtcccccc cgcctcgggg gtcccgtccc cgtcccggc      1020
ccctgtgtgt gtcccagcgg gagacggggc tggctcccca cccaccccc ggtagaggag      1080
tggggacctg ggagctggcg aagaggggag tgggctgagg gaagattggc cctggggctg      1140
ttgggagaag tttcagggac tccctccgca caccggcggt gtcaccactt tctcagcccc      1200
tctcgcggac gcgtgggtcg cgcgggggtt tccgcaggca                                1240

```

```

<210> 114
<211> 810
<212> DNA
<213> Homo sapiens

```

```

<400> 114
aatagaattc cgtcggcaca cgcacgcgta cctaggatcg tatagagcgg ccgcaatata      60
tgccgtcttc ttaaataaac tcctctctct caaaaagcct ttctttccgt gtccggaata      120
tcatccctcc ggtcctgtcc cgcagcgagt tcccggcgt tgggtcttct tattatgccg      180
gccagcggag tccaattggt ctgacttcac tgtccggaga atcctctcgc tcccaaacct      240
ccctgagaga cgacctttaa ccgtgccagc cggacctgcc taaaagacc ctctcttca      300
acctgtcccc tgtgttactc cacaaaacgg acacagaagt tegtcaacct gccagatac      360
cacgcctcaa agcggcaaca gagccgaacc cctttctcag gcttcggacg gccagaccc      420
ggcatctctt ttctcctctt cccagaccc ttccacctct ggctccgag agccccagcc      480
tcagttcccc tccaggccct aggaacccta ctctccagca gtacagtctg tagacccccg      540
aatcagttcc cactcaacc tcagaactcc tctggcgccg actggcccc ctcgggcaaa      600
ggatggcggt ggataggatg acccgaacca ccagagccag caaacttacc ccagccgcca      660
tggtgattcc gcaaagaaag ggggtggggt tctcggcgct gccgcaaagt aagcccggcc      720
gggagagaag ggaggggaa agaggagagc cgtggagaaa cagcagccga aaaacgagga      780
cgaaacagaa gacatacgta cgacagttcg                                810

```

```

<210> 115
<211> 320
<212> DNA

```

<213> Homo sapiens

<400> 115

caagagcacg	atgctgaagc	actggagagt	ggggctctgg	ggtcagtgct	ggatcagagg	60
caagaggagg	tgatgatgcg	gcctgtcct	gagtgaacac	aacctctccc	cagtactaca	120
cctgcagctg	tgctctgggc	ttcattgcct	gtccatctt	cttgcatgag	agcctgaagc	180
caaagggtcat	gctgctgaca	gtggccctgg	tggcctgtct	cgtgctcttc	aacctctccc	240
agtgtggca	gcgggactgc	tgagccaag	gcctgggcaa	cctcactgag	cccagtggca	300
ccaacaggta	gggccccgcc					320

<210> 116

<211> 456

<212> DNA

<213> Homo sapiens

<400> 116

ggcaaggcag	gcggcgcggc	cggcctcttc	gccaaagcagg	tgacagaaga	gttttagcagg	60
gcccaggaga	agtagacaag	gcggtttggg	aagacatgtc	agccagaaga	aagagcgagg	120
gaagaaagac	aagaaggacc	tgagatagag	tttgggtttt	cctttttttc	tctctctctt	180
tattaagccc	aacctgcctt	ctacaacgga	gaagttttgg	ttttctaaga	gctgatggac	240
ttagaagcat	ttggatgaac	agctctgctt	accaactgaa	atatccctat	tatcttctaa	300
aagtggagca	ctgctttgag	ccctgggaag	gcttaaaggc	aaccagctct	cccagattga	360
tttatcagca	gaaaactgat	ggaatgtaga	tgtagctcct	gactttaaga	gaccacaatg	420
gaagggaggt	tattttctat	catttgaggt	catgtg			456

<210> 117

<211> 2398

<212> DNA

<213> Homo sapiens

<400> 117

cccacgcgtc	cggtcagcct	cagtcttcaa	tgagggaccc	cgtacagagt	aacccaaacg	60
cttgttccta	tttcaggatg	tgaacactct	gcaaggaggt	gggcagcctg	tggtgactcc	120
gtccgtccag	ccctctcttc	agccggccca	tccagcggtta	ccacagatga	cctcacaggc	180
acctcagcca	tctgttactg	ggctccaggc	accttctgct	gccttaatgc	aagtgtcatc	240
tctcgattcc	cactcagctg	tatctggaaa	tgcccaatcc	tttcagccct	atgcagggtat	300
gcaagcctac	gcttatcccc	aggcatctgc	cgtcacctcc	cagctgcagc	ccgttcggcc	360
tttgtaacca	gcaccgctct	ctcagcctcc	ccattttcaa	ggatcagggt	atatggcttc	420
atttctcatg	actgaagccc	ggcaacataa	cactgaaatt	cgaatggcag	tcagcaaagt	480
ggctgataaa	atggatcatc	tcagtactaa	ggttgaagag	ttacagaaac	atagtgtctgg	540
caattccatg	cttattccta	gcatgtcagt	tacaatggaa	acaagcatga	ttatgagcaa	600
catccagcga	atcattcagg	aaaatgaaag	attgaagcaa	gagatccttg	aaaagagcaa	660
tcggatagaa	gaacagaatg	acaagattag	tgaactaatt	gaacgaaatc	agaggtatgt	720
tgagcagagt	aacctgatga	tggagaagag	gaacaactca	cttcagacag	ccacagaaaa	780

cacacaggca	agagtattgc	atgctgaaca	agagaaggcc	aagggtgacag	aggagtttagc	840
agcggccact	gcacaggtct	ctcatctgca	gctgaaaatg	actgctcacc	aaaaaaagga	900
aacagagctg	cagatgcagc	tgacagaaaag	cctgaaggag	acagatcttc	tcaggggcca	960
gctcaccaa	gtgcaggcaa	agctctcaga	gctccaagaa	acctctgagc	aagcacagtc	1020
caaattcaaa	agtgaaaagc	agaaccggaa	acaactggaa	ctcaagggtga	catccctgga	1080
ggaggaactg	actgaccttc	gagttgagaa	ggagtccttg	gaaaagaacc	tctcagaaag	1140
gaaaaagaag	tcagctcaag	agcgtttctca	ggccgaggag	gagatagatg	aaattcgcaa	1200
gtcataccag	gaggaattgg	acaaacttcg	acagctcttg	aaaaagactc	gagtgccac	1260
agaccaagca	gctgcagagc	agctgtcttt	agtacaggct	gagctacaga	cccagtgga	1320
agcaaaatgt	gaacatttgt	tggcctccgc	caaggatgag	cacctgcagc	agtaccagga	1380
ggtgtgcgca	cagagagatg	cctaccagca	gaagctggta	caacttcagg	aaaagtctgt	1440
ttgttttgca	gtgttttagcc	ctccaggccc	aatcacagc	tctcaccaag	caaaatgaac	1500
agcacatcaa	ggaactagag	aagaacaagt	cccagatgtc	tggggttgaa	gctgctgcat	1560
ctgacccttc	agagaaggtc	aagaagatca	tgaaccagggt	gttccagtcc	ttacggagag	1620
agtttgagct	ggaggaatct	tacaatggca	ggaccattct	gggaaccatc	atgaatacga	1680
tcaagatggt	gactcttcag	ctgttaaacc	aacaggagca	agagaaggaa	gagagcagca	1740
gtgaagaaga	agaagaaaa	gcagaagagc	ggccacgaag	accttcccag	gagcagtcag	1800
cctcagccag	ttctgggcag	cctcaagcac	ccctgaatag	ggagaggcca	gagtccccca	1860
tgggtgccctc	agagcagggtg	gtcgaggaag	ctgtcccgtt	gcctcctcag	gccctcacca	1920
cttcccagga	tggacacaga	aggaaagggg	actcagaagc	tgaggcactc	tcagagataa	1980
aagatgggttc	ccttcacccc	gaactgtctt	gcacccatc	ccacagagtt	ctagggcccc	2040
cgacttcaat	tccacctgag	cccctaggcc	ctgtatccat	ggactctgag	tgtgaggagt	2100
cacttgctgc	cagcccaatg	gcagctaaag	ccgcacaacc	catcaggga	aggtctgtgt	2160
tcaggggaag	taggcaccag	atggggccac	ttacaaggaa	aggttccaca	agattgttcc	2220
ctggatttca	ggaccccgag	ggagggggac	ccactggcct	tagggcttga	aaagcccagg	2280
gagagcctca	gcctccacag	cttcaaggaa	aggttgatgt	tcactagggt	ccaccgggtc	2340
cccacaaggg	agcttttcaa	gaacaggagg	gcaggtttcc	acagttttgc	agggagca	2398

<210> 118  
 <211> 800  
 <212> DNA  
 <213> Homo sapiens

<400> 118						
agcgaaacgg	cgcagcaa	tatcgaccgt	ctgcgcgtaa	aactggcgaa	agaaccgggg	60
gcgaatctgt	tcctgatggc	ggtacaggat	attcgcgttg	gtgggcgtca	gtcgaacgcc	120
agctaccagt	acacgttggt	atccgacgac	ctggcggcac	tgcgagaatg	ggagccgaaa	180
atccgcaaaa	aactggcgac	gttgccggaa	ctggcggcag	tgaactccga	tcagcaggat	240
aacggcgcg	agatgaatct	ggtttacgac	cgcgacacca	tggcacggct	gggaatcgac	300
gtacaagccg	ccaacagtct	gttaaataac	gccttcggtc	agcggcaaat	ctcgaccatt	360
taccagccga	tgaaccagta	taaagtgggt	atggaagtgg	atccgcgcta	taccaggac	420
atcagtgcgc	tggaaaaaat	gttcgttatc	aataacgaag	gcaaagcgat	cccgtgtca	480
tatttcgcta	aatggcaacc	ggcgaatgcc	ccactatcgg	tgaatcatca	gggattatcg	540
goggccttga	ccatttcggt	taacctgccg	accggaaaat	cgctctcgga	cgccagtgcg	600
gogatcgatc	gcgcaatgag	ccagcttggt	gtgccttcga	cgggtgcggg	cagttttgcc	660
ggcccggcgc	aggtgttcca	ggagaccatg	aactcgcagg	tgatcctgat	tattgcgcgc	720
atcgccacgg	tgtatatcgt	gctgggaatc	ccttacgaga	ggtacgtaca	tccgcgcagc	780
attctcttgt	gaaggcgcgc					800

<210> 119  
 <211> 427  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

aaatcatcac	acctgatg	cg atgggttgcc	agaaagatat	tgcagagaag	atacaaaaac	60
agggaggtga	ttattttatc	gctgtaaaag	gaaaccagg	gcggcttaat	aaagcctttg	120
aggaaaaatt	tccgctgaaa	gaattaaata	atccagagca	tgacagttac	gcaatcagtg	180
aaaagagtca	cggcagagaa	gaaatccgtc	ttcatattgt	ttgcgatgtc	cctgatgaac	240
ttattgattt	cacgtttgaa	tggaaagggc	tgaagaaatt	atgcgtggca	gtctcctttc	300
ggtccataat	agcagaacaa	aagaaagagc	cagaaatgac	ggtcagatac	aatatcagtt	360
agttgggtat	cgcggggat	atatcagtca	cagcgatctc	cgggacggac	gattgaatct	420
cgtaatc						427

&lt;210&gt; 120

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

ccattatttg	aaaatgctca	ctcaggcgcg	gcgggaagtg	attatcgcca	acgcctactt	60
cttccccggc	tatcgatttt	tacacgcctt	gcgtaaagcg	gcacggcgcg	gggtgoggat	120
caaactgatc	attcagggcg	aaccggatat	gccgattgtc	agagtcggtg	cgcgcttgct	180
gtataactat	ctggttaaag	gcggcggttc	ggtttttgag	taccgcccgc	gcccgcctca	240
cggcaaagtg	gcattgatgg	acgatcactg	ggcgacagta	gggtccagta	atctccatcc	300
ggtcagttag	tcggggaatc	tccaagcaaa	tgtcatcctc	cacgttctac	gggtaccgac	360
attgaatccg	taatcatg					378

&lt;210&gt; 121

&lt;211&gt; 508

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 121

ctgccgcctg	gtgaagttaa	cgccccatcg	aagccctggc	aaaagaagtc	cgtgaactga	60
aataacatac	tcgttaattg	ctcaatccag	ccacaacggc	agaactgacc	agtcctgggac	120
gaaacctgaa	ccgattgtta	aaaagtgaac	gcgaacgtta	cgacaaatac	cgtacgacgc	180
tcaccgacct	gacccatagt	ctgaaaacgc	cactggcggt	gctgcaaaag	acgctgcggt	240
ctctgcgtag	tgaaaagatg	agcgtcagtg	atgctgagcc	ggtaatgctg	gagcaaatca	300
gccgcatttc	acagcaaatt	ggctactacc	tgcacgtg	cagtatgcgc	ggcgggacat	360
tgctcagccg	cgagctgcat	ccggctgccc	cactgctgga	caatctcacc	tcagcgctga	420
tcaaaggcaa	gccgcgtaaa	ggggggcaacg	tactgtttt	tccattcaca	gcgatgtaca	480
gggacggaca	ttgaatccgt	gatcagtg				508

<210> 122  
 <211> 724  
 <212> DNA  
 <213> Homo sapiens

<400> 122  
 gggtaacact gtgatgttcc agcacctgat gcagaagcgg aagcacaccc agtggacgta 60  
 tggaccactg acctcgactc tctatgacct cacagagatc gactcctcag gggatgagca 120  
 gtccctgctg gaacttatca tcaccaccaa gaagcgggag gctcgccaga tcctggacca 180  
 gacgcccgtg aaggagctgg tgagcctcaa gtggaagcgg taaggggcggc cgtacttctg 240  
 catgctgggt gccatatatc tgctgtacat catctgcttc accatgtgct gcatctaccg 300  
 cccctcaag cccaggacca ataaccgcac gagcccccg gacaacaccc tcttacagca 360  
 gaagctactt caggaagcct acatgacccc taaggacgat atccggctgg tcggggagct 420  
 ggtgactgtc attggggcta tcatcatcct gctggtagag gttccagaca tcttcagaat 480  
 gggggctcact cgcttctttg gacagaccat ccttgggggc ccattccatg tcctcatcat 540  
 cacctatgcc ttcattggtgc tggtagccat ggtgatgcgg ctcatcagtg ccagcgggga 600  
 ggtggtagcc atgtcctttg cactcgtgct gggctggtgc aacgtcatgt acttcgcccg 660  
 aggattccag atgctaggcc ccttcacccat catgattcag aagatgattt ttggcgacct 720  
 gatg 724

<210> 123  
 <211> 435  
 <212> DNA  
 <213> Homo sapiens

<400> 123  
 gagaaagcag cagctgcca catagatgaa gtgcagaagt cagatgtatc ctctacaggg 60  
 caggggtgtca tcgacaagga tgcgctgggg cctatgatgc ttgaggtagc acatcttcat 120  
 tttagtgtctg tattttaaaa tcttgttgat cttcacatta ttacatttaa tttcaggtga 180  
 atataattta aggagaatcc acactagtac tagtactatg gacctcttga gcttgctgat 240  
 atgcctgtgt gtctctatgt atgttttggc tcctgctgcc agtataatgt tggttgaaat 300  
 taacatagaa ttaaattaac tagattagag tagacattgg caagttgtaa ttgccagttg 360  
 agcatttatt tgaaaaactg tattcacaag tcctactaaa ttctgtgttg attttagctt 420  
 gaaatgttct caaaa 435

<210> 124  
 <211> 363  
 <212> DNA  
 <213> Homo sapiens

<400> 124  
 actggaagtg ccttcagagg tcaccctttt gggctttgcc atgcaggcta caaagactct 60



cctcctcaga	acatgctgct	tgcaggaatt	caacatcatg	gaaaagaata	aaggatgggc	120
tctcctggga	ggaaaagatg	gccatcttca	gggactatth	ctccttgcca	acgcattgct	180
ggaaagaaat	cagctccttg	cacagaaggt	catgtactta	ttagtccttc	ttottaaccg	240
agggaatgat	aaacataaac	tcacatctgc	aggctthttt	gtggagcttc	tccggagtcc	300
agtggccaag	agactgcccc	gcataactc	tgttgcccc	tttaaagact	ggctacaaga	360
tgg						363

<210> 125  
 <211> 373  
 <212> DNA  
 <213> Homo sapiens

<400> 125						
agaccggccc	ccgtccctc	agctgcgcg	gaggaggcgc	ccagtcctcg	gggtgaaggg	60
tgggggatg	gcgaagcgaa	gagtgcgcg	tccggtgtgg	gggggagcag	gaggaggac	120
gaagtccgcc	cgccgcgcg	ccgccgcgc	tgacaccgag	cggagcgagg	aaggaggacg	180
agcgggtgaag	gaagcctacc	cttccagccg	tcagccgcgc	ccgccgtcgc	cgtgaccctt	240
gcgttgccgc	cggcgctgcc	accggaactt	agccccctcg	atgccaatth	caaataggga	300
aggaaaagg	aaaagaagg	aagagaaaat	ccggccgcgt	agtcccgcgt	ccactcacac	360
ctccgctcgt	gcc					373

<210> 126  
 <211> 362  
 <212> DNA  
 <213> Homo sapiens

<400> 126						
gcctacagg	ggtccatgg	agcagttcta	ctttctgcag	ctccctaagc	agtgactttg	60
accccctaga	gtactgcagc	cctaaagggg	atccccagcg	agtggacatg	cagcctagt	120
tgacctctcg	gcctcgttcc	ttggactcgg	aggtgcccac	aggggaaacc	caggtttcca	180
gccatgtcca	ctaccaccgc	caccggcacc	accactacaa	aaagcgggtc	cagaggcatg	240
gcaggaagcc	tggcccagaa	accggagtcc	ccagtcacag	gcctcctatt	cctcggacac	300
agccccagcc	agagccacct	tctcctgac	agcaagtcac	cagatccaac	tcagcagccc	360
ct						362

<210> 127  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 127

catggctgac	cccgaccccc	ggtaccctcg	ctcctcgatc	gaggacgact	tcaactatgg	60
cagcagcgag	gcctccgaca	ccgtgcacat	tcgaatggcc	tttctgagaa	gagtctacag	120
cattctatct	ctgcaggatc	tcttagctac	tgtgacttcg	acagataatt	tagcctttga	180
ggatggacgg	actgactggc	tgcaaaggcc	tgactgtgtc	tccttcaaaa	ttcatgtgct	240
gccaatgtga	cggtattaa	aggaggggcc	ttagaggggg	attagatcct	gaaaggctct	300
tactttttgg	agtgcagagg	atgcatacga	tgaagcatc	tcgtagatac	g	351

&lt;210&gt; 128

&lt;211&gt; 374

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

gaactcccca	aaggcaccat	ccagggttttt	accccgcttg	tcaaattccc	ctctggccca	60
gggctggctg	ctcagcagga	gtgtttaata	agcacttaat	tgcccgggtga	gtacagacca	120
ttccagctca	ccttaactgt	ttcctggctg	actcgcctct	cggcctgatt	gccctgctca	180
tctggctgag	tgagctggaa	tgagtgtagt	ggtagtgcc	cctatagggt	cctcttacct	240
tggtcttatt	tcacaggagc	acttcccga	cgagtttacc	tcgggagatg	gaaagaaagc	300
tcaccaggac	tttggctact	tttatggctc	gagctatgtg	gcagcctctg	acagcagccg	360
gactcctggg	ctgt					374

&lt;210&gt; 129

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

taccaccacg	cccagcccca	acatatgact	ttctgtgtgt	tttccaagag	tctagtgtga	60
ggtcagaggt	cagacaggtc	atcaggaatt	ttgcttcaag	tgagttgctg	ctgccctgac	120
tcttttcccc	cagcaattaa	gtccccccgg	ggcttggggg	ttgggtttgt	cagcttgctt	180
ttgctgtgct	gagggcttct	ccagactgaa	tcagcaggtc	ctcagctcat	ctctgctcct	240
tctctctagg	accaactgcc	cctgtaagta	cagttttttg	gataacctca	agaagttgac	300
tcctcgacgc	gatgttccca	cttaccocaa	ggtaagatga	gattccggcc	cagaagaagc	360
tcagctgtg	tccccagccc	cacgccgagc	cc			392

&lt;210&gt; 130

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

ccgggacgat	gcctgcctct	actccccagc	ctcagctccc	gaggtcatca	cagtaggggc	60
caccaatgcc	caggaccagc	cggtgacct	ggggactttg	gggaccaact	ttggccgctg	120
tgtggacctc	tttggcccag	gggaggacat	cattggagcc	tccagcgact	gcagcacctg	180
ctttgtgtca	cagagtggga	catcacaggc	tgctgcccac	gtggctggca	ttgcagccat	240
gatgctgtct	gccgagccgg	agctcaccct	ggccgagttg	aggcagagac	tgatccactt	300
ctctgccaaa	gatgtcatca	atgaggcctg	gttccctgag	gaccagcggg	tactgacct	359

&lt;210&gt; 131

&lt;211&gt; 389

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

gtagaaatc	aagttttttg	agcaggtgga	tcaattctat	gatgacaact	ttcccatgga	60
aattcggcat	ctgttgcccc	aatggattga	aaatcaagac	tggtaggatc	aaacatat	120
tccctagaag	ttgatgcaca	aatgtctgat	gctctatcca	tgtgaattta	ttttatggtc	180
cactttttac	tcagtagatg	cattcttttc	aggtaaagaa	ctttctcaag	gatttgaaag	240
ccttcccaaa	gaaggggaat	aattgtcctt	tctggttcca	ttcattgtaa	atgaaaagtt	300
aatggttcca	gtgcttcttt	tctctgtaaa	caaaaaccca	aataattttt	catgtattaa	360
aaaaagaagc	aatcaattg	attgtcagt				389

&lt;210&gt; 132

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

ggaggcagga	gatgcggatg	aagatgaggc	tgatgcta	agctctgact	gtgaaccaga	60
ggggcccgtg	gaagcggaag	agcctcctca	ggaggatagt	agcagtcagt	cagactctgt	120
ggaggaccgg	agtgaggatg	aggaagatga	acattcagag	gaggaagaaa	caagtgggaag	180
ttcagcatca	gaggaatctg	agtctgaaga	gtctgaggat	gccaatcac	agagccaagc	240
agatgaagag	gaggaagatg	atgattttgg	ggtggagtac	ttgcttgcca	gggatgaaga	300
gcagagttag	gcagatgcag	gcagtggggc	tcctactcca	ggggccacta	ctctagggtcc	360
aaagaaagaa	attactgaca	ttgctgcagc	agctgaaagt	ctccagccca	agggttacac	420
gctggccacg	accaggttaa	agacgcccac	tccctgctt	ctgcg		465

&lt;210&gt; 133

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

```

<400> 133
ctaaaaaac taaggagtt actgcttgaa gacaaccagt taccccaaat accctctggt    60
ttgccagagt ctttgacaga acttagtcta attcaaacca atatatacaa cataactaaa    120
gagggcattt caagacttat aaacttgaaa aatctctatt tggcctggaa ctgctatttt    180
aacaaagttt gcgagaaaac taacatagaa gatggagtat ttgaaacgct gacaaatttg    240
gagttgctat cactatcttt caattctctt tcacacgtgc caccctaaact gccaaagctcc    300
ctacgcaaac tttttctgag caacaccag atcaaataca ttagtgaaga agat          354

```

```

<210> 134
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(326)
<223> n = a,t,c or g

```

```

<400> 134
cccacgcgtc cggngacagg cctggccggc ctctgcagag acgtccaacc tcgtgcgcac    60
gcgagccag gccctgggccc agtcggcgcc ctgcgtcacc gccagcctga aggagctgag    120
tctccccaga agaggaagtt tccctgtgtg tccaaatgct gggagaacat cacccttgg    180
atgaattgcc accacattaa ataaaatata tccaaagctc nnnnnnnnnn nnnngggggg    240
gccgttttaa aggacccttg gggggggccaa ggtttacgcy ggctggcaag gtaatagttt    300
tttcttata gggagccgaa ttaaaa          326

```

```

<210> 135
<211> 210
<212> DNA
<213> Homo sapiens

```

```

<400> 135
cttctgtgtg tctgtcttcc tgtgggtgcc tgcccgctct tttctcttct aacagccct    60
ttgaaccagc tgatgcgtg tcttcggaaa taccaatccc ggactccag tccctccta    120
cattctgtcc ccagtgaat agtgtttgat tttgagcctg gccagtggt cagaggtagt    180
tgggctcttc tttcttggtc gacgcggccg          210

```

```

<210> 136
<211> 310
<212> DNA
<213> Homo sapiens

```

&lt;400&gt; 136

tttttccaat	acacatatataa	accatcattc	actaaaatgt	actatatatt	caatattttg	60
tgtatactca	ctgcttttcc	taacgtgaaa	aattttaccaa	aatgctaatt	gtgacttata	120
aggtatttaa	cagactcccg	acaaaaagca	gaatgatcag	cgaaatcgga	aaagaaaagc	180
tgaaccatat	gaaactagcc	aaggtagtaa	taatttcgta	tcaacaaaag	tactcaattc	240
taatgtactt	agatagaatt	ttctaactca	tactaaataa	ttagtttgta	cacagggtatt	300
cctgataaag						310

&lt;210&gt; 137

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

cttaaagtga	aattttaaaaa	gtaataataa	tttttaaaaa	tgtttaaagg	cttactttgg	60
agagacagtt	ttacatagct	taatatTTTA	tcattaaagg	catgggtggag	ctggttcctg	120
cttccgatac	cctcaggaaa	atccaagtgg	aatatgggtgt	gacaggatcc	tttaaagata	180
aaccacttgc	agagtggcta	aggaaataca	atccctctga	agaagaatat	gaaaaggcctt	240
cagagaactt	tatctattcc	tgtgctggat	gctgtgtagc	cacctatgtt	ttaggcattct	300
gtgatcgaca	caatgacaat	ataatgcttc	gaagcacggg	acacatgttt	cacattgact	360
ttggaaagtt	tttgggacat	gcacagatgt	ttggcagctt	caaaagggat	cgggctcctt	420
ttgtgctgac	ctctgatatg	gcatatgtca	ttaatggggg	tgaaaagccc	accattcggtt	480
ttcagttggt	tgtggacctc	tg				502

&lt;210&gt; 138

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

ctcctagtcc	cctccctagc	ctgtcccttc	ctcctcccg	tgctcctggt	ggccaggaga	60
gcccttcacc	ccacacagct	gaggtggaga	gtgaggcctc	accacctcct	gctcggcccc	120
tcccagggga	agccaggctg	gcgcccatct	ctgaagagg	aaagccgcag	cttggtgggc	180
gtttcccaag	tgacttcac	caaggaaacc	gctgagcctc	ttcccttgca	gccaacatcc	240
cccactctct	ctggtttctc	aaaaccttca	acccctcagc	tcacttcaga	gagctcagat	300
acagaggaca	gtgctggagg	cgggcccagag	accagggaag	ctctggctga	gagcgaccgt	360
gcagctgagg	gtctgggggc	tggagttag	gaggaaaggag	atgatgggaa	ggaaccccaa	420
gttgggggca	gcccccaacc	cctgagccat	cccagcccag	tgtggatgaa	ctactcctac	480
agcagcctgt	gtttgagcag	cgaggagtca	gaaagcagtg	gggaagatga	ggagttctgg	540
gctgagctgc	agagtcttcg	gcagaagcac	ttgtcagagg	tggaaacact	acagacacta	600
cagaaaaaag	aaattgaaga	tttgtacagc	cggctgggga	agcagcccc	accgggtatt	660
gtggccccag	ctgctatgct	gtccagccgc	cagcgccgc	tctccaagg	cagcttcccc	720
acctcccgc	gcaacagcct	acagcgctct	gagccccag	gccctggtga	gactgcagtc	780

accagcttc	catcttttcc	ctgagacccc	tttctgtoga	ctgtttttct	ccaggccctg	840
ggggtctgcc	ccgggggaat	agacccccc	tccccaccto	ccctttccto	acttagtgct	900
ctccttcccc	catcctggct	ccaggcatca	tgogaaggaa	ctctctgagt	ggcagcagca	960
ccg						963

<210> 139  
 <211> 376  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(376)  
 <223> n = a,t,c or g

<400> 139						
cgccgctttg	tttctcaaga	gactgggaat	ctgtatat	ccaaagtaga	aaaatcagat	60
gttgggaatt	atacctgtgt	ggttaccaat	accgtgacaa	accacaaggt	cctggggcca	120
cctacaccac	taatattgag	aatgatgga	gtgatgggtg	aatatgagcc	caaaatagaa	180
gtgcagttcc	cagaaacagt	tccgactgca	aaaggagcaa	cggatgaagct	ggaatgcttt	240
gctttaggaa	atccagtacc	aactattatc	tggcgaagag	ctgatggaaa	gccaatagca	300
aggaaagcca	gaagacacaa	gtcaagagtg	gggaaanntc	ttgagaaatc	ccttaatttt	360
tcagcaggga	ggatgc					376

<210> 140  
 <211> 968  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(968)  
 <223> n = a,t,c or g

<400> 140						
gcaaggggca	gttggatgaac	ttgctgcctc	cagagaat	ttcctgggtg	ggaggcagcc	60
agggacccag	gatgctccgg	acctgttaac	tgctctgttc	ccaagctggg	ccccgctcca	120
ggggctggca	gtccctgagc	tttgatggcg	gggccttcca	ccttaagggc	acaggagagc	180
tgacacgggc	cttgctgggt	ctccggctgt	gtgctgggcc	cccactcgtc	actcacgggc	240
tggtgctcca	ggcctgggtc	cggcgactcc	tgggctcccg	gctctcaggc	gcatttctcc	300
gagcatccgt	ctatggggcag	tttgtggctg	gtgagacagc	agaggaggtg	aagggtgctg	360
tgacgcagct	gcggaccctc	agcctccgac	cactgctggc	agtggccact	gaggaggagc	420
cggactctgc	tgccaagagt	ggtgaggcgt	ggtatgaggg	gaacctcggg	gctatgctgc	480
ggtgtgtgga	cctgtcacgg	ggcctcctgg	agccccccag	cctggctgag	gccagcctca	540
tgacagctgaa	ggtgacggcg	ctgaccagta	ctcggctctg	taaggagcta	gcctcgtggg	600
tcagaaggcc	aggagcctcc	ttggagctga	gccccgagag	gctggctgaa	gctatggact	660
ctgggcagaa	cctccaggtc	tcctgcctca	atgctgagca	gaaccagcac	ctccgggcct	720
ccctcagccg	cctgcatcgg	gtggcacagt	atgcccgggc	ccagcacgtg	cggctcctgg	780

tggatgcgga	gtacacctca	ctgaaccctg	cgctctcgct	gctggtgget	gccctggctg	840
tgcgctggaa	cagcccgggt	gaaggcgggc	cctgggtgtg	gaacacctac	caggcctgtc	900
taaaggacac	attctagcgg	ctggggaggg	atgcanaggc	tgcgcacagg	gccggcctgg	960
ccttcggg						968

<210> 141  
 <211> 306  
 <212> DNA  
 <213> Homo sapiens

<400> 141						
agacggctga	aaaggagggg	gtattgaggg	cggttcagag	ggcgaggaga	ggggcgtaga	60
gaacctgtgg	agaagaagtt	cactggaggg	gcattaggcc	tcgcactatg	tatccagatc	120
atcagtaggg	gaagagaaaa	gatgggcaat	atgtatagtc	agacgagaag	tgggatcaaa	180
cagagggtc	atggagaagt	aggctaccca	ccacataacc	ccatcatagg	attgcaggag	240
atacagctat	agataagaat	atccaccagt	cggtgagtga	gcagatcaag	aagaactttg	300
ccaaga						306

<210> 142  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

<400> 142						
ccacactcac	atttaataata	ctgttagggt	gtttactttg	aggcaatgtc	atcctcatta	60
gtatagggca	ttatatctct	gaatagcaga	atactcctcc	attcatgaag	ttcagtatta	120
tacattctta	ttattgcaca	acaaatagaa	gactttggat	ttccttatat	aagtaccttg	180
acagatgact	aaccttttt	tcctatgctt	tacaactatg	atcagtaact	gtaatttttt	240
taaaggctct	cctggacccc	cggttgaaaa	aggagatcga	ggtcccactg	gagaaagtgg	300
tccacgagga	tttcca					316

<210> 143  
 <211> 339  
 <212> DNA  
 <213> Homo sapiens

<400> 143						
gacaatacca	aatgaatgaa	cgtgactgtg	ttccaacaaa	actttattta	caaaaacagg	60
gatgggcccg	atgtagccag	aggccataat	ttgccaaccc	ctgattttaga	cgaaggaaag	120
gagcagtgtc	tcactgcttt	taaattaatt	ctgtattctc	acaaggccta	cattgaaatg	180

gaattatagc	ctcatttttt	cttagaacct	ttatatatttg	ttttattcat	atacaggggt	240
gtcaagctgg	acagactatt	aaagttcaag	tctcctttga	tttgcttagt	ctgatgttta	300
catttgtaag	tccatgtacc	aacgatttaa	tcatacacg			339

<210> 144  
 <211> 2018  
 <212> DNA  
 <213> Homo sapiens

<400> 144						
acaagttatc	tgtgaatcat	aggagaacac	atctttacaaa	actcatgcac	actgttgaac	60
aagctacttt	aaggatatcc	cagagcttcc	aaaagaccac	agagtttgat	acaaattcaa	120
cggatatagc	tctcaaagtt	ttcttttttg	attcatataa	catgaaacat	attcatcctc	180
atatgaatat	ggatggagac	tacataaata	tattttccaaa	gagaaaagct	gcatatgatt	240
caaatggcaa	tgttgagctt	gcattttttat	attataagag	tattggctct	ttgctttcat	300
catctgacaa	cttctttattg	aaacctcaaa	attatgataa	ttctgaagag	gaggaaagag	360
tcatatcttc	agtaatttca	gtctcaatga	gctcaaacc	acccacatta	tatgaacttg	420
aaaaaataac	atttacatta	agtcacatga	aggtcacaga	taggtatagg	agtctatgtg	480
cattttggaa	ttactcacct	gataccatga	atggcagctg	gtcttcagag	ggctgtgagc	540
tgacatactc	aaatgagacc	cacacctcat	gccgctgtaa	tcacctgaca	cattttgcaa	600
ttttgatgtc	ctctggctct	tccattggta	ttaaagatta	taataattctt	acaaggatca	660
ctcaactagg	aataattatt	tcactgattt	gtcttgccat	atgcattttt	accttctggg	720
tcttcagtga	aattcaaagc	accaggacaa	caattcacaa	aaatctttgc	tgtagcctat	780
ttcttgctga	acttggtttt	cttggttgga	tcaatacaaa	tactaataag	ctcttctggt	840
caatcattgc	cggactgcta	cactacttct	tttttagctgc	ttttgcatgg	atgtgcattg	900
aaggcataca	tctctatctc	attgtttgtg	gtgtcatcta	caacaagggg	tttttgacaa	960
agaattttta	tatctttggc	tatctaagcc	cagccgtggg	agttggattt	tcggcagcac	1020
taggatacag	atattatggc	acaaccaag	tatgttggct	tagcaccgaa	aacaacttta	1080
tttgaggttt	tataggacca	gcacgcctaa	tcattcttgt	taatctcttg	gcttttgagg	1140
tcatcatata	caaagttttt	cgtcacactg	caggggtgaa	accagaagtt	agttgctttg	1200
agaacataag	gtcttggtga	agaggagccc	tcgctcttct	gttccttctc	ggcaccacct	1260
ggatctttgg	ggttctccat	gttggtgcag	catcagtggt	tacagcttac	ctcttcacag	1320
tcagcaatgc	tttccagggg	atgttcattt	ttttattcct	gtgtgtttta	tctagaaaga	1380
ttcaagaaga	atattacaga	ttgttcaaaa	atgtccccctg	ttgttttgga	tgtttaagggt	1440
aaacatagag	aatgggtgat	aattacaact	gcacaaaaat	aaaaattcca	agctgtggat	1500
gaccaatgta	taaaaatgac	tcaccaaatt	atccaattat	taactactag	acaaaaagta	1560
ttttaaatca	gtttttctgt	ttatgtata	ggaactgtag	ataataagggt	aaaattatgt	1620
atcatataga	tatactatgt	ttttctatgt	gaaataggtc	ctgtccaaaa	atagtattgg	1680
ccagatatatt	gggaaaagta	aattgggttt	cctcaggagg	tgatatcccc	ttgcacccaa	1740
gggaaaagat	tttctttcta	acacgagaag	tatatgaatg	tcctgaaggg	aaacctggg	1800
ccttgatatt	tctgtgactc	gtgttgctt	tgaaactagt	cccctaccac	ctcggtaatg	1860
agctccatta	cagaaagtgg	aacataagag	aatgaagggg	cagaatatca	aacagtgaag	1920
agggaatgat	aagatgtatt	ttgaatgaac	tgttttttct	gtagactagc	tgagaaattg	1980
ttgacataaa	ataaagaatt	gaagaaacaa	aaaaaaaa			2018

<210> 145  
 <211> 429  
 <212> DNA  
 <213> Homo sapiens



<400> 145  
 ggcacgaggg aagctgcccc gtccagggttc atgttcctct tattttctct cactgtgtgag 60  
 ctggctgcag aagttgctgc agaagttgag aaatcctcag atggtcctgg tgctgcccag 120  
 gaacccacgt ggctcacaga tgtcccagct gccatggaat tcattgctgc cactgagggtg 180  
 gctgtcatag gcttcttcca ggatttagaa ataccagcag tgcccatact ccatagcatg 240  
 gtgcaaaaat tcccaggcgt gtcatttggg atcagcactg attctgagggt tctgacacac 300  
 tacaacatca ctgggaacac catctgcctc tttcgctgg tagacaatga acaactgaat 360  
 ttagaggacg aagacattga aagcattgat gccaccaaat tgagccgttt cattgagatc 420  
 aacagcctc 429

<210> 146  
 <211> 717  
 <212> DNA  
 <213> Homo sapiens

<400> 146  
 gatgaaactt ccggtctcat tgtccgggaa gtgagcattg agatttcgcg ccagcaagtg 60  
 gaagaactct ttggacctga agattactgg tgccagtgtg tggcctggag ctacgagggt 120  
 accacaaaga gccggaaggc gtatgtgcgc attgcatagg aactcatgac ctgacatcca 180  
 ttagcagagt catcagagtc atctggctgc tgtgttgaga atggaccatg ctgggcaagg 240  
 ggagaagcag gaagaccagt gatgagactg cagctatgag agatgttaag ctactgtaga 300  
 ttggaagcag tggagggtgg gaggccagga tttcagatat atttaaaagt agagataaca 360  
 gcttttgttg agaccttgga tgtgtgatgt gagagaaaga agagaaagga tgattttgaa 420  
 agggcctaag cctttatcca aggatttctt tcaaagtgtc ttagtgaagc cattcctgcc 480  
 tcacagaggg agggaggctg gcattccttt ctcaatactt tcagagcagt ttgtccatac 540  
 ccctaataata gtgcttgtct catttcgaat tatattcact cgtaaaattt gtgtttcatg 600  
 ccagtgaagt ccatgagatc aagaattcta ttgtacttaa ttttatatct ctctgtctta 660  
 gcacaatacc tagagtatca cagatgttta acaattttct tgaattaaaa ctgttat 717

<210> 147  
 <211> 367  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 ggcacgagat cgattcatgt aaagctggac gtgggcaagc tgcacacca gcctaagtta 60  
 gcgggccagc tcaggatggg ggacgacggc tctgggaagg tggagggcct acctgggatt 120  
 tgaccagagt ccgctgggct ccaggctctg ccacccacag gaagaagaaa ctacactgac 180  
 agatgtgaga cagtgtttcc ccttcagtct ttgaacaggc tttgtgtttt ctaaattgaca 240  
 ctggataaaa ggggaattcat tcaagagctc caaggcttcc ctttcggccc ggcttctgtt 300  
 gccctggcct gagcagcgag cagctgggag gggactgaac tgcccctaac cagggttgtg 360  
 gctggcg 367

<210> 148  
 <211> 791  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1) ... (791)  
 <223> n = a,t,c or g

<400> 148  
 cgagaccgga ccctgggctg ggtgcatcga ggtagatgca aagatgctgg ccagagcaag 60  
 tgtcgcttgg agcgggctca agccctggag caagccaaga agcctcagga agctgtgttt 120  
 gtcccagagt gtggcgagga tggctccttt acccaggtgc agtgccatac ttacactggg 180  
 tactgctggt gtgtcaccac ggatgggaag cccatcagtg gctcttctgt gcagaataaa 240  
 actcctgtat gttcagggtc agtcaccgac aagcccttga gccagggtaa ctcaggaagg 300  
 aaagatgacg ggtctaagcc gacaccacg atggagaccc agccggtgtt cgatggagat 360  
 gaaatcacag ccccaactct atggattaaa cacttgggtga tcaaggactc caaactgaac 420  
 aacaccaaca taagaaattc agagaaagtc tattogtgtg accaggagag gcagagtgcc 480  
 ctggaagagg cccagcagaa tccccgtgag ggtattgtca tccctgaatg tgcccctggg 540  
 ggactctata agccagtgc atgccaccag tccactggct actgctggtg tgtgctggtg 600  
 gacacagggc gcccgctgcc tgggacctcc acacgctacg tgatgcccag ttgtgagagc 660  
 gacgccaggg ccaagactac agaggcggat gaccocctca aggacaggga gctaccaggc 720  
 tgtccagaag ggaagaaaat ggagtttatc accagcctac tggatgctct caccactgac 780  
 atggntcagg g 791

<210> 149  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
 ggcacgagca aactcggggc tcagcttggg gacgggagtt gatagtcagg tgcttggaaac 60  
 ataattggaga ccgtccatat tggttgaatg agtggatgaa tgaattaatg aatttctttt 120  
 ctcttaagtc ctgcagctga ttaagtcaca gaaatttctg aataagttgg tgatcttggg 180  
 ggaaacggag aaggagaaga tcctgcggaa ggaatatgtt tttgctgact ccaaagtaag 240  
 tgacagcaaa cttctaaagt gggctgtgag gtaggaggag gacacaagcg ttttgaggct 300  
 cgctgtgtgc caggagtggt atcattagct cactc 335

<210> 150  
 <211> 1293  
 <212> DNA  
 <213> Homo sapiens

<400> 150  
 cgacgcctgt cctcttaga cttgcagctc ggtcctcttg gcagagaccc cccgcaggag 60  
 tgacagacct tctcccaac agacagcggg gaggagccgg ggacgtctc cctggcgtg 120  
 cagttccagc ggccgcagaa ccagcgccgc ttctccatgg aggacgtcag caagaggctc 180  
 tctctgccca tggatatccg cctgccccag gaattcctac agaagctaca gatggagagc 240  
 ccagatctgc ccaagccgct cagccgcatg tcccgccggg cctccctgtc agacattggc 300  
 tttgggaaac tggaaacata cgtgaaactg gacaaactgg gagagggcac ctatgccaca 360  
 gtcttcaaag ggccgacgaa actgacggag aaccttgttg cctgaaaga gatccggctg 420  
 gagcacgagg agggagcgcc ctgcaactgc atccgagagg tgtctctgct gaagaacctg 480  
 aagcacgcga atattgtgac cctgcatgac ctcattccaca cagatcggtc cctcaccctg 540  
 gtgtttgagt acctggacag tgacctgaag cagtatctgg accactgtgg gaacctcatg 600  
 agcatgcaca acgtcaagggt gaggcctcgg gggcagggtc ccccatctt ggcagccacc 660  
 tgccagaag ccagtggtg ggaccactc tcaccaccag ggatccggct gctgagggtg 720  
 ctcaaacctt cccagtagg aaagaggag agggcaatgc catcaacgag tccaggaact 780  
 gggttgagcg ctttacccca agaacagaca cacactgtct gccactgtct agctgttggt 840  
 ataaaacca ctctcaactc tgaacatcag tttcccagtc tgtcaaatgg gagtgtgagc 900  
 tacctgccaa aatgcaggga ggcttctggg gaagctcggg gttatgaatg acctctcctg 960  
 gtgtttgtta aagaatcaag actgggcatg gtggccacg cctgtaatcc cagcactggg 1020  
 aggccaaaggc aggaagatgg cttgagccca ggagtttgag accagcctgg gcaacatggc 1080  
 aagacctcat ctctactaaa aattgaaaaa ttagccgggc acagtagcgt gcaccatag 1140  
 tcccagctgc ttgagaggct gaggcaggag ggcacttga gcccgaggag ttgaggctgc 1200  
 agtgagccat gatcacacca ctgcaactca gcatgggtga cagagtaaaa cctgacatg 1260  
 tattgcgggc gctctagagg ataacaagca tac 1293

<210> 151  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<400> 151  
 ggacagagcg gcacgagcct tctcctactg cattagcatt tggggaccac cctattgtac 60  
 aaccaaagca attatccttt aaaattatc aggtaaatga taattaaaat gtttttttct 120  
 atggcttcta agaaccatt gactaactta ctaacaacta agatgtctgt ttgttttata 180  
 tgtagtcata aagcagaatt acacatcaag aaagataact tactaaacaa aaacaacaga 240  
 atttgtagga aggagtgaga aactgaaaca cacaatttac tatcagcttt ttaacaaccc 300  
 gttaacatgt cagttctgtt tactgattct ttctgaactt aatttccag 349

<210> 152  
 <211> 324  
 <212> DNA  
 <213> Homo sapiens

<400> 152  
 ggacagagga ccttccttgc tttcagaatt tcaccaggg tctgacaggc ctcaagaaag 60  
 gagaactagt tatgaaccga ttcattccagg cccatcccca gtggatcatg attcactgga 120  
 atcgaagcga ccacgtcttg aacaggcttc tgattctcat tatcagggtc acatcactgg 180  
 cgaatcccta ccaggacgtg tacactagca gtcctcact gtggaatctg atgggcaatg 240

ccatggtgat taccactat atccgtctta ccccatatgt tcaaagtaaa ctcggttccc 300  
tagggaaacct gatgcatgt tacc 324

<210> 153  
<211> 377  
<212> DNA  
<213> Homo sapiens

<400> 153  
ggcacgagaa aagaagaatt cagtgcagaa gaaaattttc tcattttgac ggaaatggca 60  
accaatcatg tacaggttct tgtagaattc aaaaaaagc taccaggtat tttttaaata 120  
atcacagtta atatttattg agagtttaaa tatgtgccca cagattagat tacctatttt 180  
acatacgggtg ttttaatttt caaaacattc ctgtgagatc agctctattt tcaactattac 240  
tttgccaagt attttcacat gtacttattt cactgctatt ctctacaata gtcttgtgac 300  
attgagaaag gcaggctctgt tctttgtaaa atgaaaatca tttaatatct gatttaaagt 360  
aactgtcgaa ctactat 377

<210> 154  
<211> 1224  
<212> DNA  
<213> Homo sapiens

<400> 154  
ggtttttttt ttttttcttt tgggaaaggc attggccact ttggacttta ttagcaacag 60  
taatgtcccc tgacatacgc acaagcttgt agctccacgg ccagggtcttc ccccaacctc 120  
acaatggccc cgtgatgcag gcaggcaggc gagtgggggt cccccctct tatccacagg 180  
gccaccgaaa ggcccacgag acggccttgc ccgaggtcac ccagcggagt ggcttgcctg 240  
gagccctggg aataacagtc ccacacaagg ctctctccct ccgcagctgg acctgtacgc 300  
gggggctctg tttgtgcaca tctgcctggg ctggaacttc tacctctcca ccacctcac 360  
gctcggcatc acagccctgt acaccatcgc aggtatgggt cctgcagcag ggagggtccac 420  
ccaggggacg tgtaaagggg tcagaaggcc acctccccct acaggcccga gggagcagcc 480  
caggaagtgg ccccagcagg agccccagaa gtctcctccc gtgtccctcc tccctggggc 540  
cagggccccc tccagcaacc ttgcttcac tggcaggggg cctggctgct gtaatctaca 600  
cggacgcctc gcagacgctc atcatggtgg tgggggctgt catcctgaca atcaaagggt 660  
aggacagagt ctgtggccat ggcggggctg tcccacagc gaggcctttg gactctggca 720  
ctgccggca ctgtgcagga ttcatgccgt tggggttctg ggtagcatcg ctgggagtg 780  
gtgggttcag gaggttgagc cactaggcag tcagccccc tgetggcccc tcagggactg 840  
ccctggctgg tagaggctac ccacctgct gccccgctgt taccagctct ggccctggca 900  
aggagctgac tcaggaactc agggccagcc acaccgcgat tggctcagcg cttgatgggt 960  
agggtgggct gtaggcgggt gtgaaggcac acaaccagga ggccataaaa ctgcctgggc 1020  
agctcctcca attgtttaa agcatgtaca aaatgccaa aggtgatgct acctcctgca 1080  
ggacaaaggg cagggaggaa agaagagagc tgggagagat tggcgatact agtctggaac 1140  
agataggaaa ctcacagggc tgcccggaga gagcgtgagc tcaccgtccc tgggaagtatg 1200  
taagcagagc caggagctcg tgcc 1224

<210> 155  
 <211> 345  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(345)  
 <223> n = a,t,c or g

<400> 155  
 ggcacgagcg gcacgagatc tgaagaggta tattgcttac agaaagagcg ggagatggta 60  
 aatcacagtc ttcaagagac ttctgagcaa aacgttattc tacagcatac tcttcagcaa 120  
 cagcagcaaa tgttacaaca agagacaatt agaaatggag agctagaaga tactcaaact 180  
 aaacttgaaa aacagggtgtc aaaactggaa caagaacttc aaaaacaaag ggaaagttca 240  
 gctgaaaagt tgagaaaaat ggaggagaaa tgtgaatcag ctgcacatga agcagatttg 300  
 aaaaggcaaa aagtgattga gcttactggc actgccaggc aagtn 345

<210> 156  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 ggcacgagct tctacttgta caggaaaggt tacttgagtt tgtccaaagt ggtgccgttt 60  
 tctcactatg ctgggacatt gctgctactt ctggcacgtg tggcctgcct cctaggcatt 120  
 gtccgctggg cctaccccca cttccgcgag tttctcgcca tctcctctcc gatccatctc 180  
 tacctgacgt cataactcta tatgcatggt atgcgggtcca tcttagtctt ctaaaaaggc 240  
 catttttagct tacctgccat caagctatac atgtggaaat atacactgta ttattttccc 300  
 tttccagggtg attacttacc tcatctgttc ttatatctgc 340

<210> 157  
 <211> 478  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(478)  
 <223> n = a,t,c or g

<400> 157  
 gagactccaa gccccagttt cacctcagag gcagagatga ggggtccccc ggtcctgctc 60

ctccaggccg	cccgaatgga	gtgtcctgtt	cgcagggga	tcccggccgg	gtccagtcct	120
gagcctgcac	ctgaccccc	ggggcctcat	ttcctccggc	aggagcgag	cttcgagtgc	180
cgcattgtgc	gcaaggcctt	caagcgctcg	tccacgctgt	ccaccacct	gctcatccac	240
tcagacacgc	ggccctaccc	ctgccagttc	tgcggcaagc	gtttccacca	gaagtccgac	300
atgaagaagc	acacctacat	ccacacaggt	gagaagccgc	acaagtgcc	ggtgtgcgga	360
aaggccttca	gccagagctc	caacctcatc	acccacagac	tcagagagaa	cccaccatgg	420
tgctgtctcc	tgccgacaag	accaacgtca	aggccgcctg	gngtaagggt	cgcgcgca	478

<210> 158  
 <211> 332  
 <212> DNA  
 <213> Homo sapiens

<400> 158	
ggcagcagca	gctcaccaac aacacagcca ctgccccctc tgccacgccc gtgtttgggc 60
aagtggcagc	cagcaccgca ccaagtctgt ttgggcagca gactggtatc acagccagca 120
cagcagttgc	cactccacag gtaatcagct caagggtcat taatctagat ttttagtata 180
tagtattatt	gaatatatat aatgttttat atattagact ttatacttga gacataggaa 240
ataatttatg	tataactggt aattaaattt tatattttgt agattagaaa attctattaa 300
tttattaatg	aattatatct aattatgtga ca 332

<210> 159  
 <211> 868  
 <212> DNA  
 <213> Homo sapiens

<400> 159	
cccacgcgtc	cggaataaag agagaactct gttactattg tttttacatc accaaataat 60
tatttaatat	cgtttagctaa gagaagaatt ggctatgaac tgtactttaa caactgacac 120
aactgcatac	aagttataaa gttaataaat ctttatcatc ttggaaaata aatctcttct 180
tgctaagtat	cagtttttaa aaattgcccc atgtattaga tatgtatttt tttacaaaa 240
atgttctgtg	tattaattat tttgaaataa attttaagtt cacaaaaagc cattacaaga 300
agtggaaata	gcagcaatta cacatggtgc tcttcaggga ttagcctact tacattctca 360
tactatgatt	catagagata tcaaagcagg aaatatcctt ctgacagAAC caggccaggt 420
gaaacttgct	gactttggct ctgcttccat ggcacacact gccaatcctt ttgtgggaac 480
gccgtattgg	atggccccag aagtaatttt agccatggat gaaggacaat atgatggcaa 540
agtagatgtg	tggtctcttg gaataacatg tattgaacta gcggaaagga agcctccttt 600
atttaatatg	aatgcaatga gtgccttata tcacatagcc caaaatgaat ccctacact 660
acagtcta	aatggtgag tattgttaat atatatattg ctacgtgttg aataaatgaa 720
atgctttttc	ataatctgtt atcaaagtga ttttaatttca gttaggtaaa atgtatcacc 780
ttataagata	ttaaaataga tgtattttac ccttttaaat atattttatc tttatcatgt 840
ttccatttca	tggcatacgt ataactgg 868

<210> 160

<211> 1404  
 <212> DNA  
 <213> Homo sapiens

<400> 160  
 gcgccacgcg cggcctggcg ggcggcgcca ctctaaccag cgcaaaatgt ccctggaaca 60  
 ggaggaggaa acgcaacctg ggcggctcct aggacgcaga gacgccgtcc ccgccttcat 120  
 tgagcccaac gtgcgttctt ggatcacaga gcgccaatcc tttattcgac gatttcttca 180  
 atggacagaa ttattagatc ctacaaatgt gttcatttca gttgaaagta tagaaaactc 240  
 gaggcaacta ttgtgcacaa atgaagatgt ttccagccct gcctcggcgg accaaaggat 300  
 acaggaagct tgggaagcga gtcttgcaac agtgcattccc gacagcagca acctgatccc 360  
 caagcttttt cgacctgcag cgttcctgcc tttcatggcg cccacgggat ttttgtcaat 420  
 gacgccactg aaagggatca agtccgtgat tttacctcag gttttcctct gtgcctacat 480  
 ggcagcgttc aacagcatca atggaaacag aagttacact tgtaagccac tagaaagatc 540  
 attactaatg gcgggagcgg ttgcttcttc aactttctta ggagtaatcc ctcatgttct 600  
 ccagatgaag tatggcctga ctggcccttg gattaaaaga ctcttacctg tgatcttctt 660  
 cgtgcaagcc agtggaatga atgtctacat gtcccgaggt cttgaatcca ttaaggggat 720  
 tgcggtcatt gacaaggaag gcaatgtcct gggtcattcc agaattgctg ggacaaaggc 780  
 tgtagagaaa acgctagcat ccagaatagt gctgtttggg acctcagctc tgattcctga 840  
 agtcttcacc tactttttta aaaggaccca gtatttcagg aaaaaccagc ggtcattgtg 900  
 gattttgaaa ctgtcttgta ctgtcctggc aatgggactg atggtgccat tttcttttag 960  
 tatatttcca cagattggac agatacagta ctgtagtctt gaagagaaaa ttcagtctcc 1020  
 aacagaagaa acagaaatct tttatcacag aggggtgtag gccgtgagtt ttaggtgaat 1080  
 ttatgtggtt ccctgcttga aaaccttccc cctctcccag gttcggttta gagaactttg 1140  
 cccacaggtc ttctggggac cccagagggt tctgtgctga caaggcgact tcagattcca 1200  
 tactgagatc gttcccaggc tggcgtctct ggggttttta aggctggctg gagaagacag 1260  
 tgggaagggt gccccgtctg acaccctctg ggttgctgag ggaacgggtg gagtggggat 1320  
 cggcctgcga aaggatactg tgaaatcact aattaactaa taaacctgtc tcaagttgag 1380  
 gatttgaaag aaaaaaaaaa aaag 1404

<210> 161  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 cccacgcgtc cgggagattg gaagtcttct ataacgggac ctggggcagc gtcggcagga 60  
 ggaacatcac cacagccata gcaggcattg tgtgcaggca gctgggctgt ggggagaatg 120  
 gagttgtcag cctcgccctt ttatctaaga caggctctgg tttcatgtgg gtggatgaca 180  
 ttcagtgtcc taaaacgcat atctccatat ggcagtgcct gtctgccccca tgggagcgaa 240  
 gaatctccag cccagcagaa gagacctgga tcacatgtga agatagaata agagtgcgtg 300  
 gaggagacac cgagtgtctt gggagagtgg agatctggca cgcaggctcc tggggcacag 360  
 tgtgtgatga ctctggggac ctggccgagg cggaagtggg gtgtcagcag ctgggctgtg 420  
 gctctgctct ggctgccctg agggacgctt cgtttggcca gggaaactgga accatctggg 480  
 tggatgacat gcggtgcaaa ggaaatgagt catttctatg ggactgtcac gccaaacctt 540  
 ggggacagag tgactgtgga ca 562

<210> 162

<211> 1812  
 <212> DNA  
 <213> Homo sapiens

<400> 162

gccttgcttg	gaggcaaagc	gtcctccact	ctgtcctcag	gactcagctg	tgtggccttg	60
gatttccttt	tgcgggactt	gcgccctttg	ggtgccaacg	gtccaggatc	cccctggaac	120
cagatgggtac	ggccatgccg	gtcctgcagg	gagctcatgc	ctggcatgcc	atagcagcgc	180
agccaggctc	gaaaggcagc	aaagtcctcc	tcccgcctct	ctgacccgta	gccctgccc	240
cccaactgga	ccacttcctt	gggcactgag	tgacatagct	ccagcaggtc	tggattctgc	300
agcttggtec	ttatcttctg	gctcagggtc	agctccgggc	tcggcctgtg	ctgctgcagg	360
gcctccagga	ccgagcgggc	cttctcaaag	ggggggatct	tcagccggta	caggatctct	420
gcccgcagat	agttgccaat	gccattgaag	aacctctggt	ccaggagggc	ctcgcagatg	480
ggccggctca	aggccttatc	cgctagggtt	cgtagcacat	tctccctgaa	ctgctggtac	540
tcttgcaaga	cacaggggcc	gcggcccggc	tgccactttc	ccccaaagtc	ccagcggccg	600
aaaccggcgga	tgtccacgaa	acataggcg	agccgggggc	caggcggggc	cgtgtaaaag	660
cgcaaggtggg	catggcgtgg	cagctcctcg	cggggcacca	gctgaaaaga	gccggacatg	720
ccgaagcgga	agaccagggc	cagtggctcc	tgttggggct	gggcccagg	cagagggtc	780
agtatcaggc	gcagctcctt	gcgcgggct	gaagctgaga	tgcggtaggc	actgctctca	840
aagggcacct	cagggttgcg	gctgacagag	gacttctcca	cgcagccgcc	gaacaccagc	900
gccctgcagg	cctcattcac	aaactggctg	gccaggtgca	gctcggggcc	ctcaggcatc	960
ctgagggagg	gtggcagagt	cctggctggg	aggtggcgga	agaacctgac	ttcccaactgc	1020
ctggcgccgg	cgagatgcgg	gggcaggtct	gaggccccgg	gtcgccgctg	tctctgcggg	1080
tgggggaagt	caccagcta	gcgtgggaca	gggtcggcac	cccagcagg	aaacagcagc	1140
gacgagccag	agcggagtgc	cctgcagctg	cgcgaggac	gtgcacaggt	gcgcggtacg	1200
cacaggccct	agggaccggg	tggggatctt	aagcaccaac	gaacagtcag	acctaaactca	1260
taaacaaaca	tcatcacggc	ctgccctgtc	agaagcgag	ccaagcaaca	acaacaacaa	1320
aaaaaggcga	ggaggtagac	ccacttgaga	tggttctgtt	goggagagtc	tctgaaatca	1380
gaaagcgcca	gtccgcaaaa	acgaggaaac	ccgacgtgtc	cggcggaagg	aaccgccagt	1440
acaaaggccc	tgaggcgaga	aagagattgg	tcactgaaag	aactcaaaga	agtcctgtgt	1500
ggctggagta	tagctgcggg	ttagtgtctg	caggtgaaga	cagagaagca	aaccagggtc	1560
aggctcgggt	gggcctcggg	agggcctccg	tgtggagtct	gcacttcatt	ctaagtgtat	1620
acctaaacca	tcgccacgat	ttccctcct	tcacactacc	ctgctacgtc	tccttattag	1680
gcgtaataaa	attatgtggc	tttctaagaa	attggttttt	agagatgcat	gttaaagtat	1740
tgggtatgaa	atgtcatgat	ttgtctaatt	tactttaaaa	tacttctgcc	ataataaatg	1800
aatagaatta	ac					1812

<210> 163  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<400> 163

agctgacgtg	gtctgcctgt	tattggagag	atatattaag	aatccagttg	tggattgcag	60
ctgatattct	tttgcgaaatg	cttgaaaaag	cacttcttta	tagtgaacac	cagaacatca	120
gcaacactgg	actgtcatcc	caaggcttat	tgatatttgc	ggagttgatt	cctgccatta	180
agaggacgtt	ggctcgccct	ctcgtgatca	ttgcgagcct	ggactatggc	attgagaaac	240
ctcatttagg	aacaggcatg	caccgtgtga	tcggactgat	gcttctatac	ttaatctttg	300
caaagtctga	aagcgtgatt	agagtcattg	ggg			333



<210> 164  
 <211> 134  
 <212> DNA  
 <213> Homo sapiens

<400> 164  
 tttttttttt gagatggagt ctgctctgc tgcccaggct ggagtgcagt ggtgcaatct 60  
 tggtcactg caagctctgc ctcccagggt caccgccattc tcctgcctca gcctcccgag 120  
 tagctgggac taca 134

<210> 165  
 <211> 839  
 <212> DNA  
 <213> Homo sapiens

<400> 165  
 cctgagcccg gcgagcagga gaggaggtct tccgggcccgc ggctccgag cgcgcgggat 60  
 ttgcagaact taatatgaat gtgaagaact tgcaaaagaaa cttgaaaaca gccaaaggga 120  
 tggcatatca agaaataaat tggccttggc agaattgtat gaagatgaag tgaagtgcaa 180  
 atcttccaag tctaataagac ctaaagccac agtcttcaag agcccacgga caccacctca 240  
 acggttttac tcaagtgaac atgaatacag tggattaaat atagttcgac cttcaactgg 300  
 gaaaattgtg aatgaacttt tcaaagaggc aagggaacat ggggctgtcc ctctgaatga 360  
 agccacaaga gcttcagggtg atgataaatc taagtcattt acagggtggag gatacagatt 420  
 gggtagttct ttttgtaagc ggtctgaata tatctatgga gaaaatcagc tgcaagatgt 480  
 tcagattttg cttaaactgt ggagcaatgg ttccagttta gatgatggag aattgagacc 540  
 ttacaatgaa ccaacaaatg ctcaatttct ggagtctgtt aagagagggg tgactctcat 600  
 tgcattgatg cctgaaattc agcaacttat gttagaaatc ttttaattgtg gcattactgc 660  
 tggcagaaga tttcaaaagg ttagtttgaa gttataatatt gtgaaagtaa actcagatat 720  
 tcagtgtctc caccatcca aagaacattg taacttacca gctcttcttg ctaaaggatg 780  
 aggaatcaag tgattttgct atgataataa aagcttttct gtgttatgat taacaaaaa 839

<210> 166  
 <211> 1256  
 <212> DNA  
 <213> Homo sapiens

<400> 166  
 ctcatcacc tgatggccct ggggcgcagc tcccgggttg acccacgcgt ccgagcggat 60  
 gttcactctc acgaccatga ttcaagctct tgcacctgtt atgggatggg acaggaagcc 120  
 actgaagatg ttttcatcag aagagatgag aggacatctt catcatcatc ataaatgtct 180  
 gacgaagatc ctgaagggtg aggggcaggt tccagatctg ccatcctgcc tgcccctgac 240  
 tgacaacacc cgcattgctgg cctctatcct catcaacatg ctctatgatg acctgcgctg 300

tgacccggag	cgcgatcact	tccgcaagat	ctgtgaggaa	tatatcacgg	gcaagtttga	360
ccccaggac	atggacaaga	acttgaatgc	catccagaca	gtgtcagga	tcctgcagg	420
ccctttgac	ctgggcaacc	agctgctggg	actgaaaggt	gtgatggaga	tgatggtggc	480
actatgtggc	tcagagcgcg	agacggacca	gctggtggcc	gtggaggccc	tcacccatgc	540
ctccacgaag	ctcagccgcg	ccaccttcat	catcaccaat	ggagtgtcac	tgctcaaaca	600
gatctacaag	accaccaaaa	atgagaagat	caagatccgc	acactgggtg	gactctgtaa	660
gctcggctct	gcaggtggca	cagactacgg	tctcaggcag	tttgcggaag	ggtcgacaga	720
aaaactggcc	aaacagtgtc	gcaagtggct	gtgcaatatg	tccatagaca	ctcggacccg	780
acgctgggca	gtggaggggc	tggcctacct	cacgctggac	gctgatgtga	aggacgactt	840
tgtccaggac	gtccctgccc	tgcaggccat	gtttgagctg	gccaagacca	gtgacaagac	900
catcctgtac	tcggtggcca	ccacctgggt	gaactgcacc	aacagctacg	atgtcaagga	960
ggtcatccca	gagcttgtcc	agctcgccaa	gttctccaag	cagcatgtgc	ccgaggaaca	1020
ccccaaaggac	aagaaggact	ttatagacat	gcgggtgaag	cggttctga	aggcgggtgt	1080
catctctgcc	ctggcttgca	tggtgaaagc	agatagtggc	atcctcactg	accagaccaa	1140
ggagctgctg	gccagggtat	tcctggcact	gtgtgacaac	ccaaaggacc	gaggcaccat	1200
tgtggctcaa	ggtggtggca	aggccctgat	tccctggct	ttggagggca	cagatg	1256

<210> 167  
 <211> 892  
 <212> DNA  
 <213> Homo sapiens

<400> 167						
atgtggacag	cgtgggtggc	ggcagcgagt	ctcggccct	ggactcacc	acttccagcc	60
caggcgctgg	cacgaggcag	ctggtgaagg	cttcgtccac	aggcactgag	tcctcagatg	120
actttgagga	gcgagaccct	gacctgggag	acgggctgga	gaatgggctg	ggcagccct	180
tcgggaagtg	gacactgtcc	agcgcggtc	agaccacca	gctgcggcga	ctgcggggcc	240
cagccaagtg	ccggaagtgc	gaagccttca	tggtcagcgg	gacggagtgt	gaggagtgt	300
ttctgacctg	ccacaagcgc	tgcttgaga	ctctcctgat	cctctgtgga	cacaggcggc	360
tcccagcccg	gacaccctt	tttggggttg	acttctgca	gctaccagg	gacttcccg	420
aggaggtacc	ctttgtggtc	acgaagtga	cggctgagat	agaacaccgt	gcctggatg	480
tgcaggcat	ttaccgggtc	agcgggtccc	gggtccgtgt	ggagcggctg	tgccaggctt	540
tcgagaatgg	ccgagcgttg	gtggagctgt	cggggaactc	gcctcatgac	gtctcgagt	600
tcctcaagcg	atttcttcag	gagctcaccg	agcccgatg	ccccttccac	ctctacgacg	660
ccttcatttc	ctggctaag	accttgcatg	cagaccctgg	ggacgacct	gggaccccca	720
gccccagccc	tgaggttatc	cgtcgctga	agaccctctt	ggtacagctg	cctgactcta	780
actacaacac	cctgcggcac	ctggtggccc	atctgttcag	ggtggctgca	cgatttatgg	840
aaaacaagat	gtctgccaac	aacctgggca	ttgtgtttgg	gccgacactg	ct	892

<210> 168  
 <211> 394  
 <212> DNA  
 <213> Homo sapiens

<400> 168						
ggactccatg	tcattctctt	gcacagcgct	gatggctgct	actgggagga	tcctctttct	60
gagcttgaca	gtgaacgtgt	gtctgattt	cttgctactg	agaccctgg	gttctatttg	120
ttctgtctcc	ttgcagatga	aacctgctg	ccaccagatg	ttccaagcta	cctctcttct	180

caggggaccc	tttctgaccg	acaagaaacc	gtggtcagga	cagaggggtg	ccctcaggcc	240
aatgggcaca	ttgagagcaa	tggttaaggcc	tcagtaaccg	tgaagcagag	ctctgctgtg	300
actgtgtctc	tggtgtctgg	aggtggcctc	caggtcttta	cagggcaggt	acctggcatt	360
agatggggca	aacttggtga	agccacgcg	tccg			394

<210> 169  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 169						
ctgtgacacc	tccgggcagc	cgggcacttg	ttgctccca	gacctgttgt	cattccctta	60
acccggcttt	ccccgtggcc	ccccgcctcc	tcccggttc	gtcctttttc	atgtgagcat	120
ctgggacact	gatctctcag	accccgctgc	tcgggctgga	gaatagatgg	ttttgtgaaa	180
aattaaacac	cgccctgaag	aggagccccg	ctgggcagcg	gcaggagcgc	agagtgtctg	240
cccaggtgct	gcagaggtgg	cgctcccccg	gcccgggacg	gtagccccgg	gcgccaacgg	300
catgacagac	tcggcgacag	ctaacgggga	cgacagggac	cccagatcgc	agctctttgt	360
gaaggctgga	atcgatggag	aaagcatcgg	caactgtcct	ttctctcagc	gcctcttcat	420
gacctctctg	ctgaaaggag	tcgtgttcaa	tgtcaccact	gtggatctga	aaagaaagcc	480
agctgacctg	cgcaacctag	cccccggaac	gcaccgcgcc	tttctggcct	tcaactggta	540
cgtgaagaca						550

<210> 170  
 <211> 422  
 <212> DNA  
 <213> Homo sapiens

<400> 170						
cttggattca	gtgatggaca	ggaagccagg	cctgaagaaa	ttggctgggt	aatggcttat	60
aatgaaacca	caggggaaaag	gggggacttt	ccgggaactt	acgtagaata	tattggaagg	120
aaaaaaatct	cgctccccc	accaaagccc	cgccacctc	ggcctcttcc	tgttgcacca	180
ggttcttcga	aaactgaagc	agatgttgaa	caacaagtgc	tctacaagta	tagaaagaag	240
ccttctcttt	ccaccgtccc	ccagacacca	cataatggaa	aaagcaagaa	ttttctgcat	300
aagcaaggcc	ttaaaaaaaaa	aaaagccagc	ctctgatggg	acttttttcc	tgccaaaaat	360
cccactggtc	cactgtcgca	atttttacaa	aaggccacga	taaaagagta	aggcccatth	420
tg						422

<210> 171  
 <211> 1042  
 <212> DNA  
 <213> Homo sapiens

```

<400> 171
cggacgcgtg gggatcatgga gctggcactg cggcgctctc ccgtcccgcg gtggttgctg      60
ctgctgccgc tgctgctggg cctgaacgca ggagctgtca ttgactggcc cacagaggag      120
ggcaaggaag tatgggatta tgtgacggtc cgcaaggatg cctacatgtt ctggtggctc      180
tattatgccca ccaactcctg caagaacttc tcagaactgc ccctggtcac gtggcttcag      240
ggcgggtccag gcggttctag cactggattt ggaaactttg aggaaattgg gcccttgac      300
agtgatctca aaccacggaa aaccacctgg ctccaggctg ccagtctcct atttgtggat      360
aatcccgctg gcaactgggt cagttatgtg aatggtagtg gtgcctatgc caaggacctg      420
gctatgggtg cttcagacat gatgggtctc ctgaagacct tcttcagttg ccacaaagaa      480
ttccagacag ttccattcta ctttttctca gagtcctatg gaggaaaaat ggcagctggc      540
attggtctag agctttataa ggccattcag cgagggacca tcaagtgcaa ctttgcgggg      600
gttgcccttg gtgattcctg gatctcccct gttgattcgg tgctctcctg gggaccttac      660
ctgtacagca tgtctcttct cgaagacaaa ggtctggcag aggtgtctaa ggttgacagag      720
caagtactga atgccgtaaa taaggggctc tacagagagg ccacagagct gtgggggaaa      780
gcagaaatga tcattgaaca ggtaaaaagg ggaaacactc agaggcgagc ctgcttggtc      840
ttttctggtg ggtacagggc ccatgggttg tggtgtcaaa cttggagtct acactgaggc      900
tccccacata tctgcaaatg attgcatgct ggataataaa tctcttgggt ctaagcagtg      960
atgtagtggc tccttacaga gtcagaaagc caccaggccg tgcaagactt gcttgtcctt     1020
cactaaatgt aaaaattcta tt                                     1042

```

```

<210> 172
<211> 890
<212> DNA
<213> Homo sapiens

```

```

<400> 172
aaagtagtag gttggtgcaa acgtagtaat aaattggttt ggccctgttt tcatagaact      60
atagagggtg gacctttgtc cccttcacaga tgccacaaaa caaactgatg tttttgattt     120
ttttttcttt ttaaattttg gttgccacta attcttataa aaatcctcac acaaggctgg      180
gctcagtggc tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacga      240
ggtcaggaga tcgagaccat cctggctaac acggtgaaac ccccgctctc actaaaaata      300
caaaaaaatt agccgggcgt ggtggcgggc gcctgtagtc ccagctactc gggaggctga      360
ggcaggagaa tggcgtgaac ccgggaggca gagcttgacg tgagccgaga tagcgccact      420
gcactccagc ctgggcgaca gagcaagact ccatctcaaa aaaaaaaaaa agtgataata      480
ctgtaatccc agcactttgg gaggcgagg caggcggatc acgaggtcag gagatcgaga      540
ccatcctggc taacacggtg aaaccccgtc tctactaaaa atacaaaaaa ttagctgggc      600
gtggtggcgg gcacctgtag tcccagctac ctgggaggct gaggcaggag aatggcgtga      660
accaggagg cgagacttgc agtgagcgga gatcatgcca ctgcacttca gcctgggcga      720
cagagcaaga ctccatctca aaaaacacac acacacacac acacacacaa      780
atagaaaaat aataatagtt ttaagcacct ctaaagtaca gatattgtgc caagcaattt      840
atgtgaattg attagattga taactctaaa aatagtttcc ctaatcaact      890

```

```

<210> 173
<211> 1922
<212> DNA
<213> Homo sapiens

```

<400> 173

tttctttctt	catccaaaat	agtagagatg	tctttccac	gatgacctgt	gatggtggag	60
atatcttttc	ctcgccaac	tctcctcca	tcggcttctt	tgatgtcatc	ttcaatagct	120
tcatcaattg	cttcatcaaa	ctcatcaaat	ctgtagctta	tacatttcct	tgttcttgtt	180
gacctccttt	caaagcaagt	ttgctttgga	tttttttgaa	tctttttctt	tttcttcttg	240
atcttcagaa	aagtctggct	ctttgtggag	gaatgatgtt	ttcaatactg	gataccaaca	300
tacaccaagc	gttcttttcc	ttcgttccgg	caacgctctt	tcttcttcta	aggcaacatc	360
ccaaatcctg	gaaactggtc	ctctaatttt	tccaacaaga	gcaagtttaa	tggtgggcaa	420
aaggtggggc	aagaacccat	cctcccatct	ggggatggat	catcagagga	ggggcgaaag	480
gcagggcagt	atggtatcca	ctatcgcaag	agtcacacag	agaattagc	tcaggatggt	540
ttggaaggcc	acattttttg	catggttcat	catcatctgc	taggatggct	tcttcacttt	600
ccttttcttc	ctcctcttct	gaagctgcag	atgatttttc	actgccagac	ccttcacttt	660
catcattgct	ggaatatctc	catctgccac	gtgtccgaga	accagtccat	cgaactttgc	720
ctttgggttt	taccttgctt	actttagaat	ttgtatcttt	ctctgatttt	ttcaaaattt	780
cctttttgtc	agttttttgc	aaagctgttg	actcttcttc	cacctcatct	tctccttccc	840
ctcttttttt	atcagctttc	tgatctctga	tctcagccac	ttttgcagtg	ggtctagata	900
ttcttgagga	tcttcttaaa	gtacgacca	catttgtttt	ctcctcttcc	ttttctgtct	960
tctcttgctt	gttttctggg	tctagaactt	tggggggaga	atcgggcttc	tttttccgac	1020
ttgatatcct	gattgttaat	ttgatgcctt	ctttctgcct	ttcagagggt	atctctgtat	1080
tttctgaggc	agtggtttct	tcttcaggaa	ccaacttata	tttgaatttg	cttttttgca	1140
tagaaccctt	tgtctcagaa	ggctcctcta	tgccagaggt	ctgggcattg	tccagattat	1200
ccatttctac	ctttgtgaac	tcagaatcct	cttttagggg	ttctaggtct	acttttttca	1260
cagactggcc	accaacagta	cttgtactct	ggcattctac	cacttctttt	tctgaggcta	1320
gtttctcaca	gtggtcaatg	atattagatg	gtggagaagt	ttcagctgcc	tcaggagagc	1380
caggcttttc	tgactctaga	gtactctttg	gaacttcttc	tggtattgga	ctcaatcttt	1440
gtgcgtcctt	atcaagaaaa	gtctttttgg	acttctctaa	cttttcaaga	cattctagga	1500
ttgggtggcg	cttatccttc	ttagtttttg	gagacttctc	ttcacctttc	atggtacacg	1560
actcggtgga	agataaagca	gtttttgaag	agagatcttt	tgccatctca	gaagaatcaa	1620
gagaagtttc	catttctgga	ggatcgggtt	cctctatttg	tgctttttga	ctatggatct	1680
ctaagactga	tattgaacta	tctgcatctt	tctcaaaagg	ggctgtttct	ttctcaagct	1740
cacctgtttt	catacttggt	tatgacagaa	tttaaggact	ctgttccatt	tccctccgtg	1800
atgatatttc	tgtccttagg	ggggctatag	ctctcttcc	ttgtctcata	aaactttgtc	1860
tctacttggt	tctgtcttaa	aatttgagc	taccctttca	tcactaactt	ctccatttac	1920
ca						1922

&lt;210&gt; 174

&lt;211&gt; 537

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 174

aaaagcggcg	cggctcgttc	aagatggcgg	agctcgacca	gttgctgac	gagagctctt	60
cagcaaaagc	ccttgtcagt	ttaaaagaag	gaagcttata	taacacgtgg	aatgaaaagt	120
acagttcttt	acagaaaaca	cctgtttgga	aaggcaggaa	tacaagctct	gctgtggaaa	180
tgcttttcag	aaattcaaaa	cgaagtcgac	ttttttctga	tgaagatgat	aggcaaataa	240
atacaaggtc	acctaaaaa	aaccagaggg	ttgcaatggg	tccacagaaa	tttacagcaa	300
caatgtcaac	accagataag	aaagcttcac	agaagattgg	ttttcgatta	cgtaatctgc	360
tcaagcttcc	taaagcacat	aatgggtgta	tatacgagtg	gttctattca	aatatagata	420
aaccactttt	tgaaggat	aatgactttt	gtgtatgtct	aaaggaatct	tttctaatt	480
tgaaaacaag	aaagttaaca	agagtagaat	ggggaaaaat	tcggcggctt	atgggaa	537

<210> 175  
 <211> 659  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(659)  
 <223> n = a,t,c or g

<400> 175  
 tctctctttg ccagtaatgt tggaagtggg catttcattg gcctggcagg gtcagggtgct 60  
 gctacgggca tttctgtatc agcttatgaa cttaatggct tgttttctgt gctgatgttg 120  
 gcctgggtct tcctacccat ctacattgct ggtcagggtca ccacgatgcc agaataccta 180  
 cggaagcgct tcgggtggcat cagaatcccc atcatcctgg ctgtactcta cctattttatc 240  
 tacatcttca ccaagatctc ggtagacatg tatgcgggtg ccatcttcat ccagcagtct 300  
 ttgcacctgg atctgtacct ggccatagtt gggctactgg ccatcactgc tgtatacacg 360  
 gttgctgggtg gcctggctgc tgtgatctac acggatgccc tgcagacgct gatcatgctt 420  
 ataggagcgc tcaccttgat gggctacagt ttccgcgcgg ttggtgggat ggaaggactg 480  
 aaggagaagt acttcttggc cctggctagc aaccggagtg agaacagcag ctgcgggctg 540  
 ccccggaag atgcctttca tatttttcga gatccgctga catctgatct cccgtggccg 600  
 ggggtcctat ttggaatgtc catcccatcc ctctggtact gngcacgga tcaggtgaa 659

<210> 176  
 <211> 1033  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1033)  
 <223> n = a,t,c or g

<400> 176  
 cccacgcgtc cggatgtgtg ctacacattg ggggacctga ttggggcttc agaccttggg 60  
 ggcctgtccg caggggtctcc tccatccttc ttgatttgcc tgtcattgag gctgcccgct 120  
 ctgggcgcca ttccccagcc taacacctct tctcagtcct tccttgccagg tccctggagt 180  
 ccaggccttg gggcagtgaa gaaaccgtgg ggaggggcat gagatgccag tccccaaagt 240  
 ccttgggagc ccttgtgggc caagtcattg taggacacac cctctcctgg gcattgctga 300  
 ggtcacccag tgagcctagg ctccccctc ctcccatccc cagcctgggg gaaccttcag 360  
 cgtctctcct cctgttaggc ccgggtcag ctccccagga acttttggtg gtgggtacta 420  
 gtagggttaag gcagttcttc ccatcatgag ggagaccttg ggagactttc attaccaaatt 480  
 ccattgctgc cccgaccttc ctgggactga tctgggtcac cctggtctcc tgatcttgga 540  
 gaagtcaagt tcttatcca gacttgagag gttacaagcc tccaggtctc tggcaaagtg 600  
 tggagatgat ggacagccat ttgtacacac accagccagt cccttagcat atctctcttg 660  
 gttttgtctc aggtctgcct cagccacctc cctgacgctg tcccactgtg tggatgtggg 720  
 gaaggggctt ctggatttta agaagaggag aggtcactca attgggggag cccctgagca 780  
 gcgataccag atcatccctg tgtgtgtggc tgcccgactt cctaccggg ctccaggtgt 840  
 gctgcagcct cctggccact ggaggggctg accgctgat ccacctctgg aatgttgttg 900  
 gaagtgcctt ggaggccaac cagaccctgg agggagctgg tggcagcatc accagtgttg 960  
 actttgacct ctgggctac caggtttttag cagcaactta caaccagggtt gccagttttt 1020  
 ggaaggtngg gga 1033

<210> 177  
 <211> 335  
 <212> DNA  
 <213> Homo sapiens

<400> 177  
 gtcaaaaaacg atttcctagc aactgtggcc gtgatggaaa actgtttctt tggggacaag 60  
 cacttcatat catcgcaaaa ctcttgggta agtggagaag attgggaatg gtatTTTTTT 120  
 ccttggtatt aagctattag aaataaatat gcctttgctg gcacataata gtactttggt 180  
 acaacaggat atcctatgga gtttaaaaat aagtatttaa aatataacaa atctgtatta 240  
 gtccattctc atgctactaa taaagatata cccaagactg ggtaatttat aaaggaagga 300  
 gttttaatgg cctcacagtt ccgtcgacgc gggcg 335

<210> 178  
 <211> 556  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1) ... (556)  
 <223> n = a,t,c or g

<400> 178  
 gttcacgtct gcagcagtaa gatgggagct ttgtccacgg agcggctaca gtactacact 60  
 caggaactgg gggtcggga gcgcagtggc cacagcgtgt ccctcatcga cctctggggc 120  
 ctcttgttg agtatctct gtaccaggag gagaaccctg ccaagctgtc tgaccaacag 180  
 gaggcggtcc gccagggtca gaacccttac ccattttaca ccagtgtcaa cgtccgcacc 240  
 aacttgagtg gggaagattt tgcagagtgg tgcagattca cgccctatga ggttggtctc 300  
 cccaagtacg gggcttatgt tcccaccgag ctcttcggct cagaactctt catgggacga 360  
 ttgtcgcagc tccagcctga accccggatc tgttacctgc aaggatatgt gggcagcgcc 420  
 tttgccacca gcctggatga gatcttcta aagaccgccg gctcgggcct cagcttctctg 480  
 gagtgggtaca gaggcagtgt gaatatcaca gacgactgcc agaagcctca gctgcacaac 540  
 ncctcgacgc gggaat 556

<210> 179  
 <211> 631  
 <212> DNA  
 <213> Homo sapiens

```

<400> 179
gaattttctgg gtcgtcccccac gcgtcccgca aaggatgagg gaaacgatga gggaaaggat 60
gaggggaaagg atgaggggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 120
gagagaaaagg atgaggggaaa ggatgaggga aaggatgaga gaaaggatga gggaaaggat 180
gaggggaaagg atgaggggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 240
gaggggaaagg atgaggggaaa cgatgaggga aaggatgagg gaaaggatga gggaaaggat 300
gaggggaaagg atgaggggaaa ggatgaggga aaggatgagg gaaacgatga gggaaacgat 360
gaggggaaacg atgaggggaaa ggatgaggga aaggatgaga gaaacgatga gggaaaggat 420
gaggggaaagg atgaggggaaa ggatgaggga aaggatgaga gaaacgatga gggaaaggat 480
gagagaaaagg atgaggggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 540
gaggggaaagg atgaggggaaa cgatgaggga aaggatgaga gaaaggatga gggaaaggat 600
gaggggaaagg atgaggggaaa ggataagtaa g 631

```

```

<210> 180
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(469)
<223> n = a,t,c or g

```

```

<400> 180
ggcgggggctc ntttgagacc tgatgaccat cattacgccc agcttggcac gagggggagg 60
acttcagcta cggcctgcag ccctactgcg ggtactcett ccaggttgtg ggggagatga 120
tccggaaccg ggaggtgctg ccttgccccg atgactgtcc cgcctgggcg tatgcctca 180
tgatcgaggg ctggaacgag ttccccagcc ggagggcccg ctttaaggac atccacagcc 240
ggctccgagc ctggggcaac ctttccaact acaacagctc ggagcagacc tcggggggca 300
gaaacaccac gcagaccagc tccctgagca ccagccact gtgcaatgtg agcaacgccc 360
cctacgtggg gcccaagcag aagggtccgc cctttccaca gaccaggtc atccccatga 420
agggccagat cagacccatg gtgccccgc cgcagctata cgtccccg 469

```

```

<210> 181
<211> 453
<212> DNA
<213> Homo sapiens

```

```

<400> 181
caggaattcc gggcgccacc cacgcgttcg atggatcctg gaagagcgca agcgggtgat 60
gcaggaggcc tgcgccaaagt accgggcgag cagcagccgc cgggccgtca cgcgccgcca 120
cgtgtcccgt atcttcgtgg aggaccgcca ccgcgtgctc tactgcgagg tgcccaaggc 180
cggctgctcc aattggaagc ggggtgctcat ggtgctggcc ggccctggcct cgtccactgc 240
cgacatccag cacaacaccg tccactatgg cagcgtctc aagcgccctg acaccttga 300
ccgccagggt atcttgacc gtctcagcac ctacaccaag atgctctttg tccgcgagcc 360
cttcgagagg ctggtgtccg ccttcgcgca caagtttgag caccccaaca gctactatca 420
cccgtcttc tgcattggcca tactggccc gta 453

```



<210> 182  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
 cataatgtat agtattttctc ctgccaaactc tgaggaaggc caggaacttt atgtctgcac 60  
 agtcaaggat gatgtgaact tggatacagt acttctccta ccctttttga aagaaatagc 120  
 agtaagccaa ctggatcaac tgagcccaga ggaacagttg ctggatcaagt gtgctgcaat 180  
 cattggtcac tccttccata tagatttgct gcagcacctc ctgcctggct gggataaaaa 240  
 taagctactt caggtcttga gagctcttgt ggatatacat gtgctctgct ggtctgacaa 300  
 gagccaagag cttctgtctg agcccatatt aatgccttcc tctatcgaca tcattgatgg 360  
 aaccaaagag aagaaga 377

<210> 183  
 <211> 621  
 <212> DNA  
 <213> Homo sapiens

<400> 183  
 ctcatcctta aagtgcacaga gtaaattaac tctaaggccc catccaggac tcaagctgtg 60  
 tgatttttaca aaaatgaaaa ttatattaat aatcccattg taaaatccca aaagaaagtc 120  
 aagagactag cagaaagaca ggtgggtgat gggatgtcct ggacagagcc tggatcatga 180  
 ggtcccatg tagtgcttgt actacgcaga tgtttcctct tgagctattt taaaggtgtg 240  
 gaaaaagcca aagcaatgcc ctctccacgg atactaaaga ctcaccttcc cactcagctg 300  
 ctgccaccgt ctttctggga aaacaactgc aaggtaagat accaacagct ccctgtgaca 360  
 gaaggggaaag taagccaacc aaagcgagtc ctgcagaccc caacgcagag cattcgtgat 420  
 cacctttgcc tctccactgt ctctgatgct taccagcaaa gagaaaacat aaagttctac 480  
 attcagcagg acattcacct gaacagtttc aaataggaca tgaaggcagg atccagattg 540  
 aatgtttggg gggaaactaga gacatgggga ggcagtgagt gcagtaagcg tagctgtgaa 600  
 atgaagggga gaagatggtg g 621

<210> 184  
 <211> 415  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 accgggacga cccacgcgtc cggaattta attctattat atatgcagac tttctaaaga 60

agataaagct	tttttatggg	agaaacgtta	ttattgcttc	aaacacccaa	attgtcttcc	120
taaaatatta	gcaagcgccc	caaactggaa	atgggttaat	cttgccaaaa	cttactcatt	180
gcttcaccag	tggcctgcat	tgtacccact	aattgcattg	gaacttcttg	attcaaagta	240
agtcaaatac	atttatgtgc	tcttgtttta	ttgtcagttt	ttccagtaag	gtatgttgcc	300
agaagtattt	cctttccttt	taacatgaaa	gcaattcaat	ataatccaaa	tgtgtaaatg	360
tatatttata	caaacatatc	ttctgcattg	aagttgtcaa	taaagcattg	catgt	415

&lt;210&gt; 185

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

ggaaaaatgat	gatttgaggt	ttatttgaaa	tacaacaatg	tccaatagga	aaacactgca	60
acttttcttca	ggtgttgaga	aatccaatag	agacctctgc	ttgtctcctc	ctttggcaag	120
agctccaagg	ggagagagag	gatggggccac	cacgatgaat	actacaggct	gcgggggaag	180
ataaccctag	tccagaccat	tcctacaaaa	gaaatgggga	atccgaaagg	aaaaggaaga	240
aatctcacta	gcacatgtca	aagagccagg	agaggcacia	ttcaccaagc	agaggaagaa	300
atagtgaccg	cagcgggggc	cgggtgcagcc	gcagtgataa	cggtcggagc	cgttacagg	359

&lt;210&gt; 186

&lt;211&gt; 1616

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

ggaggttgcg	gcggcggctg	cggcgcagcc	cggggcggcg	ggtgggaaga	ggactaccag	60
aggggcctgc	gggagacca	gggtcggacc	cataggagtc	ctgtcgtcag	gacctccttg	120
atcggctctc	tgcttggtt	ctcgggtgaag	gaggagcttc	ggggtgtcgg	ctgggctgcg	180
cggactctc	ttgggatccg	atgatggatc	ccaccgggtg	atcgggaatg	gggttacaat	240
gcagtgagcg	ggaaaggctc	tcgcgggggc	acagaaagat	ccccagggcc	gcaaggcgctg	300
ctgtcgcctg	caaaggcact	gaccacagag	ccactgcct	ccctccttcc	tgggtggagc	360
aggggcctgc	cttcatctcc	aaggcccggg	ggctccggca	tctcgacgcg	gcttccggcg	420
acacgggcaa	agagagacag	aggctagtcc	gagccggagc	cagtgtgacc	acacgtggca	480
ctgacgtccc	ccaagagcac	atgcagtgag	cctgtgtctc	tgaggccgta	gtgggcgacg	540
acgagacgga	cagtgatgtc	caggcctgcg	cccggggggc	actggagacc	tgcccctcaa	600
agcggaggaa	acgccaagct	cacctgaaaa	cctgcgagac	agggcctgtg	cacgagtcca	660
gtactcctac	ttcgccaagt	ctcagggacc	catccccgag	caacggtggc	ggcgcagaga	720
agagcacggc	gccggcgcag	gtgcagagag	acaggaggct	gatgggggga	agttgaggca	780
cctggggcag	agaaaaaaat	gcattgccaa	gaggtttctg	ggtcatctac	tgacgaaaat	840
gtcttcccat	cagcccttgc	gctgggtccc	agggaccctg	gcatccgtcg	ttggcgccca	900
gggtgcgcgt	cgggccacta	ggggtacccc	aactcggaca	gaaggcccat	gagttegaatt	960
tgaagtttgt	gggaatatag	gtgaggcacc	aggggcagaa	aaaaaacagg	agacctcgcc	1020
tcagacaagc	ggggcctggg	tcccccatgg	atgaaagtgc	cttcccatta	tgctgtaccc	1080
tgggcagagt	ggacagtgtg	gaccctgggt	cgagcccagg	gtgcgcttcg	ggaccgcttg	1140
cggttaccag	aaagcgaaca	aatgggtccat	gagcgggaag	tgaggcacct	gaggcagaga	1200
aagtaaagaa	acgcgcgcgc	gagaagcagt	gcctgggtcc	ctcacggagg	aaattgtctt	1260
ctccttagcc	cgttcgcttg	gcagtgaggt	cctggcgctc	cctggtttga	tcccagggta	1320

cgcctcgggc	cactagtgtt	accccaaggt	gggcagaaag	cccataaggg	gaaggcgagg	1380
cacctggggc	agagaaaaaa	aaaaacttcg	ccgcaaagaa	gcgcggcctg	attccccacg	1440
gacgaaagt	tcttcccatc	agtccttgca	ctgggacccg	gggaccctgg	tgtccctggg	1500
tcgagctcag	gggtgtgcctc	agccgctacg	tgcaccccaa	ggggagcttt	gggagcccaa	1560
aagccaataa	gggaaagtaa	tttttaaggc	ccccagtggg	gaggccctg	tcacag	1616

<210> 187  
 <211> 916  
 <212> DNA  
 <213> Homo sapiens

<400> 187

ttttgataag	aggcaacatg	aagcaagaat	ccagcaaatg	gagaatgaaa	ttcactat	60
gcaagaaaat	ctaaaaagta	tggaggaaat	ccaaggcctt	acagatctcc	aacttcagga	120
agctgatgaa	gagaaggaga	gaattctggc	ccaactccga	gagttagaga	aaaagaagaa	180
acttgaagat	gccaaatctc	aggagcaagt	ttttggttta	gataaagaac	tgaagaaact	240
aaagaaagcc	gtggccacct	ctgataagct	agccacagct	gagctcacca	ttgccaaaga	300
ccagctgaag	tcccttcacg	gaactgttat	gaaaattaac	caggagcgag	cagaggagtt	360
gcaggaagca	gagaggttca	gcagaaaggc	agcacaagca	gccagagatc	tcacccgagc	420
agaagctgag	atcgaaactc	tgcagaatct	cctcaggcag	aagggggagc	agtttcgact	480
tgagatggag	aaaacagggtg	taggtactgg	agcaaaactca	caggtcctag	aaattgagaa	540
actgaatgag	acaatggaac	gacaaaggac	agagattgca	aggctgcaga	atgtactata	600
cctcactgga	agtgacaaca	aaggaggctt	tgaaaatgtt	ttagaagaaa	ttgctgaact	660
tcgacgtgaa	ggttctttatc	agaatgatta	cataagcagc	atggcagatc	ctttcaaaag	720
acgaggctat	tggtacttta	tgccaccacc	accatcatca	aaagtttcca	gccatagttc	780
ccaggccacc	aaggactctg	gtgttgccct	taagtactca	gcctcaactc	ctgttagaaa	840
accacgccct	gggcagcagg	atgggaagga	aggcagtcaa	cctccccctg	cctcaggata	900
ctgggtttat	tctccc					916

<210> 188  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 188

cctctactgc	agcttcatca	tcagattctt	ctttctgttc	ttgggggtgct	tcttcttctc	60
ccatgggctc	ctcaacaggtt	tcagtcttgc	tgctccatac	ataaatagga	aagtttatga	120
actgtgaata	ttttttgacg	agatttttaa	ttgtatccaa	ttcaaggtaa	tcagatgctt	180
cttcttttaa	gacaagggta	attgtcgttc	cccgtcctag	agtgtttcct	cttgggtcag	240
caattacaga	aaattcattg	gagtcagact	cccagattgg	ccagtttggg	gtcggtttct	300
attccgcctt	ccttgtagca	gataaggtta	ttgtcacttc	aaaacacaac	aacgatacc	360
agcacatctg	ggagtctgac	tccaatgaat	tttctgtaat	tgctgacca	agaggaaaca	420
ctctaggacg	gggaacgaca	attacccttg	tcttaaaaga	agaagcatct	gattaccttg	480
aattggatac	aattaaaaat	ctcgtcaaaa	aataattcaca	gttcataaac	tttcctat	540
atgtatggag	cagcaagact	gaaactgttg	aggagcccat	ggaggaagaa	gaagcagcca	600
aagaagagaa	agaagaatct	gatgatgaag	ctgcagtaga	ggaagaagaa	gaagaaaaga	660
aaccaaagac	taaaaaagtt	gaaaaaactg	tctgggactg	ggaacttatg	aatgatatca	720
aaccaatatg	gcagagacca	tcaaaagaag	tagaagaaga	tgaatacaaa	gctttctaca	780

aatcattttc	aaaggaaagt	gatgacccca	tggcttatat	tcactttact	gctgaagggg	840
aagttacctt	caaatacaatt	ttattttgtac	ccacatctgc	tccacgtggt	ctgtttgacg	900
aatatggatc	taaaaagagc	gattacatta	agctctatgt	gcgccgtgta	ttcatcacag	960
acgacttcca	tgatatgatg	cctaaatacc	tcaattttgt	caaggggtgtg	gtggactcag	1020
atgatctccc	cttgaatgtt	tcccgcgaga	ctcttcagca	acataaaactg	cttaaggtga	1080

<210> 189  
 <211> 1344  
 <212> DNA  
 <213> Homo sapiens

<400> 189

tttttttttt	ttgctgctgg	gtcggggttt	atttcaaatg	cagccacaga	ggcgggtttct	60
gcacaggtac	gtgatccgac	tccacaagct	cccaccagg	gtccccatg	acccgcaatg	120
acgctgtgtg	gggtcaaagg	aaaacaggcc	acagccagg	ccctcgatgg	acgcaggcag	180
gggaccagga	atgcccggcca	cgcaggggga	tcgggaatca	ggcggaaagg	gcaggtttgc	240
agctggcggg	aggagccagc	atgccccaat	ctctaaaata	ttcccggtag	aaaaatagac	300
atttccctcc	aaagcagatt	cctggggctg	gagggtccct	ccaaggccag	gggtccgggt	360
gattccagag	catccacgct	ctgcgctgaa	ggcactgaac	ctgccatcac	tgtcacagcc	420
gtcaccggcc	aaggagggtc	tggaggagg	aaggggccc	tgcgaggctc	tggtgctggt	480
gatcccggcc	cccaccaccg	gaggagctga	aagcccttgc	tcagccgctg	ccctgctggt	540
gaaccgggcc	cccaccgccc	gaggagctgc	accctgtgtg	gtctgaggca	gccctgcact	600
gggcagcggc	cccggcccgc	gctgaacca	ctaggagagc	agctgcagca	cctgtcggat	660
gcgctggggc	ctcccggcca	gggggggata	agagccctcc	tcattccagct	cccgcacag	720
ggcttcggcc	ttctgcaccg	tcagctctcg	ggcccggccc	tcagcccctc	ccaggtaggc	780
cagcaggggtg	gagaagtgtc	catcgggaac	cttgtcactg	tcatacatgt	gcagcaggag	840
ccagctctgc	ctcgtcttct	gaaacctcca	gttcttgtgc	ttttggggccc	atctgcagag	900
gtagtccagg	gccagttcgg	cccccgagcg	cctggcaggc	gggtgctggg	ccacaaggcc	960
tgcctcccgc	agacgctgcc	tctcctcttt	cttccgttcc	tttttcagct	tcctttccag	1020
gaccctctgc	tctcttgggg	acagctctgg	ctctgcgtcc	agcccggggc	tgagcacagc	1080
ttcgcccttg	gagccggctc	cttcgccact	tggtgcagcc	tcaggggccc	gcagtggccc	1140
ctctgctgac	gccttcttca	gctttttgtt	ctttttctct	gtcacttcag	gaacttttct	1200
cttctgtttt	gccatcctgc	gcccacctgc	gcccacgtcg	cccacctaa	cgtgaacagc	1260
tgcgtcgcg	acgcgcctt	ccggcaggga	cccgcggacg	cgtgggtcga	cccggcaaaa	1320
cgggtccaac	ctagggcgtc	gagg				1344

<210> 190  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 190

cccggaacca	cgcgcgcccc	gcgcacgggc	tctccccac	accgccttat	tcgggtcgag	60
accccggggc	ccccggcgcc	gcctgctgat	gagcggatct	ccggaccccc	cgcagcagc	120
gataggctag	ctatcctaga	agactatgcg	gaccggtttg	atgttcagga	gactggcgaa	180
ggctcagcag	gagcttcagg	agccccagag	aaggccctg	aaaatgatgg	ctacatggag	240
ccctatgagg	ctcaaaagat	gatggccgag	atccggggct	ccaaggagac	agcaactcag	300
cccttgcttc	tgtatgacac	accctatgag	ccagaggagg	atggggccac	cccggaaagg	360

gagggggccc	cctggccccg	ggagtccccg	ctgccagagg	atgatgagag	gccccctgag	420
gagtatgacc	agccctggga	gtggaagaag	gagcggattt	ccaaagcctt	tgcagttgac	480
attaaggtca	tcaaagacct	accttggcct	ccacctgtgg	gacagctgga	cagcagcccc	540
tccttgcttg						550

<210> 191  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<400> 191						
caatTTTTTT	ctctTTTTTT	aaggtatcag	atacacaccg	gacttcaaca	ttctatcata	60
agacctacc	aaccaactg	tttacctctg	gacaatgcc	ccctacctca	gaaactgaag	120
gaggttgat	attcaacgca	tatggtcgga	aaatggcact	tggtttttta	cagaaaagaa	180
tgcatgccca	ccagaagagg	atgtgatacc	ttttttggtt	cccttttggg	aagtggggat	240
tactatacac	actacaaatg	tgacagtcc	gggatgtgtg	gctatgactt	gtatgaaaac	300
gacaatgctg	cctgggacta	tgacaatggc	atatactcca	cacagatgta	cactcagaga	360
gtacagcaaa	tcttagcttc	ccataacccc	acaaagccta	tatttttata	tattgcctat	420
caagctgttc	attcaccact	gcaagctcct	ggcaggtatt	tcgaacacta	cgatccatt	480
atcaacataa	acaggaggag	atatgtctgc	atgctttcct	gcttagatga	agcaatcaac	540
aacgtgacat	tggtctctaa	ag				562

<210> 192  
 <211> 2171  
 <212> DNA  
 <213> Homo sapiens

<400> 192						
cacgcgtccg	gaaaggaaga	ggcggtgaga	ggctgcaaag	ccccttgctg	gttccgcaga	60
aaccagaaag	acctccccct	ccacccaagc	ctcagttcct	aaactcaggg	gcatatcctc	120
aaaaacctct	tagaaatcag	ggagtgggtga	ggacactgtc	cagctctgcc	caagaggaca	180
tcatcoggtg	gtttaaagag	gagcagctac	cacttcgagc	gggctaccag	aaaacctcag	240
acaccatagc	ccctgggttc	catggaattc	tcacactcaa	gaaagcaaat	gaacttcttc	300
tgagcacagg	catgcccggc	agttttctca	tccgagtcag	tgaaaggatc	aaaggctatg	360
ccctgtccta	tctgtcggag	gacggctgta	aacatttcct	catcgatgcc	tctgcagacg	420
cctacagctt	cctgggcgtg	gaccagctac	agcatgccac	cttggcggat	ttggtggaat	480
atcacaagga	ggaacccatc	acttccctgg	ggaaggagct	ccttctctat	ccctgtggtc	540
agcaggacca	gctgcctgac	tacctggagc	tgtttgagtg	acagcctcca	tcagggcat	600
cctacagcct	ccaagcgggc	tttccccctg	acaaatgcc	ctgcaacatt	tatgtgtgaa	660
gccaaaatca	ccctgcagca	gagccaatac	tgatcaactg	aaagtatcca	tggagtcttc	720
attgacacct	cttttctgca	caaatactgg	aattcaatgt	caagagaaaa	tgacctctgc	780
tcaaaaggga	gaagagtctc	aatttcagca	agtacctgtc	atgaagggtg	tgaccttaat	840
gatgtacata	aaataaaaca	aatgaagaaa	tgaaaaactt	ttagaaatta	aggtgtactt	900
gaaaacgagt	atctatcata	tgacctctgc	actccctctg	tatcatctca	ggaggtttca	960
ggggcctggt	gacatgaagt	ttcgaagttt	catgttggct	ttggaatggg	agcaaaagcc	1020
tttcttggtt	gagatgatgc	ttaaaacaca	cctcacttat	tgtacatgtt	ggaaccagga	1080
catgagagac	atagaaaaac	agaagtcagt	aatgtaaatt	gaatgagagg	cttaacatgc	1140
atgaaaatca	agatggacct	gcaggaaagt	gagcaaacat	cgctgagttt	gttttcttgc	1200

tcgggagaaat	ggggccgggg	ctggcctggc	ctccccctgga	tatactctat	agtgcaccaa	1260
aaggataaaag	catctgtaca	tgtatTTTTT	tattttttat	cagaagtgt	tagacaagaa	1320
cagaataaagc	aggctgtttg	gatgctactt	gtgggttgaa	tgtgttcccc	caaaatata	1380
ggtgaagtct	taaccccat	ccccgtgaat	gggaccttgt	ttggaaatag	ggtctttgca	1440
gatatagtca	agatgaggtc	acattggatt	aggggtggg	ccaaatccaa	tgactggcat	1500
ccttaggaga	agagagagtt	ttggtaatat	acacaaatgc	agtgggaaga	agaccagggg	1560
acaagaggca	agttggagtg	atgcagccgg	aagggaagg	acaccaagga	tctccggcca	1620
ccagcagaag	ccagcagaga	ggcatgggac	aggttcccc	caagccttag	aaggaaagcat	1680
ggccctgact	tcagaattcc	agactccaga	actggaagaa	taaatgtctg	ttgttttaag	1740
ctgcttagtt	catgctgagt	tcagctgac	ttgttactat	agccccagaa	agctaataca	1800
gtcgtttatg	taattacata	acctgacaca	caagatcgac	ccattcactg	ctgcccagtc	1860
caccatttttc	ataatgaagt	agaaatggga	ggtaagaaaa	acattccagc	cagttctgtt	1920
tagccctggg	acacatat	gtcccgctcag	gaatcttatg	ccctcctgga	acccccgcc	1980
acctcagtc	agtcacagtc	aggcgaacgg	cctctggaca	gggactgagg	tggctttgag	2040
ccactggaga	tcatttttct	tggaggatgg	agattggcta	gtacctctgg	cctaactgtg	2100
taggtcaata	ctcttttaca	ttgccttcta	ataaaagcag	aatgatacac	cagtgttgtt	2160
aaaaaaaaa	a					2171

<210> 193  
 <211> 2095  
 <212> DNA  
 <213> Homo sapiens

<400> 193

ggggaagtct	ggagaaggca	ttgtttcaat	tattaaaagt	gtgggggcag	tgggcggaac	60
aaacgcgcgc	actacagagg	ctggacgtaa	gcttatcggt	ggcgcgcgtg	cgcagcgccg	120
gcccaggttg	ccaaaacaaa	ggggatttgg	tgatggaggc	tttgttagaa	ggaatacaaa	180
atcgagggca	tggtggggga	tttttgacat	cttgtgaagc	agaactacag	gagctcatga	240
aacagattga	cataatggtg	gctcataaaa	aatctgaatg	ggaaggacgt	acacatgctc	300
tagaaaactg	cttgaaaatc	cgtgaacagg	aacttaagag	tcttaggagt	cagttggatg	360
tgacacataa	ggaggttgga	atgttgcac	agcaggtaga	agaacatgaa	aaaatcaagc	420
aagagatgac	catggaatat	aagcaggagt	tgaagaaact	acatgaagaa	ttatgcatac	480
tgaagagaag	ctatgaaaag	cttcagaaaa	agcaaatgag	ggaattcaga	ggaaatacca	540
aaaatcacag	ggaagatcgg	tctgaaattg	agaggttaac	tgcaaaaata	gaggaattcc	600
gtcagaaaac	gctggactgg	gagaagcaac	gcttgattta	tcagcaacag	gtatcttcac	660
tggaggcaca	aaggaaggct	ctggctgaac	aatcagagat	aattcaggct	cagcttgtca	720
atcggaacaa	gaaatttagag	tctgtggaac	ttcttagcca	atcagaaatt	caacacttaa	780
gcagtaaaact	ggagcgggct	aatgacacta	tctgtgccaa	tgagttggaa	atagagcgcc	840
tcaccatgag	ggtcaatgac	ttgggttgga	ccagtatgac	tgtcctacag	gagcagcagc	900
aaaaagaaga	aaaattgagg	gaatctgaaa	aactattaga	ggctctgcag	gaagaaaaga	960
gagaattgaa	ggcagctctt	cagtctcaag	aaaatctcat	acatgaggcc	agaatacaaa	1020
aggagaagtt	acaagaaaaa	gtaaaggcaa	ctaactctca	acatgctgta	gaagctataa	1080
gtttggaatc	tgtgagtga	acgtgtaaac	agctgagcca	agaactaatg	gaaaaatatg	1140
aagaactgaa	gaggatggaa	gcacataaca	atgaatacaa	agcagagatt	aagaagttga	1200
aagaacagat	tttacagggt	gaacaaagtt	acagttctgc	actagaagga	atgaagatag	1260
aaatctccca	tctaactcag	gagttacatc	agcgagatat	cactattgct	tccaccaagg	1320
gttcttctct	agacatggaa	aagcgactca	gagcagagat	gcaaaaggca	gaagacaaag	1380
cagtagagca	taaggagatt	ttggatcagc	tggagtcact	caaattagaa	aatcgctatc	1440
tttctgaaat	ggtgatgaaa	ttggaattgg	gtttacatga	gtgttccctg	cctgtatctc	1500
cccttggttc	aatagctacc	agatTTTTTg	aagaggagga	actgagggtc	catcacattc	1560
tagagcgctt	ggatgccc	attgaagaac	taaaaagaga	gagtgaagaa	acagtggagac	1620
aattcacagc	ctttaaagtag	cctcttaaaa	aaatcacaa	cttggaaata	aaaataaaca	1680
ccaaagagtt	actgtcatct	gaagtgcag	ctcttttaaa	acatgaagag	ataaaattat	1740
aaaaatgata	catctaaagc	agtggtgaag	aaagctgaaa	aactgatact	tttgataaggc	1800
attttctctg	cactggTTTT	tttaaaggac	ttcttccagc	aataagttga	aagaataaac	1860
cactttgcta	gactTTTTTc	tcatacgaat	atttattatc	ataaagtgat	acttaccttg	1920

ctgacttaaa	tgtgaatagc	tatgtactaa	ttgaaataag	gatttttatga	tacatgttga	1980
aaataaagta	actgcaggaa	ctttcttttag	gggaaatgtg	tagaagcatg	gattttagggg	2040
tcaaacatac	ctggatcgat	agactgggtt	tgcacttac	cagccaacgg	ggctt	2095

<210> 194  
 <211> 1051  
 <212> DNA  
 <213> Homo sapiens

<400> 194						
gagaccttgt	cttaaaaaaa	taaaatgctg	tcagaataaa	aagcagtcaa	cagaaatgaa	60
acccttataa	gagacaaata	aatgtgggca	attattttct	gcaaaatgcc	ctccaagccc	120
ctgggcgcca	ttgccttctg	taataggaca	tcacctgaac	aggctttctg	ggctggagcc	180
aaggacctc	cctgactccc	acctcccttt	ctgccttgta	ccccagccag	gtggaagaga	240
ccggagtgg	gctgtccctg	gagcaaacgg	agcaacactc	tgcagacccc	attcagcggg	300
gcgccccctc	tcagaaggac	acctctaacc	ctggggacag	ccttgacacc	cctggccccc	360
ggatccttgc	cttctgcac	ccgccttccc	tgagcgaggc	tgccctggcc	gctgaccccc	420
gccgtttctg	cagccctgac	ctccgtcgcc	tcctgggacc	catcctggat	ggggcttcag	480
tagcagccac	tcccagcacc	ccgctggcca	cacggcacc	ccaaagtcct	ctttcggtcg	540
atctccaga	tgaactacct	gtgggcaccg	agaatgtgca	cagactcttc	acctccggga	600
aagacactga	ggcagtggag	acagatttag	atatagetca	ggatgctgat	gctctggatt	660
tggagatgct	ggccccctac	atctccatgg	atgatgactt	ccagctcaac	gccagcgagc	720
agctacccag	ggcctaccac	agacctctgg	gggctgtccc	ccggccccgt	gctcggagct	780
tccatggcct	gtcacctcca	gcccttgagc	cctccctgct	accccgctgg	gggagtgaac	840
cccggtgag	ctgctccagc	ccttccagag	gggacccctc	agcatcctct	cccatggctg	900
gggctcggaa	gaggaccctg	gcccagagct	caaaggacga	ggacgaggga	gtggagctgc	960
tgggagtga	acctcccaaa	aggtcccca	gccagaaca	cgaaaacttt	ctgctctttc	1020
ctctcagcct	gagtttccct	ctgacaggag	g			1051

<210> 195  
 <211> 423  
 <212> DNA  
 <213> Homo sapiens

<400> 195						
gtgaactcca	agactgtttt	gatgttcattg	atgcatcttg	ggaagagcag	atattctggg	60
gatggcataa	tgatgtccac	atatttgaca	caaagacaca	gacttggttt	caaccagaaa	120
ttaaagggtg	agttccacca	cagccacgag	ccgcgcatac	gtgtgcagtt	cttggaataa	180
agggttatat	ctttggcgga	cgtgttctgc	aaactaggat	gaatgatttg	cactatctaa	240
acctagacac	ctggacttgg	tctggaagga	ttactattaa	tggagaaagc	ccaaaacatc	300
ggtcatggca	tactttaaca	cctatagctg	atgataaact	tttcctatgt	ggtggactaa	360
atgcatataa	tatgccatta	agtgatgggt	ggattcataa	tgtcacaaca	cattgttggg	420
aac						423

<210> 196  
 <211> 411  
 <212> DNA  
 <213> Homo sapiens

<400> 196  
 tttttttttt ttgaggacaa ggtctcactc tgtcacccca aggtgggagt gcagtgcga 60  
 catcacagct cactggcagc ctcaaccctg gggttcaagt gatcctctca ccttcagcct 120  
 ccccaagtag ttgtgcctcc taggcacaca acactatgcc cgggcaaatt tttttgtatt 180  
 ttgtattttt tgtagaaaca ggatttcgcc atgttggcca ggctgggtctc gaacaccctg 240  
 ggctcaactg atccgcctgc ctccggcctcc caaagtgcctg ggattacagg tgtgagccac 300  
 cctgctcaac cagggttttat tatttaagtt agttaaactt tggatagatt gtataatata 360  
 tagtttaagt taatcatgct catatttttt aaataaataa aacactatac t 411

<210> 197  
 <211> 751  
 <212> DNA  
 <213> Homo sapiens

<400> 197  
 cccacgggaa gggcaggtga agcaggggct gctgggggat tgctgggtcc tgtgtgcctg 60  
 cgccgcgctg cagaagagca ggcacctoct ggaccaggtc attcctccgg gacagccgag 120  
 ctgggcecgac caggagtacc ggggctcctt cacctgtcgc atttggcagt ttggacgctg 180  
 ggtggagggtg accacagatg accgcctgcc gtgccttgca gggagactct gtttctcccg 240  
 ctgccagagg gaggatgtgt tctggctccc cttactggaa aaggtctacg ccaaggtcca 300  
 tgggtcctac gagcacctgt gggccgggca ggtggcggat gccctggtgg acctgaccgg 360  
 cggcctggca gaaagatgga acctgaaggg cgtagcagga agcggaggcc agcaggacag 420  
 gccaggccgc tgggagcaca ggacttgtcg gcagctgctc cacctgaagg accagtgtct 480  
 gatcagctgc tgcgtgctca gccccagagc aggtgaggca cgtggccagc atgggagggc 540  
 tgcagccagc gtgcccccca ctgccaggcc tcaggcacac tgtagctttt tatgtgactg 600  
 gctacacagc cctgtcagga ctaagtggga agaagtaagc ttgttctcaa ggggtggtgc 660  
 ctcaatttgt gaccttcccc tgctgtcctc ttccagaggg acgtggccct tctctccct 720  
 gaccagtcct ttccactagt gcgaggcagg g 751

<210> 198  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 198  
 gggccgagtg tctggaggcc tctattgccc gatatgccc cctgtgcgcc aatagccggt 60  
 atacctttga cgggtgaaacc gtgacgcttt cgccaagtca ggcggttaac cagctgcacg 120  
 gcgggcccga agggttcgac aaacgtcgct ggagattgt gaaccagaac gatcgtcagg 180  
 tgctgtttgc cctgagttca gatgatggtg atcagggtct cccgggtaac ctccggcgcga 240



cgggtgcaata	tcgtctgacc	gacgataacc	gtatctccat	tacttatcgc	gccacagttg	300
ataaaccttg	cccgggtgaat	atgactaatc	acgtctatct	caatcttgac	ggcgagcagt	360
ctgacgtgcg	caatcacaag	ttgcagattc	tggcggacga	atatctgccg	gttgatgaag	420
gcggcattcc	gcacgacggc	ctgaaatctg	tcgccggaac	gtcttttgat	ttccgcagcg	480
ccaaaatcat	cgccagtgag	tttcttgccg	acgacgatca	gcgcaaagtg	aaagggttacg	540
atcacgcatt	cttggttacag	gccaaaggcg	atggcaagaa	agtggcggcg	catgtctggt	600
cagcagatga	aaaattgcag	ctgaaggtct	acacca			636

<210> 199  
 <211> 690  
 <212> DNA  
 <213> Homo sapiens

<400> 199						
aaagtggcag	tgtttcttct	gaaattctca	ggcagtcaga	ctgtcttagg	caaatcttga	60
taaaatagcc	cttatccagg	tttttatcta	aggaatccca	agaagactgg	ggaatggaga	120
gacagtcaag	ggttatgtca	gaaaaggatg	agtatcagtt	tcaacatcag	ggagcgggtgg	180
agctgcttgt	cttcaatttt	ttgctcatcc	ttaccatttt	gacaatctgg	ttatttataaa	240
atcatcgatt	ccgcttcttg	catgaaactg	gaggagcaat	ggtgtatgac	aagccgccga	300
aatttgccat	gtcacgagag	caaatgtcac	agtcatgttc	tcacacggca	cataatgcaa	360
gtctgttgac	agatgcgggt	ccattgtcat	gtggggagtc	gagggcgagc	tgtttggttt	420
tgtaacgatg	ttgggaagtg	atggctctgc	agtcacaaag	agcagccttc	tctcactggc	480
tgcaaccgatg	aacattacga	agttctagaa	caaacatcac	ttcaaaatgc	ctggagtaat	540
tcctcttata	tcaactaatt	tcaagaagaa	aacctgcaga	aactaaccac	accctctca	600
acgagaatat	tgtgtccacg	tcctctttac	ttatacgacc	ogtctcttat	tctcttataa	660
cacaacgtca	taactaaaag	agcacaacac				690

<210> 200  
 <211> 433  
 <212> DNA  
 <213> Homo sapiens

<400> 200						
gtgactccaa	ggaaccaaga	ctgcagcagc	tgggcctcct	ggaggaggaa	cagctgagag	60
gccttggtatt	ccgacagact	cgaggataca	agagcttagc	aggggtgtctt	ggccatggtc	120
ccctgggtgct	gcaactcctc	tccttcacgc	tcttggtctg	gctccttgtc	caagtgtcca	180
aggtccccag	ctccataagt	caggacaat	ccaggcaaga	cgcgatctac	cagaacctga	240
cccagcttaa	agctgcagtg	ggtgagctct	cagagaaatc	caagctgcag	gagatctacc	300
aggagctgac	ccagctgaag	gtgcagtg	gtgagcttcc	agagaaatct	aagctgcagg	360
agatctacca	ggagctgacc	tggctgaagg	ctgcagtg	tgagcttcca	gagaaatcta	420
agatgcagga	gag					433

<210> 201  
 <211> 782

<212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> (1)...(782)  
 <223> n = a,t,c or g

<400> 201  
 gaagaagggg aaaagaggct ccaggcccct tctccaatca ctccctgccca ccctttctcc 60  
 tttggattcc ttggctgctt tagcaggtct tcctagaggc taactttgat ctttcttgct 120  
 gcagtttctt tttgggagag ctatgcagtc ccacagagtg gtatccctag aaggggagaag 180  
 taaggattgc cctcttcttt aaaatgaaag ccagctattt ttacagccct ttaactgcag 240  
 gtctgtctta ttttcttttc tctctctgga gctgagagtc agagggccct tctcctcctc 300  
 ctttcagccc ccaacactaa gctgatggat tgataaatac ctacagccct cgcctttctc 360  
 aaccacactg gcaagtcttc ttaggatctg atcccagttt tctggaagca atcctacccc 420  
 agcccattct tcccagagtc gagecctaat ccttctcact tctcagtgtc agagcagaaa 480  
 tgaatcctgg ggttgactgt gtccattcgg gttattagca gctaagaagc ccagacgagt 540  
 agtgtagagc gccttgggag cctcagtgag ggcactggga ctggcctcac tctcttgccc 600  
 ccagcctagt gggctttctc ctctgtctct cgggtggccc caggcaatcg actgcatcac 660  
 gcanggacgt gagttggagc ggccacgtgc ctgcccacca gaggtctacg ccacatgccc 720  
 gggctgctgg gcagcggagc cccagcaacg ccacagcatc aaggatgtgc acgcccgtgc 780  
 ca 782

<210> 202  
 <211> 714  
 <212> DNA  
 <213> Homo sapiens

<400> 202  
 ttccagagccc tatccatgag gggaattcct cacatgctgg ctttggggcc acagcagctg 60  
 ctggcccagg atgaggaggg ggacacgctc cttcacctgt ttgcggctcg ggggctgcgc 120  
 tggcgggcat atgctgcggc tgaggtgctc caggtgtacc ggcgtcttga cattcgtgag 180  
 cataagggca agacccctct cctggtggcg gctgctgcca accagcccct gattgtggag 240  
 gatctgttga acctgggagc agagcccaat gccgctgacc atcagggacg ttccggtcttg 300  
 cacgtggcgg ctacctacgg gctcccagga gttctcttgg ctgtgcttaa ctctggggtc 360  
 caggttgacc tggaagccag agacttcgag ggccctaccc cgctccacac ggccatcctg 420  
 gcccttaacg ttgctatgcg cccttccgac ctctgtcccc ggggtgctgag cacacaggcc 480  
 cgagacaggc tggatttgtt ccacatgttg ctgcaaatgg gtgctaatac caccatccag 540  
 gtgagcgggg atgtgggcgg tcagaccctg ggagatttgt tggaatgggg ccacttggtat 600  
 gtccgggagc tccaggcaaa tgctgacttt gcctcttctt tgctgcgtgc ccttgaacat 660  
 gttacttcac ttctctgtgc cttaagggtt ttttgcttgt ttctttgtca gtta 714

<210> 203  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 203

cggacgcgtg	ggcggacgcg	tgggtgggga	ccaagatggc	ggaccttgat	tgcctccga	60
agctgtcagg	ggtgcagcag	cgtctgagg	gggtgggagg	tggccgctgc	tccgaaatct	120
ccgtgagct	cattcgctcc	ctgacagagc	tgcaggagct	ggaggctgta	tacgaacggc	180
tctgcggcga	ggagaaagt	gtggagagag	agctggatgc	tcttttgaa	cagcaaaaca	240
ccattgaaag	taagatggtc	actctccacc	gaatgggtcc	taatctgcag	ctgattgagg	300
gagatgcaaa	gcagctggct	ggaatgatca	cctttacctg	caacctggct	gagaatgtgt	360
ccagcaaagt	tgcctcagctt	gacctggcca	agaaccgcct	ctatcaggcc	attcagagag	420
ctgatgacat	cttggaacctg	aagttctgca	tggatggagt	tcagactgct	ttgagga	477

&lt;210&gt; 204

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

gcggtggaat	tccgggttcc	cgttctggt	tggcatatc	tctacagcta	tgtcactgtg	60
ggtgaactct	gggccttcac	cactggctgg	aacctcatcc	tctcctatgt	cattgggtaca	120
gccagtgtgg	cccgggcctg	gagctctgct	tttgacaacc	tgattgggaa	ccacatctct	180
aagactctgc	aggggtccat	tgcactgcac	gtgccccatg	tccttgacga	atatccagat	240
ttctttgctt	tgggcctcgt	gttgctgctc	actggattgt	tggctctcgg	ggctagttag	300
tgggccttgg	ttaccaaagt	gttcacaggc	gtgaaccttt	tggttcttgg	gttcgtcatg	360
atctctggct	tgtttaagg	ggacgtgcac	aactggaagc	tcacagaaga	ggactacgaa	420
ttggccatgg	ctgaactcaa	tgacacctat	agcttgggtc	ctctgggctc	tggaggattt	480
gtgcctttcg	gcttcgagg	aattctcgt	ggagcagcga	cctgtttcta	tgcatttgtt	540
ggtttcgact	gtattgtctac	cactggagaa	gaagcccaga	atccccagcg	ttccatcccg	600
atgggcattg	ggatctcact	gtctgtctgc	tttttgccgg	attttgtctg	ctcttctgca	660
ctcaccctga	tgatgcctta	ctaccagctt	cagcctgaga	gcctg		706

&lt;210&gt; 205

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

ggcttccatc	ctaatacgac	tcactatagg	gctcgagcgg	cgcggcgggc	aggtgctggg	60
tgttttggg	gcgaagtaag	tgctgtagat	aaagactttg	ggccaaatgg	agaagtaagg	120
tattcttttg	aaatgggtgca	gccagatttt	gagttgcatg	ccatcagtgg	ggaaattaca	180
aatactcatc	agtttgacag	ggagtctctt	atgaggcgga	gagggactgc	tgtgttttagc	240
tttacagtca	tagcaacaga	tcaggggatc	cctcagcctc	tcaaggatca	ggccactgta	300
catgtttaca	tgaaggatat	aaatgataat	gctcccaaat	ttttaaaaga	cttttaccac	360
gctacaatat	cagaatcagc	agccaatctg	acacaagtgt	taagagtatc	tgcctcagat	420
gttgatgaag	gtaataatgg	acttattcac	tattctataa	taaaaggaaa	tgaagaaaga	480
cagtttgcta	tagacagtac	ctctggtcag	gtaacactaa	ttggcaaatt	agactatgaa	540

gcaacacctg	cctattccct	tgtaattcaa	gcagtggatt	cagggacaat	ccccctcaat	600
tcaacgtgta	ctttaaatat	tgatatttta	gatgaaaatg	acaatacccc	tttctttccc	660
taaatacaaca	cttctttgtt	gatgttttgg	aaaacatgag	aattggtgaa	ctcggggcct	720
ctgggtactgc	aactgattcc	cgattcaggt	gacattgctg	atttatatta	caagtttact	780
gggactaaac	acccccccgg	aacttttagc	attagcccca	aacacttggg	agtatttttc	840
ttggcccaaa	aa					852

<210> 206  
 <211> 361  
 <212> DNA  
 <213> Homo sapiens

<400> 206						
ctgggtgattg	ctatgacctg	tatggagggg	agaagtttgc	cactttggct	gagttgggtcc	60
agtattacat	ggaacatcat	gggcaattaa	aagagaagaa	tggagatgtt	attgagctta	120
aaaatcctct	gaactgtgca	gacccactct	ctcaaagggtg	gtttcatgga	cacctctctg	180
gaaaagaagc	agagaaattg	ttaactgaaa	aaggaaagca	tagtagcttt	cttgtacgag	240
agagccagag	ccaccctgga	gattttgttc	tctccgtgtg	caccggtgat	gacaaaggag	300
agagcaatga	cggcaagtct	aaagtgactc	atgtcatgat	tcactgtcag	gaactgaaat	360
c						361

<210> 207  
 <211> 2483  
 <212> DNA  
 <213> Homo sapiens

<400> 207						
ataaaatgga	catagtagta	ggacttacct	cccagggctg	tggttataga	ggttttgtaa	60
gaattaaatg	acatcatcca	tgtaaagcat	atagcagaat	gcctggcaca	tagatgccct	120
tagtgaattt	ttgctgttgt	tgtgattctt	ttgggagcag	tcatagtaac	atattctcat	180
atgttgggtat	gttctttcat	attgcattgt	cttatgaata	gattctggaa	acaaaaatgg	240
aggaaatgat	gataagacta	agaatgctga	gaggaactat	ttaaattgtt	tacctgggga	300
attttatatt	acacggcatt	ctaattctct	agaaatccat	gttgctttcc	atctctgtgt	360
ggatgaccat	gtgaaatcgg	gaaacatcac	tgctcgtgat	cctgccatta	tgggactccg	420
aaatatactc	aaagtttgct	gtacccatga	catcacaaca	ataagcattc	ctctcttgct	480
ggtacatgat	atgtcagagg	aaatgactat	accctgggtg	ttaaggagag	cggaaactgt	540
gttcaagtgt	gtcaaagggt	tcattgatga	aatggcttca	tgggatggag	gaatttctag	600
gacagtgcac	tttctagtac	cacagagtat	ttctgaagaa	atgttttata	aacttagtaa	660
catgcttccc	cagatcttcc	gagtatcatc	aacactcact	ctgacatcca	agcactaaac	720
ccttatagat	tgacatgctg	gcagaagatg	attgttaaac	tctccaggaa	cttgtgtcat	780
gctgggaatc	tgtcaagcaa	aagatgcccc	gaaagagaac	ttgcagctca	atccacaaat	840
caagatacat	gtgtgtgaaa	cccattccaa	aaatttatat	actggcacia	actggtggat	900
caacccttaa	cttaaacact	taaagtctct	ttatgaattt	ctcttttttt	cttctctgtg	960
ttacctgtgg	aatattaggt	aatctaaaa	tttttattta	ttcacacagg	gacacttggg	1020
gggaaaggga	aacttgatta	tatttacatg	ggagggcatt	tgactttttt	caaggagggc	1080
ttggacttcg	tcttcagggtg	gcaatcctta	attaacata	caaacaaaat	tttcctttta	1140
ctttctttgc	caaaacaaaa	tgtaaaagca	ctgaaatata	cattgcaagt	acaaatttcc	1200
tgtgaaaatc	tttttataga	aacacaaatg	tataagacaa	atgtgcttgt	tcttttaa	1260

tctcctgttt	cagaatctct	ttttaatcta	ctcctaagga	tgtacaagtt	agagtcagaa	1320
gacgttttgg	atTTTTtccc	tctctctcat	cctcccgtg	tgcccttgca	cttgcatatt	1380
aataacatTT	catggactgg	gaaatagtgt	tctTTTTtgc	aagcttgatg	tcaagttagt	1440
ctaaaccagc	acctggcagt	atTTtagtgc	tcatcaacat	tgtgacaatc	acacaaggaa	1500
gatcattttct	acattttctgt	cctccctgcg	ttctcagctt	gcttaaccat	tcctctacct	1560
cttgcatTTT	tttgcggata	aatgtatccc	cattttctgct	tctctgtttc	ccctcctttt	1620
ccattgtttt	tccttatggg	actactttct	caggtgctac	atatcatata	tttgtcccat	1680
ctataacata	tttaaatgct	ataagtagta	actccattaa	acaaaggcat	ttacaaaagc	1740
acacaggtga	ttagaaaagc	aatagtttca	tcaattccaä	gttatgtgga	tattgttaact	1800
ggccacaaga	atgaaatgga	gggcatttgg	tgtcataaga	tggcatgtct	tgatgacaag	1860
aaacaaaacg	cccttcatta	atatgcctca	gtgtaataac	tattatagaa	actgttggca	1920
agcagagtgc	tttcctataa	cagaatgtgt	cttaattttc	tacttgaggg	aaaggtttgt	1980
ccaggtaaca	acactaaaga	caaccctaag	aacaccact	ccagcagtat	gtccattaga	2040
cactaaaact	ctccaaatta	tttgtcaggg	agcctggcga	ttctgccaag	aaggcaggtg	2100
ttttgccctt	agagcctata	cagttctctt	ggagaaattg	tctttcaggc	accactgtta	2160
atcactgaga	ctgattctaa	tgcaaagcag	ggaagacaga	ggcagaaaacc	aggagagtgg	2220
tagatcagtg	cagcccagat	atcggaatgg	aggagcaaag	tttcattcac	ggatgtttgt	2280
tgaatgctgc	tgcccaactc	ttcctttgtc	acctctaggc	tattccacta	agttacttat	2340
aaactgggtg	ctttaactga	gggctgtgta	aaggtaactat	ttggcatgtg	aagtcaggat	2400
aaatTTtatcg	aatgtccgtt	ttccacatgc	aactgtgtta	cagaagtagt	aaaattggaa	2460
gaatcatgtt	tatggtgtta	cca				2483

&lt;210&gt; 208

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 208

caagcatcct	gcccgcctg	ctggtgacca	tcctgatctt	catggaccag	cagatcactg	60
ccgtcattgt	caaccggaag	gagaacaaac	tgaagaaggc	tgccggctac	catctggacc	120
tgttctgggt	gggcatectc	atggctttgt	gtccttttat	ggggctcccc	tggtacgtgg	180
ctgccacggt	catctccatc	gcccacatcg	acagcctcaa	gatggagaca	gagaccagtg	240
cccctgggga	gcagccccag	tttctgggag	tcagggaaca	gagagtaacc	ggcatcatcg	300
tcttcatect	gacgggaatc	tctgtcttcc	tggctcccat	cctaaagtgt	atccccctgc	360
cggtgc						366

&lt;210&gt; 209

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 209

cggcgttca	cgcgtagagg	caggcagtg	gaatggaatg	ctcattgatg	gtggtagcca	60
gatagtaaaa	gttcaagggc	acgtgatgg	tacaacgata	aataagtctg	gctctcagga	120
cgtagtacaa	ggaagtctgg	caacgaacac	aaccataaat	ggtggctgcc	agtatgttga	180
acagagcaca	gtagaaacaa	caaccattaa	aaatggcgg	gagcaaagag	tatatgagag	240
ccgtgcgctg	gacacgacga	ttgaaggcgg	aactcagctc	ctgaatagta	agtcaacggc	300
aaaaaatacy	catatctatt	ctggtggcac	gcaaattgtt	gataacacca	gcacctcgga	360

tggtattgaa	gtttattctg	gtggcgtgct	tgatgttagg	ggcgttacgg	caacaaatgt	420
taccacgac	gatgggtgca	ttttaaaaa	taacactaac	ggtagcgacg	tgagcgggtac	480
gaatagtga	ggcgcattct	ccatccacaa	tcacgtggca	gacaatgtgt	tgctggaaaa	540
cggtgggtcat	ttagacataa	acgcatatgg	ttcg			574

&lt;210&gt; 210

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(383)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 210

tttttctctt	ccatccagct	gactgatgat	cagggccccc	tcctgatgac	caactgtagcc	60
atgcctgtgt	ttagtaagca	gaacgaaacc	agatcgaagg	gcattcttct	gggagtgggt	120
ggcacagatg	tcccagtga	agaacttctg	aagaccatcc	caaatacaa	ggtaatgaat	180
gacctaatcc	ctgaaatcaa	agcaacagag	atgcccagag	cctgttttcc	acaaagttca	240
ggcttcaaac	tctactttgg	agcgatgttt	ttgctcacca	ctattacagc	ctgttagctt	300
gtctttatac	catctgcaca	gttattttaa	aggnnnnnnn	nnnattattt	acaaggactg	360
gctgtttttc	ttattttac	cct				383

&lt;210&gt; 211

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

tttctgtgtc	aggaactggc	accaatgcgt	gttacatgga	ggacatgagc	aacattgacc	60
tggtggaggg	cgacgagggc	aggatgtgca	tcaacacaga	gtggggggcc	ttcgggggacg	120
acggggccct	ggaggacatt	cgcactgagt	tcgacaggga	gctggacctc	ggctctctca	180
accaggaaa	gcaactgttc	gagaagatga	tcagtggcct	gtacctgggg	gagcttgtca	240
ggcttatctt	gctgaagatg	gccaaaggctg	gcctcctgtt	tggtgggtgag	aaatcttctg	300
ctctccacac	taagggcaag	atcgaaacac	ggcacgtggc	tgccatggag	aagtataaag	360
aaggccttgc	taataacaaga	gagatcctgg	tggacctggg	tctggaaccg	tctgaggctg	420
actgcattgc	cgtccagcat	gtctgtacca	tcgtctcctt	ccgctcggcc	aatctctgtg	480
cagcagctct	ggcggccatc	ctgacacgcc	tccggggagaa	caagaagggtg	gaacggctcc	540
ggaccacagt	gggcattggac	ggcacccctct	acaagataca	ccctcagtac	cc	592

&lt;210&gt; 212

&lt;211&gt; 2166

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 212

```

tttcgttgca attgcaacga atggtgttgt gctgtctggt ggctcctact acatgatttc      60
caggtctctg gggccagagt ttgggggtgc cgtggggcctc tgcttctacc tgggcactac      120
ctttgcagga gccatgtaca tcctgggcac catcgaaatc ctgctggcctt acctcttccc      180
agccatggcc atcttcaagg cagaagatgc cagtggggag gcagcagcca tgctgaacaa      240
catgctgtgt tacggcacct gtgtgctcac ctgcatggcc actgtggtgt ttgtgggtgt      300
caagtatgtc aacaagtttg cccttgtctt cctgggttgt gtcactcctc ccatcctggc      360
catctatgct ggggtcatca agtctgcctt cgacccaccc aacttcccga tctgcctcct      420
gggtaaccgc acgctgtctc gccatggcct tgatgtctgt gccaagctgg cttgggaagg      480
aaatgagacg gtgaccacac ggctatgggg ccttttctgc tcctctcgct tcctcaacgc      540
cacctgtgat gaatacttca cccgaaacaa tgtcacagag atccagggca tccctggtgc      600
tgccagtggc ctcatcaaag agaacctctg gagctcctac ctgaccaagg gcgtgattgt      660
ggagaggagt gggatgacct cgggtggcct ggccgatggc actcctatcg acatggacca      720
cccttatgtc ttcagtata tgacctcta cttcacctg ctggttggca tctacttccc      780
ctcagtcaca gggatcatgg ctggttctaa ccgctctggg gacctgaggg atgccagaa      840
gtcaatcccc actggcacca tcctggccat cgccaccacc tctgctgtct acatcagctc      900
cgttgttctg tttggggcct gcattgaggg ggtcgtcctg cgggacaagt ttggcgaagc      960
tgtgaatggc aacctcgtgg tgggcactct ggccctggcca tctccatggg taattgtcat     1020
cgcatccttc ttctccacct gtggggctgg gctgcagagc ctcacggggg cccacgcctc     1080
gctgcaggcc atctcgaggg atggcattgt gcccttctg caggtctttg gccatggcaa     1140
ggccaatgga gagccgacct gggccctgct cctgactgcc tgcactctcg agattggcat     1200
cctcattgca tccctcgacg aggtggcccc catcctctct atgttcttcc tgatgtgcta     1260
catgtttgtg aatctggcct gtgcagtga gacgctgctg aggacacca actggaggcc     1320
acgctttcga tattaccact ggacctctc cttcctgggc atgagcctct gcctggccct     1380
catgttcacg tgctcctggt attatgcaat ggtagccatg ctcatgtctg gactcatcta     1440
caagtacatt gagtaccgtg gggcaaagaa ggagtggggc gatgggatac gaggtctgtc     1500
tctcagtgcc gctcgctatg ccctcttacg cctggaggaa gggcccccac acaccaagaa     1560
ctggaggcca cagctgctgg tgctggtgcg tgtggacca gaccagaatg tgggtgcacc     1620
ccagctgctc tcactgacct ccagctgaa ggcagggaag ggcctgacca tcgtgggctc     1680
tgtccttgag ggcacctttc tggaaaatca tccacaggcc cagcgggcag aagagtctat     1740
caggcgccctg atggaggcag agaaggtgaa gggcttctgc caggtggtga tctcctccaa     1800
cttgcgctgat ggcgtgtccc atctgatcca gtctgggggc ctcggggggc tgcagcacia     1860
cactgtgctt gttggctggc ccgcgaactg gcgccagaag gaagatcatc agacgtggag     1920
gaacttcatt gagctggtcc gggaaaccac agctggccac ttagccctgc tggtcaccaa     1980
gaacgtttcc atgtttcctg ggaaccttga gcgcttctct gaaggcagca tgcaccgttg     2040
ggggattggg cacgatggag gcatgctcat gctggtgccc ttcctgctgc ggcaccacia     2100
ggtctggcgg aagtgaaga tgcgtatctt cactgtggcc cagatggttg acatgcatgc     2160
catgag

```

&lt;210&gt; 213

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (392)

&lt;223&gt; n = a, t, c or g

&lt;400&gt; 213

ttctatctga	ggctactgtc	ttttttctgc	tttcaggagc	atgagaagag	gtgttggagc	60
gttgacttta	atttgatgga	tcctaaactc	ttggcttcag	gttctgatga	tgcaaaaggt	120
actgtttgaa	tctctttctc	agcacctcct	tctccctggc	cctcttaact	gtaattcctt	180
tcacgggcag	aaatacaaat	atttactcaa	actcatgtca	gtcctttgtg	attactgatt	240
attattatct	ccannnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	300
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	360
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nn			392

<210> 214  
 <211> 425  
 <212> DNA  
 <213> Homo sapiens

<400> 214						
ggcgggaattc	aaaagcaatg	cacaggtctt	cctgtgacgg	gccgctactc	tctctgccct	60
cagtgggacg	gtcagccacc	catgccctgg	tccaggccca	gctgatctgc	tcaggagcca	120
ggcggggcat	gcacgctttt	attgtgcaa	tccggagtct	tcaggaccac	acccactgc	180
caggtaagcc	cataatgctc	cctcaaggaa	cctgcccagg	aggagagccc	aggtggcctc	240
cctgacctgg	ggccccagag	ggccacagga	gtagctaaga	catgtctccc	ttgggcaggg	300
agcgggtccag	ttggacagac	ttggtgctaa	ctggctaggt	gaacttgagc	aagatttagc	360
atctttctga	cctcagcttg	ttcacctgca	aaataggtag	aataatccca	gtgtcacagg	420
ctgct						425

<210> 215  
 <211> 608  
 <212> DNA  
 <213> Homo sapiens

<400> 215						
ctgcgggacc	ctcatcttgc	aggcccgggc	ctatgtggga	ccgcacgtcc	tggcagtggt	60
gaccgcgaca	gggttctgca	cggcaaaagg	gggcctgggtg	agctccatct	tgcaccccg	120
gcccatcaac	ttcaagttct	ataaacacag	catgaagttt	gtggctgccc	tctctgtcct	180
ggctctcttc	ggcaccatct	acagcatctt	catcctctac	cgaaaccggg	tgccctgtaa	240
tgagattgta	atccgggctc	tcgacctggt	gaccgtgggtg	gtgccacctg	cctgcctgc	300
tgccatgact	gtgtgcacgc	tctacgcccc	gagccgactg	cggagacagg	gcattttctg	360
catccacca	ctgcgcacga	acctgggggg	caagctgcag	ctgggtgtgt	tcgacaagac	420
gggcaccctc	actgaggacg	gcttagacgt	gatgggggtg	gtgcccctga	aggggcaggg	480
attoctgccc	ctgggtcccag	agcctgcgcg	cctgcctgtg	gggcccctgc	tccgagcact	540
ggccacctgc	catgccctca	gccgggtcca	ggacaccccc	gtgggcgacc	ccatggactt	600
gaagatgt						608

<210> 216  
 <211> 858  
 <212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 216

ctatctgggc	actggccact	gtggctttgt	attcctctaa	cgtggctgcc	aaggctgctt	60
ttcctttctg	ctcagactca	ataattegct	ccatatgggtg	actgcgttct	ttgagtggcc	120
ctatcatttc	ttgagcttcc	ttattgtctt	gttctgccat	tttcaaagta	ttgcttaaat	180
gctgctggac	accaagaagc	tgctcccgtt	caaaacgggc	attctcagcg	aggtccatgt	240
aacgttgctc	taattccata	tagcgccac	tttttacatc	ttcatctatg	acagattgaa	300
tacttccgct	ctcttctaga	tgagcatcac	atttcttatg	tcatagatga	agatgtaaaa	360
agtggcgct	atatggaatt	agagcaacgt	tacatggacc	tcgctgagaa	tgcccgtttt	420
gaacgggagc	agcttcttgg	tgtccagcag	catttaagca	atactttgaa	aatggcagaa	480
caagacaata	aggaagctca	agaaatgata	ggggcactca	aagaacgcag	tcaccatatg	540
gagcgaatta	ttgagtctga	gcagaaagga	aaagcagcct	tggcagccac	gttagaggaa	600
tacaaagcca	cagtggccag	tgaccagata	gagatgaatc	gcctgaaggc	tcagctggag	660
aatgaaaagc	agaaagtggc	agagctgtat	tctatccata	actctggaga	caaactctgat	720
attcaggacc	tcctggagag	tgtcaggctg	gacaaagaaa	aagcagagac	tttggtcagt	780
agcttgccagg	aagatctggc	tcatacccg	aatgatgcc	atcgattaca	ggatgccatt	840
gctaaaggta	gaggatga					858

&lt;210&gt; 217

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 217

agcacgctac	cgttttacc	tcagcgccag	gacgcagggtg	ggctctgggg	aagccgtcac	60
agaggagtca	ccagcacc	cgaatgaagc	tactccaacc	gcagctcctc	ccacattgcc	120
cccgactacc	gtgggtgcga	cgggcgctgt	gagcagtacc	gatgctactg	ccattgctgc	180
caccaccgaa	gccacaacag	tccccatcat	cccaactgtc	gcacctacca	ccatggccac	240
caccaccacc	gtgccacaa	ctactacaac	cactgctgcc	gccaccacca	ccacggagag	300
tcctcccacc	accacctccg	ggactaagat	acacgaatcc	gccccgatg	agcagtccat	360
atggaacgtc	acggtgctcc	ccaacagtaa	atgggccaa			399

&lt;210&gt; 218

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 218

ctgaagtcaa	cgcaagacga	aatcaaccag	gcaaggagca	aactgtccca	gctgcatgaa	60
agccgccagg	aggccacag	gagcctggag	cagtatgacc	aggtgctcga	tggagcccat	120
ggtgccagcc	tgaccgacct	ggccaacctg	agcgaaggcg	tctccctggc	agagaggggc	180
agttttggag	ccatggatga	tcctttcaaa	aataaagcct	tgttatttag	caacaacacg	240
caagagttgc	atccggatcc	tttccagaca	gaagaccctt	tcaaactctga	cccatttaaa	300

ggagctgacc	ccttcaaagg	cgacccgttc	cagaatgacc	cctttgcaga	acagcagaca	360
acttcaacag	atccatttgg	aggggaccct	ttcaaagaaa	gtgaccatt	ccgtggctct	420
gccactgacg	acttcttcaa	gaaacagaca	aagaatgacc	catttacctc	ggatccattc	480
acgaaaaacc	cttccttacc	ttcgaagctc	gacccctttg	aatccagtga	tcccttttca	540
tcctccagtg	tctcctcaaa	aggatcagat	ccctttggaa	ccttagatcc	cttcggaagt	600
gggtccttca	atagtgtctga	aggctttgcc	gacttcagca	ctattgaagg	tcgacgcggc	660
cg						662

&lt;210&gt; 219

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 219

cggacgcgtg	gggatcttgg	caatagctcc	caaccctcac	ttcgtgaggg	ccacgacaaa	60
cctgttttta	atggagctgg	aaagcctcat	tccagcacct	cttcaccaag	tgtcccaaag	120
acttctgcta	gcaggactca	gaaatctgct	gttgagcaca	aagccaaaaa	atctctgtcc	180
catcctagcc	attccaggcc	tgggcccatg	gtcaccctac	acaataaggc	taagagtcca	240
ggtgtcaggc	agccaggcag	cagctctagc	tcagcccttg	ggcagcccag	caagggggtt	300
gctcgaccca	cagttagtct	tggccctgtg	cctaggcgcc	agaatggcag	ctccagctca	360
ggacctgagc	gatcaatcag	tgggtccaag	aagccaacca	atgactcaaa	tcctcttagg	420
cggacagtca	gtggtacatg	tggccctgga	caacctgcaa	gcagctcagg	tggccctggg	480
cgaccatca	gtggttcagt	tagttctgca	agacccttgg	gcagctctcg	tggccctggc	540
cggcctgtga	gcagtcacca	tgaacttcga	cgaccagtga	gtggtctggg	ccccccgggg	600
cggctctgtca	gtggccctgg	gagatccata	agtggctcaa	ttccagctgg	acggactgtc	660
agtaattcag	tcccaggaag	accagtgagc	agcttgggac	ctgggcaaac	agttagtagc	720
tcaggtccca	ctataaagcc	taagtgcact	gt			752

&lt;210&gt; 220

&lt;211&gt; 582.

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

ttattattat	tttgcataga	gacaagcact	cactgtgtta	cccaggctgg	ttttgaactc	60
ctgagcttaa	tcagttctca	cctgctttgc	cctcccaaag	tgctatgatt	acagggtgtga	120
gccaccacgc	ttggccctgc	ccaggagtca	tttttgtatc	tacaggatc	ttcctatgct	180
gtagacagat	gccctttttc	aaggcaaaaa	ccctagccat	ttttctcttc	tccttcagag	240
tctgcaacat	cctctcaact	catccaagtg	actactgcct	ggtgctcttg	gggatgcagg	300
gaggcctgag	aaggccaatg	tctatacaga	aagttctaac	atagtgcact	gagtcaatgt	360
gggcacttta	aagccctttc	acctgccaa	tcacgaagca	cccttatagt	tgtgtttgta	420
aaatactggg	gggtttgaag	gggaaaagg	ataactccaa	ggtaccatct	ttgcatttca	480
gatccacaca	acttaaagat	ctgctgtcga	gtgaatgggg	aagtgggtcca	gagcagcaac	540
accaaccaga	tggtattcaa	gacagaggac	ctgatagcct	gg		582

<210> 221  
 <211> 440  
 <212> DNA  
 <213> Homo sapiens

<400> 221  
 ggaattcgat cagtagaagt ttgggggata tagaaacgaa ggttttctaa ctttttagctt 60  
 tcaaggagat tgtccggttg ggaaagcaag atatgaaaaa taaatatgtc aagaatataa 120  
 tccaaaacaa tctaattaag tgctagaagt ttgccatgga cagacaaagt gctacttggg 180  
 aaggaagttc cagaaacacc acagctgggt acattcttca ccactctgag tgggtggcagt 240  
 gacgcgttg ctttgtgaga atgggtgtgtc ttacttgaga aagtgtgtgt gttctgcctg 300  
 caggcatggg actcgctgtg ctggagaagt ggcagccgct gcaaacaatt cgcactgcac 360  
 agtcggaatt gctttcaacg ccaagatcgg aggtatggga aaccaactca cgtggatgta 420  
 gaaatgcgcc agttagctct 440

<210> 222  
 <211> 489  
 <212> DNA  
 <213> Homo sapiens

<400> 222  
 ccgacgattt cgtgaggcgg cagccagggtg gggttccagc cagagcacgc acgcacggag 60  
 ccgggagcat gcagcctgca ctgcggggga tgtgatgtc ggctctaact cgcctggctg 120  
 gcccgccacg gacgcctcag cttgcaacca tggtaacgtt tctggcgggg gacacccccg 180  
 ggagcccacc gcgatgggca gcctcctgggt gactgatgga cgagtgtcca cctcccagac 240  
 cgagagcgct tagtaggtcg gaggaagtgg agaggatgta acacgcccc agccgggagt 300  
 gaagccctga ggagctcctc ccccttctgt tcccaccctc aagtctgacg atgacacctc 360  
 caattttgat gaaccaaaga agaattcgtg ggtttcatcc tctccgtgcc agctgagccc 420  
 ctcaggcttc tcgggtgaag aactgccgtt tgtgggggtt tcgtacagca aggcactggg 480  
 gattcttg 489

<210> 223  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 223  
 ttctgtcgag cgccttgccg acctccacgc tgctgcgcc ccgcgcgcga aggtggcgct 60  
 cctcttgag gtgtgcagag atgtctatgc gggcctggct cgaggcgaga accaagatcc 120  
 cctggggggc gacgccttcc tgccggcgct gaccgaggaa ctcatctgga gcccgacat 180  
 tggggacacg cagctggacg tagagtttct tatggagctc ttagatccag atgagctgcg 240  
 gggagaggct ggggtactacc tgaccacgtg gtttggggcg ctgcaccaca ttgccacta 300  
 ccagcccga acagaccgcg ctccccgggg gctcagctcc gagggccgcg cctccctgca 360

ccagtggcac	cgcaggcgga	cgctgcacag	aaaggatcat	cccagagccc	aacagctgga	420
ctgaccctgg	ctggtcgaag	agccctggcc	agatgtcctg	tggacagacc	caatttctgg	480
cctcgtctgc	tgg					493

<210> 224  
 <211> 883  
 <212> DNA  
 <213> Homo sapiens

<400> 224						
agtgacctgg	aaacaagttc	tgatccagaa	ggtgaggatt	gggatgagga	agctgaggat	60
gatgggtttg	atagtgatag	ctcactgtca	gactcagacc	ttgaacaaga	ccctgaaggg	120
cttcaccttt	ggaactcttt	ctgcagtgtg	gacccctata	atccccagaa	ctttacagca	180
acaattcaga	ctgctgccag	aattgttctc	gaagagcctt	ctgattcaga	gaaggatttg	240
tctggcaagt	ctgatctaga	gaattcctcc	cagtctggaa	gccttcctga	gacccttgag	300
catagtctcg	gggaggaaga	tgactgggaa	tctagtgcag	atgaagcaga	gagtcttcaa	360
actgtgggaa	cttcattctg	ttaattctgg	atggaccctt	acaacccttt	aaattttaag	420
gctccttttc	aaacatcagg	ggaaaatgag	aaaggctgtc	gtgactcaaa	gaccccatct	480
gagtcatttg	tggccatttc	tgagtgtcac	accttacttt	cttctaaggt	gcagctgttg	540
gggagccaag	aaagtgaatg	tccagactcg	gtacagcgtg	acgttctttc	tggaggaaga	600
cacacacatg	tcaaaagaaa	aaaggtaacc	ttccttgaag	aagttactga	gtattatata	660
agtgggtgatg	aggatcgcaa	aggaccatgg	gaagaatttg	caagggatgg	atgcaggttc	720
cagaaacgaa	ttcaagaaac	agaagatgct	attggatatt	gcttgacatt	tgaacacaga	780
gaaagaatgt	ttaatagact	ccaggaaca	tgcttcaaag	gacttaatgt	tctcaagcaa	840
tggtgagttg	gcagcctgta	gtcctagcta	gcatacacta	cct		883

<210> 225  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

<400> 225						
cggcgcgctc	tacggcatat	tctttttttg	gaactgtgga	gaatatggct	ccaaaagtgg	60
ttaatcgctc	aggtcatact	cagagtgcgt	actgggggtc	ttttgggggg	ttaatgggaa	120
ggtttgaaat	tgggattttt	ttaaagggga	aggagattgt	taagtgagga	tcaacaggga	180
atggtaaaga	aactgggggt	tttattttct	ttattttatg	ccctatgtaa	taaataacca	240
aaaaacatta	ttgcgtgcag	tataaaagga	ctatgaaatc	tgtagctgc	gtctatctca	300
tcctaatttg	aaagggcaaa	aaaaaatatt	accatagatt	tcctgcta	agtaacaatc	360
taaagcatta	atggtgttgg	gtccttttgg				389

<210> 226  
 <211> 412  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 226

gggtttgttt	ttcttccagg	ccccatgtct	gtgggttttg	acttctctct	gccaggcatg	60
gagcatgtct	atgggatccc	tgagcatgca	gacaacctga	ggctgaaggt	cactgagtga	120
gtcctatgg	gacatcagga	agatggaggt	gggcaggaag	gagtcaggcc	tttagggaga	180
tggtgtgca	tattggatac	tctaggcaag	catgggtcat	ttcttgtgtc	cagaatcacc	240
tttggtgata	gaaaattttt	tgagaaagga	caagaggagc	ctttgcttat	ctctcaccgt	300
tgtctgtgga	gtggtgttag	catataacgc	agcctggggc	cagttagcag	cccaagtctg	360
tctgtttgcc	tgcaggggtg	gggagccata	tgcctctac	aatttggatg	tg	412

&lt;210&gt; 227

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

gggagtga	gccaggcac	tgacctggac	acccgcaact	gtaccagtga	cctctgtgta	60
cacactgctt	ctggccctga	ggacgtggcc	ctctatgtgg	gcctcatcgc	cgtggccgctc	120
tgcttggtcc	tgctgctgct	gtccctcatc	ctcgtttatt	gccggaagaa	ggaggggctg	180
gactcagatg	tggtgactc	gtccattctc	acctcaggt	tccagcccgt	cagcatcaag	240
cccagcaaag	cagacaaccc	ccatctgctc	accatccagc	cggacctcag	caccaccacc	300
accacctacc	agggcagtct	ctgtccccgg	caggatgggc	ccagcccaa	gttccagctc	360
accaatgggc	acctgctcag	ccccctgggt				390

&lt;210&gt; 228

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 228

cttattttata	atgaagatat	gatttgttgg	attgaatcaa	gagaatcttc	aatcaactc	60
aatgtatcc	agataacaaa	agcaggagga	ttaacagatg	aatggacaat	caatattctt	120
caatccttcc	acaatgtgca	acaaatggcg	attgactggc	tcactcgaaa	tctctatttt	180
gtggaccatg	tgggtgaccg	gatctttgtt	tgtaattcca	acggttctgt	atgtgtcacc	240
ctgattgatc	tggagcttca	caatcctaaa	gcaatagcag	tagatccaat	agcaggaaaa	300
cttttcttta	ctgactacgg	gaatgtcgcc	aaagtggaga	gatgtgacat	ggatgggatg	360
aaccgaacaa	ggataattga	ttcaaagaca	gagcagccag	ctgcactggc	actagacctc	420
gtcaacaaat	tggtttactg	ggtagatctt	tacttggact	atgtgggagt	agtggactat	480
caaggaaaaa	atagacacgc	tgtcattcaa	ggcagacaag	tcagacatct	ttatggtata	540
actgtgtttg	aagattattt	gtatgcaacc	aattctgata	gctacaatat	cgtaaggata	600
agccgattta	atgggactga	tattcactca	ttaatataaa	ttgagaatgc	ttggggaatc	660
cgaatttatc	aaaaaagaac	tcaaccaaca	gtcagaagcc	atgcatgtga	agtcgatcca	720
tatggaatgc	cagggggctg	ttcacacatc	tgtctactca	gcagcagtta	cacgaaa	777

<210> 229  
 <211> 486  
 <212> DNA  
 <213> Homo sapiens

<400> 229  
 tttcgtctgg gaaccgcgag cctggggact cctccggcgg gggcgctggg ggcgggctgc 60  
 cgtcccctgg ggagcaggag ctgagccggc gcttgacgag cctgtatccc gcggtcaacc 120  
 agcaagagac tccgctgccg cgctcctgga gcccgaagga caaatataac tacattgggtc 180  
 tctcccaggg caacctccgc gtccactaca aaggatcatg caaaaatcac aaagatgcgg 240  
 cctcagtgcg tgccaccac cccatacctg ctgcctgtgg catttattac tttgaagtga 300  
 agattgtcag caaaggaaga gatggttaca tgggaatagg actctcggct caaggcgtca 360  
 acatgaacag acttcctggt tgggacaaac attcctatgg ttaccatggt gatgatgggc 420  
 attcgttctg ctctcgggg actggccagc cctatggtcc cacattcacc acaggagacg 480  
 tgatcg 486

<210> 230  
 <211> 396  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
 tttttttttt ttaagatggg gtctcgtctc gtcaccagc ctggagtgcg gtgggtgtgat 60  
 gtcagctcac tgcaagctcc gcctcccagg ttcacactat tctgcctcag cctcccaagt 120  
 agctgggact acaggtgcgt gccaccatgc ccggctaatt tttttgtatt tttagtagag 180  
 acgggggttc accgtgttag ccagtatggt cttgatctcc tgacctcgtg atccacctgc 240  
 ctgggcctcc caaaagtgc tggattacag gtgtgagctg ctgcgcctgg cttatgagtc 300  
 gtatgttctg atcctccctc ttgaagtgc cttctgtggt ctaaggaggg cctgaagggt 360  
 caggtaaaaa cttcagggtg accttcaact ggggtg 396

<210> 231  
 <211> 713  
 <212> DNA  
 <213> Homo sapiens

<400> 231  
 tcagctcagc ttggcacgag gaaagggtgt cttgtgtgcc ttgtcttttg tttactttgc 60  
 caaagcattg gcagaaggct atctgaagag caccatcact cagatagaga gaagggttga 120  
 tatcccttct tcaactgggtg gagttattga tggtagtttt gaaattggga atctcttagt 180  
 tataacattt gtttagctact ttggagccaa acttcacagg ccaaaaataa ttggagcagg 240

gtgtgtaatc	atgggagttg	gaacactgct	cattgcaatg	cctcagttct	tcatggagca	300
gtacaaatat	gagagatatt	ctccttcctc	caattccact	ctcagcatct	ctccgtgtct	360
cctagagtca	agcagtcaat	taccagtttc	agttatggaa	aaatcaaaat	ccaaaataag	420
taacgaatgt	gaagtggaca	ctagctcttc	catgtggatt	tatgttttcc	tgggcaatct	480
tcttcgtgga	ataggagaaa	ctcccattca	gcctttgggc	attgcctacc	tggatgattt	540
tgccagtga	gacaatgcag	ctttctatat	tgggtgtgtg	cagacgggtg	caattatagg	600
accaatcttt	ggtttcctgt	taggctcatt	atgtgccaaa	ctatatgttg	acattggcct	660
tgtaaaccta	gtcattttta	ggtggaagca	tgttacagca	cattatcgag	gaa	713

<210> 232  
 <211> 1067  
 <212> DNA  
 <213> Homo sapiens

<400> 232						
cagccttcca	aggtagggca	caccaaggcc	taaggaatca	gaaagggccc	gaggggtgggc	60
tgtgtcctgg	ctttcaggcc	ctggggcgac	caccagcctc	tgctcactct	gaggctccag	120
ccagggcgcc	aagcctcagg	accgtgggtg	gggcccagg	acactctgga	ccccgttcc	180
attcatgaga	ggcctcagc	acgccacgtg	tctgctgtga	cagcccgag	ggaggggtgga	240
agccttctgt	aaattccaca	tgtgggccga	gggcatgacg	tccttgatga	aggccgcgct	300
ggacctcacc	taccccatca	cgtccatggt	ctccggagcc	ggcttcaaca	gcagcatctt	360
cagcgtcttc	aaggaccagc	agatcgagga	cctgtggatt	ccttatttcc	ccatcaccac	420
cgacatcaca	gcctcggcca	tgcgggtcca	caccgacggc	tcctgtgtgc	ggtacgtgcg	480
tgccagcatg	tccctgtccg	gttacatgcc	ccctctctgt	gaccggaagg	acggacacct	540
gctgatggac	ggggggtaca	tcaacaacct	cccagcggat	gtggcccggg	ccatgggggg	600
aaaagtgggtg	atcgccattg	acgtgggcag	cagagatgag	acggacctca	ccaactatgg	660
ggatgcgctg	tctgggtggg	ggctgctgtg	gaaacgctgg	aacccttgg	ccacgaaagt	720
caaggtgttg	aacatggcag	agattcagac	gcgcctggcc	tacgtgtgtt	gcgtgcggca	780
gctggagggtg	gtgaagagca	gtgactactg	cgagtacctg	cgccccccca	tcgacagcta	840
cagcaccctg	gacttcggca	agttcaacga	gatctgcgaa	gtgggctacc	agcacgggag	900
cacggtgttt	gacatctggg	gccgcagcgg	cgtgtctggg	aagatgctcc	gcgaccagca	960
ggggccgagc	aagaagccc	cgagtgcggg	cctcacctgt	cccaacgcct	ccttcacgga	1020
ccttgccgaa	attgtgtctc	gcattgagcc	cgccaagccc	gccatgg		1067

<210> 233  
 <211> 704  
 <212> DNA  
 <213> Homo sapiens

<400> 233						
tttcgtgtga	gggagagccg	agggaaaccag	cgcggtgcct	agcggaaactc	cagggctgga	60
atcccagagac	acaagtgcac	ctgctagctg	ttagcaacttg	gcagacggag	ttctcctcta	120
gggtagttct	aactttgggt	aataatgttt	gtcagctacc	tgatattaac	attgctccac	180
gttcaaacag	cagtgttagc	aagacctggg	ggagagagca	ttggctgtga	tgactactta	240
ggctccgaca	aagtcgtgga	caaagtgtgg	gtgtgtggag	gagacaacac	gggctgtcag	300
gttgtgtcgg	gcgtgtttta	gcatgccctc	accagcctgg	gctaccaccg	cgtcgtggag	360
attcccagg	gagccacgaa	aatcaacatc	acggagatgt	acaagagcaa	caactatttg	420
gccctgagaa	gtcgtttctg	acgctccatc	atcaatggga	actgggcaat	tgatcgacca	480

ggaaaaatcag	agggcggagg	gaccatgttc	acctacaagc	gtccaaatga	gatttcgagc	540
actgccggag	agtccttttt	ggcgggaagg	cccaccaacg	agatcttgga	tgtctacgtg	600
agtttgatg	tttctggact	gttctttgga	ttttgaatct	tgtcacttct	aaggaacata	660
ctctgaacaa	ataagcaaca	aatcattgcc	catactcaat	aaaa		704

<210> 234  
 <211> 420  
 <212> DNA  
 <213> Homo sapiens

<400> 234						
atttcaggag	ggaccagaag	cgcaggcccg	ctcaggagga	attacaactt	catcgccgcg	60
gtggtggaga	aggtggcgcc	atcggtggtt	cacgtgcagc	tgtggggcag	gaaccagcag	120
tggattgagg	tgggtgctcca	gaatggggcc	cgttatgaag	ctggtgtcaa	ggatattgac	180
cttaaatgg	atcttgcggt	gattaagatt	gaatcaaatg	ctgaacttcc	tgtactgatg	240
ctgggaagat	catctgacct	tcgggctgga	gagtttgtgg	tggctttggg	cagcccattt	300
tctctgcaga	acacagctac	tgcaaggaatt	gtcagcacca	aacagcgagg	gggcaaagaa	360
ctggggatga	aggattcaga	tatggactac	gtccagattg	atgccacaat	taactatggg	420

<210> 235  
 <211> 1057  
 <212> DNA  
 <213> Homo sapiens

<400> 235						
cccacgcgtc	cgagaactca	aagaaattct	ggataggaaa	gggcatttct	cagagaatga	60
gacaaggtgg	atcattcaaa	gtctcgcatc	agctatagca	tatcttcaca	ataatgatat	120
tgtacataga	gatctgaaac	tggaaaatat	aatggttaaa	agcagtctta	ttgatgataa	180
caatgaaata	aacttaaaaca	taaagggtgac	tgattttggc	ttagcgttga	agaagcaaag	240
taggagtga	gccatgctgc	aggccacatg	tgggactcct	atctatatgg	cccctgaagt	300
tatcagtgcc	cacgactata	gccagcagtg	tgacatttgg	agcataggcg	tcgtaatgta	360
catgttatta	cgtggagaac	cacccttttt	ggcaagctca	gaagagaagc	tttttgagtt	420
aataagaaaa	ggagaactac	atthtgaaaa	tgacgtctgg	aattccataa	gtgactgtgc	480
taaaagtgtt	ttgaaacaac	ttatgaaagt	agatcctgct	cacagaatca	cagctaagga	540
actactagat	aaccagtggg	taacaggcaa	taaactttct	tcggtgagac	caaccaatgt	600
attagagatg	atgaaggaat	ggaaaaataa	cccagaaagt	gttgaggaaa	acacaacaga	660
agagaagaat	aagccgtcca	ctgaagaaaa	gttgaaaagt	taccaaccct	ggggaaatgt	720
ccctgagacc	aattacactt	cagatgaaga	ggaggaaaaa	caggtaggaa	gaatcattgc	780
tgcattttct	ccaagtgtaa	aataccctca	ccacacctgg	aacatttttt	tgcaaatctg	840
tctttttgtt	gttagtttgt	aacaaaggcc	gagcgttata	tagcaagtaa	agttctttct	900
gccttataag	gctagcatga	tttagcgagg	tggcctacat	gtttatttta	aggttgggtga	960
ttatgtaggg	caggtgtctg	caaacttttt	ctgtaaggga	acaaacagta	aatatttttag	1020
gctttgtggg	ccctagtagt	ctttgtcaca	actactc			1057



<210> 236  
 <211> 467  
 <212> DNA  
 <213> Homo sapiens

<400> 236  
 ttgagtatta gtgtcagtga tgtgtctctc tctgatgaag gacagtacac ctgttcttta 60  
 tttaacaatgc ctgtcaaaac ttccaaggca tatctcaccg ttctgggtgt tctgaaaag 120  
 cctcagatta gtggattctc atcaccagtt atggagggtg acttgatgca gctgacttgc 180  
 aaaacatctg gtagtaaac tgcagctgat ataagatggt tcaaaaatga caaagagatt 240  
 aaagatgtaa aatattttaaa agaagaggat gcaaatacgca agacattcac tgtcagcagc 300  
 aacttgagct tccgagtggg ccggagtgat gatggagtgg cggatcatctg cagagtagat 360  
 cagcaatccc tcaatgccac ccctcaggta gccatgcagg tgctagaaat gcactataca 420  
 ccatcagtta agattatacc atcgactcct ttccacaag aaggacg 467

<210> 237  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(416)  
 <223> n = a, t, c or g

<400> 237  
 ggtacaacca gaaagtggat ctcttcagcc tgggaattat cttctttgag atgtccctatc 60  
 accccatggt cacggcttca gaaaggatct ttgttctcaa ccaactcaga gatccactt 120  
 cgcctaagtt tccagaagac tttagcatg gagagcatgc aaagcagaaa tcagtcactt 180  
 cctggctggt gaaccacgat ccagcaaac ggccacagc cacagaactg ctcaagagtg 240  
 agtctctgcc cccaccccag atggaggagt cagagctgca tgaagtgtg caccacacgc 300  
 tgaccaacgt ggatggaaag gcctaccgca ccattgatgg gccagatct ttctggcagc 360  
 gcatctcccc tgccatcgnt ttacacctat gaccagcgac atattgaagg gcaact 416

<210> 238  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 238  
 ggaccaggac tacaagtacg acagtacctc agacgacagc aacttcctca accccccag 60  
 ggggtgggac catacagccc caggccaccg gacttttgaa accaaagatc agccagaata 120  
 tgattccaca gatggcgagg gtgactggag tctctggtct gtctgcagcg tcacctgcgg 180  
 gaacggcaac cagaaacgga ccggtcttg tggctacgag tgcactgcaa cagaatcgag 240

gacctgtgac	cgtccaaact	gcccaggaat	tgaagacact	tttaggacag	ctgccaccga	300
agtgagtctg	cttgcgggaa	gcgaggagtt	taatgccacc	aaactgtttg	aagttgacac	360
agacagctgt	gagcgctgga	tgagctgcaa	aagcgagttc	ttaaagaagt	acatgcacaa	420
ggtgatgaat	gacctgcca	gctgcccctg	ctcctacccc	actgaggtgg	cctacagcac	480
ggccgacatc	ttcgaccgca	tcaagcgcaa	ggacttccgc	tggaaggacg	ccagcgggcc	540
caaggagaag	ctggagatct	acaagcccac	tgcccggtac	tgcattccgt	ccatgctgtc	600
cctggagagc	accacgctgg	cggcacagca	ctgctgctac	ggcgacaaca	tgcagctcat	660
caccaggggc	aagggggcgg	gcacgcccac	cctcatcagc	accgagttct	ccgcggagct	720
ccactacaag	gtggacgctc					739

<210> 239  
 <211> 611  
 <212> DNA  
 <213> Homo sapiens

<400> 239		
ggaatcgga	gaaaatggag agagtgcaat ggacagcaca gtggccaaag aaggcactaa 60	
tgtaccatta	gttgctgctg gtccttgtga tgatgaaggc attgtgacta gcacaggcgc 120	
aaaagaggaa	gacgaggaag gggaggatgt tgtgactagt actggaagag gaaatgaaat 180	
tgggcatgct	tcaacttgta cagggtagg agaagaaagt gaaggggtct tgatttgtga 240	
aagtgcagaa	ggggacagtc agattggtac tgtggtagag catgtggaag ctgaggctgg 300	
agctgccatc	atgaatgcaa atgaaaataa tgttgacagc atgagtggca cagagaaagg 360	
aagtaaagac	acagatatct gctccagtgc aaaagggatt gtagaaagca gtgtgaccag 420	
tgcagtctca	ggaaaggatg aagtgcacac agttccagga ggttgtgagg gtcctatgac 480	
tagtgctgca	tctgatcaaa gtgacagtca gctcgaaaaa gttgaagata ccactatttc 540	
cactggcctg	gtcgggggtg gttacgatgt tcttgtatct ggtgaagtcc cagaatgtga 600	
agttgtctac	a	611

<210> 240  
 <211> 1090  
 <212> DNA  
 <213> Homo sapiens

<400> 240	
tttttttttt	ttaagcttga aataaaatth ttattttgtt ttgaattaaa tcaaccatga 60
ttattcacag	tgcagtaagt gtgtatcatc tgtttgatat ttatcatatta cagttttgat 120
agtgtctctc	agtctgcgaa atcttctttg ggtggaaatg atgaactgtc agctactttc 180
ttagaaatga	aaggacatth ctatatgtat gctggtcttc tgctcttgaa gatgggtcag 240
catggtaata	atgttcaatg gcgagctctt tctgagctgg ctgcgttggt ctatctcata 300
gcatttcagg	taagtcttcc acttggagca attgacatth cacggagtct tgatgtgttt 360
taaatgaagg	tgtgctctgg tatgtaatga caaatatgtg acaaacctgt ggaattaaag 420
ttaaaatgaa	atagtcaatt tgatacagtg gaaaataact aagcatacac aatactggtg 480
aggctggtga	aacagggatg ttgaatgcac tcttgtcgaa agcctgcatt gccatgattt 540
gtttgtagac	aaatttgaag agtttgatct ttttactctg ccatttttgg gaacatgata 600
aagatgtaat	ctcgtattat gggtaaagct tgattcaaaa agatgtgtta cttggacaaa 660
atcctaataa	gtagacgtag ggcaatggct ttatagccta tgatagaaga atatgattgc 720
aatttaacat	gttaattgaa acacatgtat ataacattta tgactgtatt gtgtatatgt 780
aacagtatat	ctattaatct ttgaaaacat aaaacctttt cttatttttt atttttttat 840

ttttttttga	gaccaagtct	ctctctgtcg	ccaggctgga	gtgcagtggg	gtgatctcgg	900
ctcactgcag	cctccacctc	ctgggttcga	gtgattctcc	tgccctcagcc	tcccagatag	960
ctgggactac	aggcccatgc	taccaagccc	agctaatttt	ttgtattttt	aatagagatg	1020
gggtttcacc	atgttgGCCA	ggatggtcgc	aatctcttga	cctcttgatc	tacctgcctt	1080
ggtctcccaa						1090

<210> 241  
 <211> 680  
 <212> DNA  
 <213> Homo sapiens

<400> 241		
gcaacaccca	tcccaggaaa agccacaagt cctgaccccc agccccagga agcagaagct 60	
gaacagaaag	tacagggtccc accatgacca gatgatctgc aagtgcctct ccctgagcat 120	
atcctactcc	gctaccattg gcggcctgac caccatcatc ggacacctca ccagcctcat 180	
cttctctgga	cacttcaaca accagtatcc agcctcagag gtggtgaact ttggcacctg 240	
gttctctctc	agcttcccca tateccctcat catgctgggt gtcagctggg tctggatgca 300	
ctggctgttc	ctgggctgca attttaaaga gacctgctct ctgagcaaga agaagaagac 360	
caaaagggaa	cagttgtcag agaagaggat ccaagaagaa tatgaaaaac tgggagacat 420	
tagctaccca	gaaatggtga ctggattttt cttcatcctg atgaccgtac tgtggtttac 480	
ccgggagcct	ggctttgtcc ctggctggga ttctttcttt gaaaagaaag gctaccgtac 540	
tgatgccaca	gtctctgtct tccttggett cctcctcttc ctcattccag cgaagaagcc 600	
ctgctttggg	aaaaagaatg atggagagaa ccaggagcac tcaactgggga ccgagcccat 660	
catcacgtgg	aaggacttcc	680

<210> 242  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

<400> 242		
cttgaaagag	aaggggacaa aggaacacca gtattaagag gattttccag tgtttctggc 60	
agttggtcca	gaaggatgcc tccattcctg cttctcacc	gctcttcat cacaggcacc 120
tccgtgtcac	ccgtggccct agatccttgt tctgcttaca tcagcctgaa tgagccctgg 180	
aggaacactg	accaccagtt ggatgagtct caaggctctc ctctatgtga caaccatgtg 240	
aatggggagt	ggtaccactt cacgggcatg gcgggagatg ccatgcctac cttctgcata 300	
ccagaaaacc	actgtggaac ccacgcacct gtctggctca atggcagcca cccctagaa 360	
ggcgacggca	ttgtgcaacg ccaggcttgt gccagcttca atgggaactg ctgtctctgg 420	
aacaccacgg	tggaaagtaa ggcttgccct ggaggctact atgtgtatcg tctgaccaag 480	
cccagcgttt	g	491

<210> 243  
 <211> 983  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

tgcgcccgca	ccatgagcga	catccgccac	tcgctgctgc	gccgcgatgc	gctgagcgcc	60
gccaaggagg	tggtgtacca	cctggacatc	tacttcagca	gccagctgca	gagcgcgcgcg	120
ctgcccacgc	tggacaagg	ccccgtggag	ctgctggagg	agttcgtgtt	ccagggtgccc	180
aaggagcgca	gcgcgcagcc	caagagactg	aattcccttc	aggagcttca	acttcttgaa	240
atcatgtgca	attattttcca	ggagcaaacc	aaggactctg	ttcggcagat	tattttttca	300
tcccttttca	gccctcaagg	gaacaaagcc	gatgacagcc	ggatgagctt	gttgggaaaa	360
ctggtctcca	tggcggtggc	tgtgtgtcga	atcccggtgt	tggagtgtgc	tgctctctgg	420
cttcagcgga	cgcgcgtgg	ttactgtgtg	aggtagcca	aggcccttgt	agatgactac	480
tgctgtttgg	tgccgggac	cattcagacg	ctgaagcaga	tattcagtgc	cagcccagaga	540
ttctgctgcc	agttcatcac	ctcgcgttacc	gcgctctatg	acctgtcatc	agatgacctc	600
attccaccta	tggacttgct	tgaatgatt	gtcacctgga	tttttgagga	cccaagggtg	660
attctcatca	ctttttttaa	tactccgatt	gcggccaatc	tgccaatagg	attcttagag	720
ctcaccccg	tcgttggatt	gatccgctgg	tgctgaagg	caccctggc	ttataaaagg	780
aaaaagaagc	cccccttacc	caatggccat	gtcagcaaca	aggtcacaaa	ggacccgggc	840
gtggggatgg	acagagactc	ccacctcttg	tactcaaaac	tccacctcag	cgtcctgcaa	900
gtgctcatga	cgtgcagct	gcacctgacc	gagaagaatc	tgtatgggcc	gcctggggct	960
gacctcttc	gaccacatgg	tcc				983

&lt;210&gt; 244

&lt;211&gt; 526

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (526)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 244

cggtcgtcc	nnatttgaac	cccttctttg	atcggcctgc	agtaccgggc	cggaattacc	60
cggtcgagcc	acgcgttcgc	tcacgcgtcc	ggccaaccag	aagggttgcg	acggggaccg	120
cctgtactac	gacggctgtg	ccatgatcgc	catgaacgga	agcgtctttg	ctcaaggatc	180
ccagttttct	ctggatgacg	tggaaagcct	gacggccacg	ctggatctgg	aggacgtccg	240
gagctacagg	gcggagattt	catctcgaaa	cctggcggtg	agtgtccag	tagacacctg	300
tgtgggatgc	tcatcaaaga	cgtggaaagt	ggcccatc	gtgcgggcct	ggtggaggcc	360
gtgaggggtg	agtgcctgaa	aagtctgaca	gggaagtcc	ggacttccc	agcgtggaaa	420
ggggctgggtg	ccgcagacag	aacctgcttc	catctgttcc	ccgtcatcct	ctgcttgggc	480
caggccctga	gctgggggtga	gctgggggaca	ggcaggcagg	tgtatt		526

&lt;210&gt; 245

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 245  
 ggggcgggcc cccaggtag gcatggctgc tgccccagc ccattttctt tgaatctgtt 60  
 cactcctatt cactcctact tgccactcct tctattcatt actcactgcc cctgccccta 120  
 gtccccatgg taccctgag ccattgggcat ttcttgagcc ccactcagca ggctctgctt 180  
 cccccaggtc ctggtgaacg agggcggtgg ctttgaccgg gcctctggct ccttcgtagc 240  
 ccctgtccgg ggtgtctaca gcttcgggtt ccattgtggt aaggtgtaca accgccaac 300  
 tgtccaggtg acctcagcac tggccccat ccccggtca ggagggtgg gagggggaag 360  
 aaggggagcc cagctgacct ccgggtggac tctccattga cctgtgtcct ggaagaaa 418

<210> 246  
 <211> 706  
 <212> DNA  
 <213> Homo sapiens

<400> 246  
 acctcatatt attggagcag aagatgatga ttttgggtact gaacatgaac agatcaatgg 60  
 acagtgcagc tgtttccaga gcattgaatt gctaaaatct cggccggctc atttggctgt 120  
 tttcttacgc catgtagtgt cacaatttga ccctggcact ttgctttgtt atctctattc 180  
 agacctgtat aaacatacca attccaaaga aactcgctgc atcttccttg agtttcatca 240  
 gttctttcta gatcgatcag cacacctgaa agtttctgtt cctgatgaaa tgtctgcaga 300  
 tctagaaaag agaagacctg agctcattcc tgaggatctg catcgccact atatccaaac 360  
 tatgcaagaa agagtccatc cagaagttca aaggcactta gaagattttc ggcagaaaac 420  
 tagtatggga ctgaccttgg ctgaaagcga gctgactaaa cttgatgcag agcgagacaa 480  
 ggaccgattg actttggaga aggagcggac atgtgcagaa cagattgttg ccaaaattga 540  
 agaagtattg atgactgctc aggtgttaga ggaagataag agctccacca tgcagtatgt 600  
 tattctcatg tatatgaagc atttgggagt aaaagtgaag gagcctcgaa atttggagca 660  
 caaacggggt cggattggat ttcttcccaa aatcaagcaa agtatg 706

<210> 247  
 <211> 439  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
 caagggaggg gggttgatcc cctggcacag gtgagggcc tggaccaca tcctttgtct 60  
 gcctcccccac cccacagtgc ccgttcacgc acgatttcat cctggccctc cataggaaga 120  
 tcaagaatga gcccggtgtg tttcctgagg ggccagaaat cagcgaggag ctcaaggacc 180  
 tgatcctgaa gatgttagac aagaatccc agacgagaat tggggtgcc gacatcaagt 240  
 tgcacccttg ggtgaccaag aacggggagg agccccttc ttggaggag gacactgca 300  
 gcgtggtgga ggtgacagag gaggaggta agaactcagt caggctcatc ccagctgga 360  
 ccacggtgat cctggtgaag tccatgctga ggaagcgttc ctttgggaac ccgtttgagc 420  
 cccaagcacg aatggcgaa 439

<210> 248  
 <211> 730  
 <212> DNA  
 <213> Homo sapiens

<400> 248  
 cccacgcgctc cggaataaaag atagataaga cttccgatgg accaaaaactt ttcttaacag 60  
 aagaagatca aaagaaactt catgattttg aagagcagtg tgttgaaatg tatttcaatg 120  
 aaaaagatga caaatttcat tctgggagtg aagagagaat tctgtgctact tttgaaagag 180  
 tggaacagat gtgcattcag attaaagaag ttggagatcg tgtcaactac ataaaaagat 240  
 cattacaatc attagattct caaattggcc atttgcaaga tctttcagcc ctgacggtag 300  
 atacattaaa aacactcact gccacagaaag cgtcggaagc tagcaaagtt cataatgaaa 360  
 tcacacgaga actgagcatt tccaaacact tggctcaaaa ccttattgat gatggtcctg 420  
 taagaccttc tgtatggaaa aagcatgggtg ttgtaaatac acttagctcc tctcttcctc 480  
 aaggggatct tgaagtaat aatccttttc attgtaatat tttaatgaaa gatgacaaaag 540  
 atccccagtg taatatattt ggtcaagact tacctgcagt accccagaga aaagaattta 600  
 attttccaga ggctgggttc tcttctgggtg ccttattccc aagtgcgtgtt tcccctccag 660  
 aactgcgaca gagactacat ggggtagaac tcttaaaaat atttaataaa aaacaaaaaa 720  
 aaaggcgggc 730

<210> 249  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<400> 249  
 attgctgccg ctggatcgac tgctttgcct tgtacgacca gcaggaggag ctctgctggc 60  
 acatcgagaa ggtccacatc gaccagegca aaggggagga cttcacttgc ttctgggccc 120  
 gttgccctcg aagatacaag cccttcaacg ccgctataa actgctgac ccatgagag 180  
 tccactctgg ggagaagccc aacaagtgtg cgtttgaagg ttgcgagaag gccttttcaa 240  
 ggcttgaaaa tctcaagatc cacttgcgga gccacacagg cgagaagccg tatttgtgcc 300  
 agcatccggg ttgtcagaag gccttcagta actccagtga ccgcgccaaa caccagcgga 360  
 cgcatctgga cactaaacct tatgcttgtc aaattccagg atgtaccaa cgctacacag 420  
 acccaagttc cctaagaaag catgtgaagg cacattcttc caaaga 466

<210> 250  
 <211> 963  
 <212> DNA  
 <213> Homo sapiens

<400> 250  
 ggagcggtcg ccacggaaaa cgctggccg gacgggtggct ggcgccctg cctggggcgcg 60

gagggcggcg	gtggcgggccc	ccgcggcctt	ctctcagctt	cctttctcct	cacgacggcc	120
tccacagtc	ggagcccggc	ggagcccga	cctggggggg	agagctgcct	ccacggccgg	180
gcacccagac	cccaccgtcg	cagtcgccac	cacctcagtc	catccttgg	accggcaatg	240
ggcttcgtat	cctccagtgc	acttgtaact	gacttggaca	cggaaatacta	agaactcact	300
tctgtcctca	tcccagtcgc	gccggcggcg	accatctcgg	ctcttttggg	cttaactgcc	360
gctcctctgg	actctgtctg	actttggggg	caccatggac	caaagtggga	tggagattcc	420
tgtgaccttc	atcattaaag	caccgaatca	gaaatacagt	gaccagacta	ttagctgctt	480
cttgaactgg	accgtgggga	aactaaaaac	gcattctatct	aacgtttacc	ctagcaaacc	540
agtaagtgtg	taaaagctgg	gggcagctgc	tctgaccagc	agcttttcgt	gccgtgtacc	600
ctcctttttc	ctgctttctcc	cctccagctct	tgaatcaaat	aggtctcttt	tggtagaccg	660
cgaggatattt	tgagttctga	ggttgtgtct	cctgagtgtt	cgaaccatca	ttaatatttt	720
cctgatgagg	ttcagttaat	tagtaagagg	aagcagaaat	atcaaggga	ttagaattg	780
gcaggcaaaag	aocggggcgcg	gtgggtcacg	cctgtaatcc	cagcactttg	ggaggccaag	840
gcggggggat	cacgaggtca	ggagttcgag	accagcctta	ccggcatggg	gaaacctgt	900
gtctactgaa	aatacaaaaa	ttactgggc	gtgggtggcg	atgcttgtaa	tcccagctac	960
tcg						963

<210> 251  
 <211> 894  
 <212> DNA  
 <213> Homo sapiens

<400> 251						
gcggggaccc	ggatgtgtgt	ggtggcggcg	gccgaagagc	ttgtgtgcgg	agctgagagg	60
cctatggatg	aggaggacgc	ggcggccccg	gtttgttctc	atgaacaaga	tggatgacct	120
caacctgcac	taocggtttc	tgaattggcg	ccgggggatc	cgggagattc	gagagggtccg	180
agctttccga	tatcaggaga	ggttcaaaca	tatccttgta	gatggagata	ctttaagtta	240
tcatggaaac	tctggtgaag	ttggctgcta	cgtggcttct	cgaccctga	ccaaggacag	300
caattatttt	gaggtgtota	ttgtggacag	tggagtccgg	ggcaccattg	ctgtggggct	360
ggtccctcag	tactacagct	tggatcacca	gcctggctgg	ttgcctgact	ctgtagccta	420
ccatgctgat	gatggcaagc	tgtacaatgg	ccgagccaag	ggccgccagt	ttgggtcaaa	480
gtgcaactcc	ggggaccgga	ttggctgtgg	cattgagcct	gtgtcctttg	atgtgcagac	540
cgcccagatc	ttcttcacca	aaaatgggaa	gcgggtgggc	tctaccatca	tgcccattgc	600
cccagatgga	ctgttcccag	cagtgggcat	gcactccctg	ggtgaggagg	tgcggctgca	660
cctcaacgct	gagctgggccc	gtgaggacga	cagcgtcatg	atggtggaca	gttacgagga	720
tgaatggggc	cggctacatg	atgtcagagt	ctgtgggact	ctgctggagt	acttagggaa	780
gggcaaaagc	atcgtggatg	tggggctggc	ccaggcccgg	cacccactca	gcaccgcgag	840
ccactacttc	gaggtggaga	tcgtggaccc	tggagagaaa	tgctacatcg	ccct	894

<210> 252  
 <211> 861  
 <212> DNA  
 <213> Homo sapiens

<400> 252						
tcccgggtcg	acgatttcgt	ctggagtgtt	agcaaccagta	ctggatgtga	cagcaggcag	60
aggagcactt	agcagcttat	tcaagtgtccg	attotgatcc	cggcaaggat	ccaagcatgg	120
aatgctgcog	tcgggcaact	cctggcacac	tgctcctctt	tctggcttcc	ctgctcctga	180

gttccaggac	cgcacgctcc	gaggaggacc	gggacggcct	atgggatgcc	tggggcccat	240
ggagtgaatg	ctcacgcacc	tgcgggggag	gggcctccta	ctctctgagg	cgctgcctga	300
gcagcaagag	ctgtgaagga	agaaatatcc	gatacagaac	atgcagtaat	gtggactgcc	360
caccagaagc	aggtgatattc	cgagctcagc	aatgctcagc	tcataatgat	gtcaagcacc	420
atggccagtt	ttatgaatgg	cttcctgtgt	ctaattgacc	tgacaaccca	tgttcactca	480
agtgccaagc	caaaggaaca	accctgggtg	ttgaactagc	acctaaggtc	ttagatggta	540
cgcgttgcta	tacagaatct	ttggatatgt	gcatacagtgg	tttatgcca	gtaagtgtg	600
atttgttctc	attcaacttg	tccagagggt	ttcaatgtct	ttgtgtaaat	ggtttacata	660
gtctcactct	ctgaatcact	catctttaca	cttttttagag	tttgtaaatg	gtgaaagatt	720
tgaaaattaa	ggtatgattt	cagtgtaaaag	taccaagtgt	tgtattgtgc	gaaggaaaag	780
tagactagag	ttatttttct	ttccttgagt	gtcacttgaa	tataaaagaa	taaaaatttt	840
tgaatagtgt	taaaaaaaaa	a				861

&lt;210&gt; 253

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 253

caggetgtta	agacaagagc	tttgtgtgct	ttgccacctt	caccacccca	gtttgatatc	60
tttgctggca	gctgggattc	gtccccggat	gttggtgatg	gagttagcct	ccaagggttc	120
cttggatcgc	ctgcttcagc	aggacaaagc	cagcctcact	agaaccctac	agcacaggat	180
tgcactccac	gtagctgatg	gtttgagata	cctccactca	gccatgatta	tataccgaga	240
cctgaaaccc	cacaatgtgc	tgcttttcac	actgtatccc	aatgctgcca	tcattgcaaa	300
gattgctgac	tacggcattg	ctcagtactg	ctgtagaatg	gggataaaaa	catcagaggg	360
cacaccaggg	tttcgtgcac	ctgaagttgc	cagaggaaat	gtcattttata	accaacaggc	420
tgatgtttat	tcattttggt	tactactcta	tgacattttg	acaactggag	gtagaatagt	480
agagggtttg	aagttttccaa	atgagtttga	tgaattagaa	atacaaggaa	aattacctga	540
tccagttaaa	gaatag					556

&lt;210&gt; 254

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

caaaggccag	taatagtacc	catgagtttc	gtattggcct	acctgagggg	tgggaatccg	60
aaaaaaaggc	agttatcccc	ctggggatcg	ggccacccct	gactttaatc	tgcctagggg	120
ttctgggggg	tattctcatc	tacgggagga	aaggcttcca	aactgcccac	ttttacttaa	180
aggacagtcc	atccccataa	gtaatatcca	cccctccacc	acctatcttt	ccaatttcaa	240
aggaggtcgg	accaattcca	ataaagcact	ttccaaagca	tgtggcaa	ttacatgcaa	300
gtaggggggt	tactgaaaaa	tttgaaacac	tgaaaaagtt	ttaccaggaa	gggcaaagct	360
gtactgttga	cttaggtatt	acagcaaaca	gtcccaacca	cccagacaac	aggcacagga	420
atcgatcctt	aattg					435



<210> 255  
 <211> 698  
 <212> DNA  
 <213> Homo sapiens

<400> 255  
 cctcatttcc tgategaaca gctcacttg tgttgctgtc agtgccagta gggcaggcag 60  
 gaatgcagca gagaggactc gccatcgtgg ccttggtgtg ctgtgcggcc ctacatgcct 120  
 caccagccat acttcccatt gcctccagct gttgcacgga ggtttcacat catatttcca 180  
 gaaggctcct ggaaagagtg aatatgtgtc gcatccagag agctgatggg gatttgtgact 240  
 tggctgctgt catccttcat gtcaagcgca gaagaatctg tgtcagcccg cacaaccata 300  
 ctgttaagca gtggatgaaa gtgcaagctg ccaagaaaaa tggtaaagga aatgtttgcc 360  
 acaggaagaa acaccatggc aagaggaaca gtaacagggc acatcagggg aaacacgaaa 420  
 catacggcca taaaactcct tattagagag tctacagata aatctacaga gacaattcct 480  
 caagtggact tggccatgat tggttagtct cgctctgtca cacaggctgg agggcagtgg 540  
 cgggatctcg gttcacccca acctttgctt caggggttca agggattctc gtgcctcagc 600  
 cttccaagtg gctgggattg caggtgtgcg ccagtacgcc tggctagttt tagtattttt 660  
 tgttacagac ggggtttcac catgttggct gggctggt 698

<210> 256  
 <211> 736  
 <212> DNA  
 <213> Homo sapiens

<400> 256  
 gtttgaacag cccggaaacc cgggcgaccc acgcgtacga actccgcccc catggggggc 60  
 ccactttttc gctttgattc cttcttcccc caaagaggtc ccagctaccc catcctccag 120  
 aagggacccc attgcccac cagcgactct tctctctaaa aagaccccag caactctagc 180  
 ccccaaagag gccctcattc cccagctat gactgttccc tcccctaaaa agaccccagc 240  
 aattccaacc cccaaagaag cccagctac cccatcctcc aaagaggcct ccagtcccc 300  
 agcagtgact ccttccactt acaaaggggc cccatcccc aaagagctcc tcattccacc 360  
 agctgtgact tctccttccc ccaaagaggc acctactcct ccagctgtga ctctccatc 420  
 ccccgaaaag gggccagcaa ctccagcccc caaagggact cccacttccc cacctgtgac 480  
 tcttctctcc ctcaaagact cccctacttc cccagcttct gtcacatgta aaatgggggc 540  
 cactgttctt caagcatcta aagggcttcc agcaaagaaa ggccccacag ctctgaaaga 600  
 agtacttggt gccccagctc cagaaagcac gccaatcatc acagctccca ctcggaagg 660  
 tccacagacc aaaaagagtt ctgctacttc acctcctata tgcccagatc cctcagctaa 720  
 gaatggttct aaagga 736

<210> 257  
 <211> 77  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 ctccgcctcc caaagtactg ggattacagg tgtgagccac cgtgcccagc caagaccttg 60  
 tatcctttaa aaaaaaa 77

<210> 258  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

<400> 258  
 aatgctcctt tggtaagaac aattatatgg ctaaattaat ctcagccacc tagttctaaa 60  
 tgtagagcaa ggattgcaag ggattattta gacaagttca tcaattaagt aaaattagac 120  
 atgaaggata taagaatgaa tgataaagca agctaaaaat ggtgaaacaa gggatgtctg 180  
 attggaagta gaagatattt atttagggtc taggacatta gtatcagtga ggacagtaat 240  
 ttctgtcttg tttgtatttc agtgatcaca tacacttctt tacctgataa cgtctctctt 300  
 ctctaggtctg gttttgggta cggcttgcca atttctcgtc tgtatgccaa gtactttcaa 360  
 ggagatctga atctctactc tttatcagga tatggaacag atgctatcat ctacttaaag 420  
 gtatcccttg aattcaatag caaaatcctg tttctaaaac cattgctcct tttatagccc 480  
 tgagtgtctat ggtccggag 499

<210> 259  
 <211> 621  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 tttcgtgact gtagtcagcc cttagtggat gagagcgcc atgcttcaga aacagcaggc 60  
 tcccaggatg gacacccgc cccctgaaga acgcttagag aagcaaatg aaaaactgaa 120  
 caaccaggaa gaggagacgg agtttaagga actggacggg ctgaggggaag ccttggcaaa 180  
 cctccgggga ctgtcagagg aggagaggag cgagaaggct atgcttcgct cccgcattga 240  
 agagcagtc cagctcatct gcacctgaa gcggagggtca gatgaggccc tggagcgctg 300  
 ccagatccta gagctgctca atgcagagct ggaggagaag atgatgcagg aggctgagaa 360  
 gctcaaggcc cagggtgagt acagtcggaa actagaggaa cgctttatga ccctagcagc 420  
 caaccacgag ttgatgctcc gcttcaagga tgaatacaag agtgagaaca tcaagctgag 480  
 ggaggagaat gagaagctga ggctggagaa taacagcctc ttcagccagg ctctgaagga 540  
 tgaggaggcg aaagtattac agctcacagt ccggtgtgag gccctcactg gggagctaga 600  
 aacgctgaag gagaggtgtg c 621

<210> 260  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

```

<400> 260
agatccgggt gcgagccacg cgtccgtgca ggtgcaggta ctgaaagagc aactttttgc      60
tgggcgtagt ccttcaccct tccgctcctg cgcactcatg ggaatgtgtg gcagtagaag    120
cgctgataac ttgtcatgcc cttctccatt gaatgtaatg gaaccagtaa gcttctttcc    180
tcttaaatca ctggggaagg gaatgataca acatttcaga cacatagttt ccctagttta    240
gatgaaatat atgtttatatt taaatacata atttgataaa ttattgttga ttggaagtga    300
ctttcacctt tgaagtcca ttgctgtctg aagccactag aaagccacct gaattgcaat    360
agtgatttat ctttctgact aaaggaggta atgcaccata aaaacatgta cagt          414

```

```

<210> 261
<211> 620
<212> DNA
<213> Homo sapiens

```

```

<400> 261
gtaaccacca ctactcatag cgttggacga gggcatgagc tacagttgct taatgaagaa      60
ctgagaaaca ttgagcttga gtgtcagaat atcatgcagg ctcacaggct ccagaaagtg    120
acagaccagt atggagacat ctggacattg catgatggag gattccggaa ttataacacc    180
agcatagata tgcaaagggg aaagctagat gacatcatgg agcatccaga aaagtctgac    240
aaggacagtt ctagtgttta caacacagct gagagctgca gaagtactcc gctcactgta    300
gaccgttccc ctgacagttc ccttccaagg gtgatcaacc tcaccaataa gaaaaacctg    360
agaagcacia tggcagccac ccagtcctct tccggacaga gcagtaaaga gtcgacctcc    420
accaaagcca aaaccactga gcaaggttgt agcgtgaaa gcaaggagaa ggttttagaa    480
ggcagcaagc ttctgatca agagaaggca gtcagcgaac acatccctta cctctctcct    540
taccacagct cctcatatag atatgcaaac atcccagcac acgcccggca ttatcaaagc    600
tacatgcagt taattcaacg

```

```

<210> 262
<211> 418
<212> DNA
<213> Homo sapiens

```

```

<400> 262
gggtctgggg ctgcctggcc accgtgtcca cccacaagaa gatccaagga ctgccatttg      60
ggaactgcct gcccgtcagt gatggccct tcaacaatag cactgggatt cctttctctt    120
acatgacagc caaggacccc gtggtggctg atctgatgaa gaaccccatg gcctcgctga    180
tgctgccaga atcagaaggg gagttctgca gaaaaaacat cgttgatccg gaagatcccc    240
gatgtgtcca gttaacgctc actggccaga tgatcgagc gtctccagaa gaagtagaat    300
ttgccaagca agccatgttt tcaaggcacc cagggatgag gaagtggcct cgtcaatatg    360
aatggttctt tatgaagatg aggatagaac atatctggct tcagaaatgg tatggagg    418

```

<210> 263  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 tttcgtcaga gccgcgggag gacgggttgcc tgggtattatt agcaagcagc aaatatggcg 60  
 gtggcgcgcg tggacgcggc ttgcctccc ggagaaggat cagtggtaa ttggtcagga 120  
 cagggactac agaaattagg tccaaattta ccctgtgaag ctgatattca cactttgatt 180  
 ctggataaaa atcagattat taaattggaa aatctggaga aatgcaaacg attaatacag 240  
 ttatcagtag ctaataatcg gctgggttcgg atgatgggtg tggccaagct gacgttgctt 300  
 cgtgtattaa attgcctca taatagcatt ggctgtgtgg aagggtctaaa ggaactagta 360  
 catctggaat ggctgaattt ggcaggaaat aatcttatag ccatggaaca gatcaatagc 420  
 tgcacagctc tacagcatct c 441

<210> 264  
 <211> 832  
 <212> DNA  
 <213> Homo sapiens

<400> 264  
 tatttcgagc ggcagttggg gcggtaccag aggggtgcctg gaaggatacg gccagctcc 60  
 acaagagcga ggaggcgaag cgggtgctgc ggtattacct cttccagggc cagcgtata 120  
 tctggatcga gaccagcaa gccttctacc aggtcagcct cctggaccat ggccgctctt 180  
 gtgacgacgt ccacgcctcc cgccatggcc tcagcctcca ggaccaaag gagaggaagg 240  
 ccatttacgg cccaacgtg atcagcatac cgtcaagtc ctaccccag ctgctggtgg 300  
 acgaggcctt cagcatcgcg ctgtggctgg ctgaccacta ctactggtac gccctgtgca 360  
 tcttctcat ttctccatc tccatctgcc tgtcgtgta caagaccaga aagcaaagcc 420  
 agactctaag ggacatggtc aagttgtcca tgcgggtgtg cgtgtgccgg ccagggggag 480  
 aggaagagtg ggtggactcc agtgagctag tgccggaga ctgcctggtg ctgtcccagg 540  
 aggggtgggt gatgccctgt gatgccgcc tggtgccgg cgagtgcatt gtgaatgata 600  
 gctctctgac aggagagagc attccagtgc tgaagacggc actgccggag gggctggggc 660  
 cctactgtgc agagacacac cggcggcaca cactctctc cggaaccctc atcttgcatt 720  
 cccgggccta tgtgggaccg cagtcctgg cagtggtag ccgcacaggt atgagccggg 780  
 aggtctgggt tgagagagat ccgggctcag cacccttgaa gaggtggagt gg 832

<210> 265  
 <211> 714  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 tttcgtcggg ggcgggctcc accttcacct ctgcctctc ctctgcttca tgctgccga 60

ggacgctgcc	atggctgtgc	tgacggcctc	caaccacgtg	agcaacgtca	ccgtgaacta	120
caacatcacc	gtggagcgga	tgaacaggat	gcagggcctg	cgggtctcta	cagtgccagc	180
cgtgctgtcc	cccaatgcc	cgtggcact	gacggcgggc	gtgctggtgg	actcggccgt	240
ggaggtggcc	ttcctgtgga	cctttgggga	tggggagcag	gcctccacc	agttccagcc	300
tcatacaac	gagtccttcc	cggttocaga	ccctcgggtg	gccaggtgc	tgggtggagca	360
caatgtcacc	cacacctacg	ctgccccagg	tgagtacgtc	ctgaccgtgc	tggcatctaa	420
tgcttctcag	aaccggacgc	agcagggtgt	gatccgcagt	ggccgggtgc	ccattgtgtc	480
cttggagtg	gtgtcctgca	aggcacaggc	cgtgtacgaa	gtgagccgca	gctcctacgt	540
gtacctggag	ggccgctgcc	tcaattgcag	cagcggtccc	aagcgagggc	ggtgggtgtc	600
acgtacgttc	agcaacaaga	cgtcgggtgt	ggatgagacc	accacatcca	cgggcagcgc	660
aagcatgtga	ctgggtgtgc	ggcggggcgt	gctgcgggac	ggcgagggat	acac	714

<210> 266  
 <211> 1872  
 <212> DNA  
 <213> Homo sapiens

<400> 266						
cccgaattc	ctgggtcgac	tatttcgtgg	aaaggctgcc	actctgcatg	tgcacagtga	60
ccagaagccc	cttcacgatg	gggcccctcg	gtcgcagcag	aacttggttc	gcatgaagga	120
ggcgtgagg	gccagcacca	tggacgtcac	cgtggtcctg	cctagtgggc	tggagaagag	180
gagcgtgtc	aatgggagcc	atgcgatgat	ggacctactg	gttgaaacttt	gccttcagaa	240
ccacctgaat	ccatcccacc	atgcccttga	aattcgggtc	tcagaaaccc	aacaaccttt	300
gagttttaag	ccaaatactt	tgattgggac	cctgaatgtg	catactgtgt	ttctgaaaga	360
aaaagttcct	gaagagaagg	ttaagcctgg	tccccctaag	gtgcttgaga	aatctgtgcg	420
tttggtcgtg	aattacctgc	ggacacaaaa	agctgttgtg	cgtgtgagcc	ctgaggttcc	480
tctccagaat	attctcccag	tcatattgtg	aaagtgtgag	gtcagcccag	agcacgtggt	540
tctcctcagg	gacaacattg	ccggagagga	gctggagctg	tccaagtccc	tgaacgagct	600
cgggataaaag	gagctctacg	cgtggggacaa	cagaagagaa	accttttagga	aatcatcact	660
tggcaatgat	gagacagata	aagagaagaa	aaaattttctg	ggatttttca	aagttaataa	720
aagaagcaat	agtaagggtc	gtttaacgac	ccccaaactcc	ccatccatgc	actcacgttc	780
tcttacgctg	ggtccatccc	tctcgtcggg	cagcatctca	ggggtgtccg	tgaagtcgga	840
gatgaagaag	cgccgagccc	ctcctcctcc	aggttcaggg	ccacctgtgc	aagacaaggc	900
atcggaagaa	gtatctcttg	ggtcacagat	tgatttacag	aagaagaagc	ggcgagcgcc	960
agctccccct	ccaccacagc	caccaccacc	gagtcccctg	atcccccaacc	gcactgagga	1020
taaggaggag	aacaggaaga	gcacgatggt	ttattgctgt	gcgtcattcc	ctactcaggc	1080
caagcgcttc	tgatggacgg	gcctcttctc	gacctcggac	ctttcccagt	gtctcttctg	1140
ccttggtctc	gatttttctg	ttgttcttcc	tcctttcagg	ataaaagggc	tcattgtata	1200
cccagaattt	acttcctttg	gggtttacat	ataaatgcat	taataacaga	gatttggttg	1260
attgaggttt	atattttttt	gaaggaggta	aatttatatg	aaatttttagg	ttgataatat	1320
tcacctgtct	gaaattcact	gatacttgga	aatgttcctg	tgaagaactc	tgctttatatt	1380
taatttcatta	ttaattcatg	tttttcttat	tggatattca	gttccagaat	ttattgcca	1440
tttttcttaa	aactagattg	tatccataaa	ttgaccagta	tagtcaattt	ggatagaact	1500
gaaactttct	gtctacctgg	taaaactaag	tgcttaaaaa	catgaactat	aaatgtagtt	1560
actaggaact	cacaacttat	atatactatc	cattcaatga	tacataggac	ccaatgtctt	1620
tgtgtttttg	aggttttcct	gttactgtgt	actttgcat	tttacatagt	tcactaaaaa	1680
gaaagaagtg	ggagaagaag	gggggtctat	tcattattct	atattatgat	tctcttcatt	1740
attctgttct	cttcattatt	ctattcattt	cttcacccat	ttattcacta	aacagtgaca	1800
tagtacttac	ttgatgctag	gtattacacc	agttttgtgg	gctataagag	tgaataacaa	1860
gcacgtgacc	tt					1872

<210> 267

<211> 684  
 <212> DNA  
 <213> Homo sapiens

<400> 267

tgtagataca	gagtagctaa	ttctaaaatt	catatggaag	gcaaagaaac	taaattagcc	60
aaaacaat	tgaaaaagat	ttcaaaaaaa	ttttgaagga	atcatgctgc	ccagttttta	120
gacttactat	aaagctgtga	taatcaaggc	aatctggtat	ttatgaaagg	ataaacacat	180
agatcaatgg	aataaagtcc	aaaaccagac	tcacataaat	agcaattgat	ttctgacaaa	240
ggtgaaaaga	caactcaatg	gggaatggag	agtttttcaa	cagatgattt	taaaacaact	300
gaacatccat	atgcaaaaaa	ataaacctac	ctaaatttca	cagcttatac	aaaaattaac	360
ctaaaatgga	tcacggatct	aaatgtagaa	ctaaatttat	aaaattttta	gaagaaaaaa	420
atccataggc	cgggcacggg	ggctcatgcc	tgtaatccca	gcacttcaga	ggctgaggcg	480
ggcagatccg	ttgaggtcag	ttcaagacca	gcctagccta	tgtggtgaaa	tcccaactct	540
actaaaaata	aaaaataaaa	aaaaaatggg	ctgggagtg	tggtgcacac	ctgtagtcct	600
agctacttgg	gagactgaag	cacaagaatc	acttgaaccc	agcaggcaga	ggttgagtg	660
agtggagatt	gtgccactgc	accc				684

<210> 268  
 <211> 453  
 <212> DNA  
 <213> Homo sapiens

<400> 268

ggtcgacgat	ttcgcccgcc	gtcggacgag	gagcgggagc	cgtgggagcc	gtggacgcag	60
ctgcgcctgt	cgggccacct	gaagccgctg	cactacaatc	tgatgctcac	cgccttcctg	120
gagaacttca	ccttctccgg	ggaggtcaac	gtggagatcg	cgtgccggaa	cgccaccg	180
tacgtagtgc	tgcacgcttc	ccgagtggcg	gtggagaaag	tgcagctggc	cgaggaccgg	240
gcgttcgggg	ctgtccctgt	agccggtttt	ttcctctacc	cgcaaaccca	ggtcttagtg	300
gtggtgctga	ataggacact	ggacgcgcag	aggaattaca	atctgaagat	tatctacaac	360
gcgctcatcg	agaatgagct	cctgggcttc	tttcgcagct	cctatgtgct	ccacggggag	420
agaagattcc	ttggggttac	tcagttttcg	cct			453

<210> 269  
 <211> 525  
 <212> DNA  
 <213> Homo sapiens

<400> 269

ggcagagaa	ctggtgctta	atttaatgcc	aattcatgat	gtaggtttct	aagcagcaca	60
taaaaggggc	tttttaggta	gcactgagta	ctttactaaa	aatacaaaaa	ttagccaggg	120
gggggggtgc	acgtctttta	tcccagctac	tcagggcggg	ggccaggggg	tggggtaggg	180
tgggggctga	gacaggagaa	gcacttgaac	ccaggaggcg	gagggtgcag	tgagctgaga	240
ttgtgctact	gtactccaac	ctgggcaaca	aacagagtga	gacactgtct	caaataaata	300

aataaataga	taaataaaat	aaaataaaat	aaaaagaact	cgaccctttt	tacaatagct	360
aaaggaaaat	aaaatactta	agaatatact	taaccaagga	ggtgaaagac	ctctacaaag	420
aaaactacaa	aacactgctg	aaagaaatca	cagatgacac	aaacaaaaac	acatcccaag	480
ctcatggaca	ggtagaatca	atactgtgaa	aatgactata	ctgcc		525

<210> 270  
 <211> 880  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1) ... (880)  
 <223> n = a,t,c or g

<400> 270						
cccagtccca	cattgagccc	tgatcccata	caagtccata	gacttggcct	ctgaccaaac	60
ctgaccctgc	acttgctact	taagggtggc	ccatattcag	ctcagaccct	gaaccgagct	120
ctgaccctgg	cttctgactg	aatctgtgac	agactaaggc	ctgaccctgg	ccctatacca	180
cgtctccacc	cgtgtcctca	actgagtgc	gaccccaaac	ctagacagcc	ctacctgac	240
cttccccccag	gcctgtcccc	gccgcttcat	ctcaaaagtt	gaagggtgagg	agccggtaaa	300
caggtctgga	gcctgggtctc	agactcagcc	tgagcaagct	cagtctgggg	tcattggggc	360
tgtaaccccg	ggcaggccct	tgttagggat	gcagggtctc	accctagggg	tataagggat	420
ttctgtgccc	atcagaactt	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	480
nnnnnnnnnn	nnnnnnnnnn	attttgtctg	tagcatatgt	gatgaccttg	acttcacctc	540
cctggcgcca	atatcctctt	ctgtaaaatg	gcttatgcat	tacaaagtga	ggtcctgcca	600
gtgactacac	ctagaggcat	taagtgcctt	tgtggactcc	tgccctgcac	ctcacctctc	660
ccagcttttt	aacccccctga	ggaaccttct	taccttgagt	ccctcaccgg	ctacaggcca	720
tccatgagca	gatgaactgc	aaggagtatc	aggaggacct	ggccctgcgg	gctcagaacg	780
atgcggtctc	ccggcgggccg	tcagagatgt	ttaagggtgag	gctggctcag	ggtcgtggcc	840
tagcatcttt	aagttctggg	atccagtctg	gggtaggggag			880

<210> 271  
 <211> 1066  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1) ... (1066)  
 <223> n = a,t,c or g

<400> 271						
tgaccctcgt	aagngcggtg	gaattccctc	acctgtgtgg	tcctcacctt	cctggggccac	60
cgctctgtga	aacggtttct	ggtgccaaag	ctgaggagggt	ttctcaagcc	tcaggggccat	120
ccccgcctgc	tgctctgggt	taagagggtga	gtgagctcac	agccccgagg	cagggcaggg	180
gagggccctc	gagctgaggg	ggtggctcca	gggttatggc	caggggctga	ggaggaggaa	240
ggctctgtgt	catggagaac	tctctggcgc	cccaggggcag	gagccagtgg	gtggcttcaa	300

acaaagcagc	atctttgtgg	tgtttcacca	gttcttagtc	ccagttacag	caggtgactg	360
tggtggacga	aaactggact	caacagtttc	ctccattcag	ggatcccagg	ccatggagca	420
aggagggccc	gaatcagtac	ctccctcaga	tcacctggac	agtgtgagac	aaaaagccgc	480
agggaccatc	cctggagggg	gattcagcag	gctcgatcgg	ggtccagggtg	ctggtatttt	540
tcattagcct	ccaggggatt	ctgatgtagc	cagcagcgtc	cttgacaac	agtttgagat	600
ctgctgcttt	tcaaactgga	ttccttggag	cgctggaaat	ctcagcgatg	tcacagggca	660
ggagagggag	gttgtggagg	gaaaattcag	acttcccgc	cagcccacca	tttcaccagg	720
cagctctaaa	tttatgtgtt	ttataagcca	aggttcacac	aaaaaagaaa	attcgctggg	780
gggaaaaaaa	cagtttctat	ggcttaaaaa	aaagtctgaa	gaccaccagt	ctatttcaat	840
actctatttt	gttgatgaag	aagctgggtg	ccaaagatac	ccaaagacta	agtcaggggg	900
atgcaggggt	acaggggtgc	ctctcacttt	cccaaagtga	gatccacata	ccacagcaaa	960
atgatttgag	ccagcctgtg	gatgaacaca	tttaaaattt	tatttataaa	tacatttact	1020
gttacatttg	acttctcttt	attaaatata	tttgtgattt	ataaaa		1066

&lt;210&gt; 272

&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

tacggggaat	tgcacaccta	ccaaggggtg	gctgtgacgc	ggagccggaa	agaaggcatc	60
gcacacaact	acaaaaatga	gacggagtgg	agagcgaaca	tcgacacagt	gatggcgtgg	120
ttcacagagg	aggacctgga	tctggtcaca	ctctacttcg	gggagccgga	ctccacgggc	180
cacaggtacg	gccccgagtc	cccggagagg	agggagatgg	tgcggcaggt	ggaccggacc	240
gtgggctacc	tccgggagag	catcgcgcg	aaccacctca	cagaccgcct	caacctgatc	300
atcacatccg	accacggcat	gacgaccgtg	gacaaacggg	ctggcgacct	ggttgaattc	360
cacaagttcc	ccaacttcac	cttcggggac	atcgagtttg	agctcctgga	ctacggacca	420
aacgggatgc	tgctccctaa	agaagggagg	ctggagaagg	tgtacgatgc	cctcaaggac	480
gcccacccca	agctccacgt	ctacaagaag	gaggcgcttc	ccgaggcctt	ccactacgcc	540
aacaacccca	gggtcacacc	cctgctgatg	tacagcgacc	ttggctacgt	catccatggg	600
gtgagtcgcc	tgctggaggc	accacctcca	ggggctccct	ccccaggctc	tgggtcttc	659

&lt;210&gt; 273

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

acgcgacttc	tcggttcgac	ccacgcgtcc	gcacatataa	cacatcacgc	accttttgag	60
tggctacctt	ggttctcgcc	tttcttttca	agagaccatt	cttcaacaga	actgtaagga	120
ttcttcttgg	ctgaatcaga	tgtgacgcat	cccacttctg	cgtttgaggt	ctagcacata	180
ccgctccaag	ggctttgacg	tcacagtga	gcactcacac	ggaagctgga	cgggcttcgg	240
tggggaagac	ctcgccacca	tccccaaagg	gttgaatact	tattttcttg	tcaacattgc	300
cactattttt	gaatcaaaga	atttcttttt	gcctgggatt	aaatggaatg	gaatacttgg	360
cctatcttat	gccacacttg	ccaagccatc	aagttctctg	gagaccttct	tc	412



<210> 274  
 <211> 522  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
 gaattaagag ttactccggg ccaaattggcc ggagttgtca gatctggcag cgtcttcgct 60  
 ggggctccag ggagctgctg ctgggggtgga agctctcaca ctctttctcc acgtgccctt 120  
 tccagttccc tgacatcgtg gagttctgcg aggccatggc caacgccggg aagaccgtaa 180  
 ttgtggctgc actggatggg accttcaga ggaaggtaag gcgtctgac caggtctgga 240  
 gctgggattg aggagggcaa gaggtctctg gatgggcaca gagacaccag ctctgggtga 300  
 ccagggtca gccaccacag ggttacggcc gagctgctca ggccttggct gagccaaggg 360  
 actccatggt ctgtgcagac tgcgtgccat ctgttgccgc aggtgctttg aattggcaaa 420  
 gggacagagc cgggcatggt gctctggggg ttgggggaag gactaaggct agagcaaact 480  
 ctctggctt cagtacttgt gaatcagagg gtttaaaaga aa 522

<210> 275  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1) ... (650)  
 <223> n = a,t,c or g

<400> 275  
 gaattctgct tatgcaccaa tttgcagctc ctgcaaccat gatgcagcct caccgggacc 60  
 tttcaacatt ttccctttca cctaaaactg tattttttct tgctaagacc ggctacccta 120  
 ctttcathtt cctttcactc ttcttggtc ttttgggcct tttaggaatt tgggatgatt 180  
 caggctctga caggcatggt actagattta ttttaggctg ctcttttgct gttgtccaac 240  
 aggccaagga gagatttaaa tgatttatcc aatatttgct aaatagtcac gtgtttcatt 300  
 tatcccatat atagttcagc cttaatatgt tttttgtttt gatttggtac actagtgcac 360  
 acatagagac gtgaagccag aaaatatcct catcacgaaa cattccgtga ttaagctttg 420  
 tgactttgga tttgctcggc ttttgactgg accgagtgc tactatacag actacgtggc 480  
 taccaggtgg taccgctccc ctgagctgcn ggtgggggac acgcagtacc ggcccccg 540  
 tgggatgttt ggggcaattg gctgtgtctn tgctgagctn gctgtcaggg aagtgcctct 600  
 ggtggccagg aaaatcggaa tgttgatca gctgtatctg attaggaaga 650

<210> 276  
 <211> 497  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 276

cccttgatga	ccatctagtc	agtgcggtgg	aattcccatg	acagacgtat	ctgactggtc	60
atgtggtcag	caagcctcgc	ctttggtcag	gccttggagg	gtacagctga	cccatagggc	120
cacttccatg	gcactgggca	agtggctgta	ttggaaatga	agtcgttgcc	cccgatttct	180
ttggggccag	gttgagcttt	cctgcccaga	gcacggaggc	taaagggggt	gggctttgga	240
ctggattggg	gctgacctca	gcctacacct	gcaggaggag	gtggagacag	aggtaggcctg	300
ggaggaatgt	gggcacgtcc	tactgtcact	gtgctacagc	tctcagcagg	gtggcttgct	360
ggtaggtgtg	ctgcgtgctg	cccacctggc	ccccatggat	gccaatgggt	actcggaccc	420
cttcgtgcgc	ctgtgagtga	actggggtag	gcaggcggga	ggtgaggata	aggcgggtgac	480
tcctcacctc	tccaggg					497

&lt;210&gt; 277

&lt;211&gt; 428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 277

tgggtggaatt	ctcgccatgg	aatatgcacc	aggcggcact	ctggctgagt	tcatccaaaa	60
gcgctgtaat	tccctgctgg	aggaggagac	catcctgcac	ttcttcgtgc	agatcctgct	120
tgcactgcat	catgtgcaca	cccacctcat	cctgcaccga	gacctcaaga	cccagaacat	180
cctgcttgac	aaacaccgca	tggtcgtcaa	gatcgggtgat	ttcggcatct	ccaagatcct	240
tagcagcaag	agcaaggcct	acacggtggt	gggtacccca	tgctatatct	cccctgagct	300
gtgtgagggc	aagccctaca	accagaagag	tgacatctgg	gccttgggct	gtgtcctcta	360
cgagctggcc	agcctcaaga	gggctttcga	ggctgcgaac	ttgccagcac	tggtgctgaa	420
gatcatgg						428

&lt;210&gt; 278

&lt;211&gt; 427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 278

gtccagtgtg	gtggaattca	ccagggtgtcc	ggggcagtg	tagtatctgg	gctgctgcag	60
ggcatgatgg	ggctgctggg	gagtcccggc	cacgtgttcc	cccactgtgg	gccctgggtg	120
ctggctccca	gcctggttgt	ggcagggctc	tctgcccaca	gggaggtagc	ccagttctgc	180
ttcacacact	gggggttgcc	cttgctgtac	gtgagtctctg	agaggcgtgg	gatggtgcc	240
agtgggggtg	tatgggggga	ctaggggagg	gcagaactgc	tggtcctatc	agattcagca	300
gcgactggaa	tagggacata	ttttatattt	ggaatccaag	acttttcctt	gattcatctg	360
gtctccttga	atttcacact	gttttctgct	gtcccccaag	gtcacttctt	attccttcca	420
tgggagt						427

&lt;210&gt; 279

<211> 561  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
 cccagaatga cggggtcgac ccaegcgctc gcaccagct atggaggcag ctgcaggaac 60  
 aacttgtttt accgagaaga aacctacact ccaaaagctg agacggacga gatgaatgag 120  
 gtggaaacgg ctccatttcc tgaagaaaac catgtttggc tccaaccgag ggtgatgaga 180  
 cccaccaagc ccaagaaaac ctctgcggtc aactacatga cccaagtcgt cagatgtgac 240  
 accaagatga aggacaggtg cataggggtc acgtgtaaca ggtaccagtg cccagcagggc 300  
 tgcctgaacc acaaggcgaa gatctttgga agtctgttct atgaaagctt cgctagcata 360  
 tgccgcgcgc ccatccacta cgggatcctg gatgacaagg gaggcctggg ggatatcacc 420  
 aggaacggga aggtccccct ctctgtgaag tctgagagac acggcgctgca gtccctcagg 480  
 taactactct gtgatcgggg ctctgtgaaa cggttttcct gtttatgacg gtgttgttga 540  
 aattttgaaa aataccacac a 561

<210> 280  
 <211> 792  
 <212> DNA  
 <213> Homo sapiens

<400> 280  
 atttttgatg ccatgtggct acattgggtt tagaatacta ataaaatcca ttgcttttaa 60  
 aataaataaa taaaccccat agcacatcct ccatacaaca tctgttgctc ctcaagatac 120  
 aattgttacc actatcatct aaccattatt ttatgataac tttaaaatat caacttggca 180  
 agaaaatatt ccacaaaaca cactctgcct ttttacttta aagagtcctt ggctacctgg 240  
 gccaatatta ttctcatttg taggatttag gttccacaga atataatatg tgcctttttc 300  
 tgtgttccct gcagatttgc aagtaccatc cctttttggg gccttacttt gcacctccag 360  
 catctgggaa acaatgtttt cctgttgagc actctctttg gtgcagtcac cctcctggcc 420  
 aattgtgttg caccttgggc actgaatcac atgagccgtc gactaagcca gatgcttctc 480  
 atgttcttac tggcaacctg ccttctggcc atcatatttg tgcctcaaga aatgcagacc 540  
 ctgcgtgtgg ttttggcaac cctgggtgtg ggagctgctt ctcttggcat tacctgttct 600  
 actgccaag aaaatgaact aattccttcc ataatcaggg gaagagctac tggaatcact 660  
 ggaaactttg ctaatatttg gggagccctg gcttccctcg tgatgatcct aagcatatat 720  
 tctcgacccc tgccttggat catctatgga gtctttgcca tcctctctgg ccttgttgtc 780  
 ctccctcttc cg 792

<210> 281  
 <211> 1047  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 ggtcttggtt tcaagggatc atatgaaaag tgcccagcag ttcttccagt tgggtgggagg 60

atcagctagt	gaatgtgata	caataccagg	gaggcagtgc	atggcttctt	gtttcttctt	120
gcttaagcaa	tttgatgatg	ttttgattta	cctcaactca	tttaagagcc	acttctataa	180
tgatgacatc	tttaacttta	attatgccca	agccaaagct	gcaacaggca	ataccagtga	240
gggcgaagag	gcgttcctct	tgatccaaag	tgagaagatg	aaaaatgatt	acattttacct	300
cagctgggtta	gctcggggct	atattatgaa	taagaaacca	agactagcct	gggaacttta	360
tcttaagatg	gaaacctccg	gcgagtcctt	cagtctctta	cagctcattg	ctaattgactg	420
ctacaagatg	ggccagtttt	actattctgc	caaagctttt	gatgtccttg	agaggctgga	480
tcctaaccct	gaatattggg	aaggcaaacg	gggtgcctgt	gtgggcattt	tccagatgat	540
catagctggg	agagaacca	aagagaccct	tcgagaagtg	ctccattttac	tgagaagcac	600
aggtaacacc	caagtagaat	acatgatccg	gatcatgaag	aatggggcca	aagaaaacag	660
agtgtccatc	ctaaaatagc	gccagtgcac	taggaaccag	cttctacttt	gacataaaac	720
tggaaatcat	tttctactca	gctttaatct	gtgatacagg	gctctgtttt	attgacattt	780
tccttccttg	ctctttaagc	ctcaaggcca	gagactgact	tgctgagact	tagtctcctg	840
gctgaacaga	gtgccatagt	ctgtgaccct	gtatgatcct	agtagcaata	agattttgga	900
cttatctggt	gcctttcttc	caaaaatgct	cagagtactt	ttatgcaatt	tactgacttt	960
aaggaaaaca	gtataacttt	tttttgtag	cattttatgg	cattgtctcc	tggctgcaat	1020
aacaaacatc	tttgatgttc	aagaatc				1047

&lt;210&gt; 282

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

ctttaaaagt	ttctgatgaa	ttagtgagc	aatatcaa	taaaaaccag	tgtctttcag	60
caatagcatc	tgatgcagaa	caagaacct	aaattgatcc	atatgcattt	gttgaaggag	120
atgaggaatt	cctttttcct	gataaaaaag	atagacaaaa	tagtgagaga	gaagctggaa	180
aaaaacacaa	ggtaagagaa	atcacagtac	accaaagggg	cactgttgat	ttttagtcac	240
tgcatatagt	aacactctta	ctaccacagt	tatctcactt	cttttgtctt	agaatagaaa	300
gagtaatcat	ttatttagaa	aaacctat	ttgccgggct	gcggtggctc	atgcctg	357

&lt;210&gt; 283

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 283

ctgggggtgcc	ccgcaacctg	ccttccagcc	tggagtatct	gctgttgtcc	tacaaccgca	60
tcgtcaaact	ggcgctgag	gacctggcca	atctgaccgc	cctgcgtgtg	ctcgatgtgg	120
gcggaaattg	ccgccgctgc	gaccacgctc	ccaaccctg	catggagtgc	cctcgtcact	180
tccccagct	acatcccgat	accttcagcc	acctgagccg	tcttgaaggc	ctgggtgtga	240
aggacagttc	tctctcctgg	ctgaatgcc	gttggttcgg	tgggtctggga	aacctccgag	300
tgctggacct	gagtgagaac	ttcctctaca	aatgcatcac	taaaaccaag	gccttccagg	360
gcctaacaca	gctgcgcaag	cttaacctgt	ccttcaatta	ccaaaagagg	gtgtcctttg	420
cccaccttgt	ctctggggcc	cctttccttc	ggggaagcct	gggtcgcccc	ttgaaggagg	480
ctggggacatg	gcacggcaat	ctttcttttc	cgctccactt	cgaatggggg	aagacc	536

<210> 284  
 <211> 440  
 <212> DNA  
 <213> Homo sapiens

<400> 284  
 gtatcttatt tgcggcgctg atctggagtt cgttcgatga gaatatagaa gcttcagccg 60  
 gaggcggcgg tggttcgtcc atcgacgctg tcatggttga ttcagggtgc gtagttgagc 120  
 agtacaacg catgcaaagc caggaatcaa gcgcgaagcg ttctgatgaa cagcgcaaga 180  
 tgaaggaaca gcaggctgct gaagaactgc gtgagaaaca agcggctgaa caggaaacgcc 240  
 tgaagcaact tgagaaagag cggtttagcgg ctcaggagca gaaaaagcag gctgaagaag 300  
 ccgcaaaaca ggccgagtta aagcagaagc aagctgaaga ggccggcagcg aaagcggcgg 360  
 cagatgctaa agcgaaggcc gaagcagatg ctaaagctgc ggaagaagca gcgaagaaag 420  
 cggctgcaga cgcaaagaaa 440

<210> 285  
 <211> 119  
 <212> DNA  
 <213> Homo sapiens

<400> 285  
 gcgatggaaa tcgtccacga gccgcgcgac ctcgagcggtt acatgcgcga ggccgtgaag 60  
 gtgtcgaaag attcgccggt gctgctcgac cgcttctctga acgacgcgat cgagtgcga 119

<210> 286  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
 aaacagggga ttttaagtgtg tcttttgtgt ttgcaaggca ctaacaccac tcccgtctgt 60  
 atttaaatgc tgtccccagg ttacgactat ggctatgtct gcgtggagtt ttcactcttg 120  
 gaagatgcc a tcggatgcat ggaggccaac cagggttgctt tataacttcgg tcaaatgatg 180  
 ctggaaggat atatTTTTTT atatatgggg agggaggggt tcaaatgatt ttactttgga 240  
 aaggtacaag aagtcctatc gtggagcata ctgtattcca accatcggtt gtgaggaaaa 300  
 tctttaaaaa ggctggaaag ctttctctag aaaacttaat gggcacagag tgcattttta 360  
 aagctagagc ccagttgctt ttggactaga ttccaaaa 398

<210> 287  
 <211> 1177  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1177)  
 <223> n = a,t,c or g

<400> 287  
 cccacgcgtc cgctcctctg ggggtcaaga ggaccccgcc agccagcagt gggcacgacc 60  
 gcgcttcaca cagccctcca agatgaggcg ccgggtgata gcacggcccg tgggtagctc 120  
 cgtgcggctc aagtgcgtgg ccagcgggca ccctcgcccc gacatcacgt ggatgaagga 180  
 cgaccaggcc ttgacgcgcc cagaggccgc tgagcccagg aagaagaagt ggacactgag 240  
 cctgaagaac ctgcggcccg aggacagcgg caaatacacc tgccgcgtgt cgaaccgcgc 300  
 gggcgccatc aacgccacct acaaggtgga tgtgatccag cggacccggt ccaagcccggt 360  
 gctcacaggc acgcaccccg tgaacacgac ggtggacttc ggggggacca cgtccttcca 420  
 gtgcaagggt cgacgcgacg tgaagccggt gatccagtgg ctgaagcgcg tggagtacgg 480  
 cgccgagggc cgccacaact ccaccatcga tgtgggcggc cagaagtttg tgggtctgcc 540  
 cacgggtgac gtgtggtcgc ggcccgacgg ctctacctc aataagctgc tcatcacccg 600  
 tgcccgccag gacgatgcgg gcatgtacat ctgccttggc gccaacacca tgggctacag 660  
 cttccgcagc gccttcctca ccgtgctgcc agacccaaaa ccgccagggc cacctgtggc 720  
 ctctcgtcc tcggccacta gcctgcccgt gcccggtggtc atcggcattc cagccggcgc 780  
 tgtcttcate ctgggcaccc tgctcctgtg gctttgccag gcccagaaga agccgtgcac 840  
 ccccggcct gccctcccc tgctgggca ccgcccgcgc gggacggccc gcgaccgcag 900  
 cgagacaag gaccttcct cgttggcgc cctcagcgt ggccctgggt tggggctgtg 960  
 tgaggagcat ggggtctcgg cagcccccca gcaactactg ggcccaggcc cagttgctgg 1020  
 ccctaagttg taccctaaac tctacacagg acattccaca ccacacacat acacacaccc 1080  
 cccaccctcc tgccaattaa acagtagcca tccccnaaa atnnnnnnnn nnnnnnnn 1140  
 nnnnnnnnnn nnnnnctcgg cccccgcta ttcacgg 1177

<210> 288  
 <211> 100  
 <212> DNA  
 <213> Homo sapiens

<400> 288  
 tgaattttca ttttacaggg aagtgtttgt ttatgtcagg gctcagttag gtccagctga 60  
 cccatattga tgatcacact ctaccagggt attgaagctc 100

<210> 289  
 <211> 406  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 cggcagcagc ggcacgagag tcagagggtt ttaatttact tgtgaagctc acactattga 60  
 aactaattgc aatgcttgac tttattttct ttagagtcca agaaagagaa aaacaaggca 120  
 tagcacaaat cccctctag agtgtcatgt tgggtgggta atggattcca gagaccatgg 180  
 gccaggaaca tcctctgtca gcacttcaaa tgcttcacct tcagaaggcg caccactagc 240  
 aggaagtatt ggatgtactc ctcatctcatt cccaaagttc cagcatcctt ctcatgaact 300  
 tttgaaggaa aatggcttta cccaacaagt gtaccacaag tatcgtcgaa gatgcctaag 360  
 tgagagaaaa cgcttgggaa ttggtcagtc ccaagaaatg aatacc 406

<210> 290  
 <211> 359  
 <212> DNA  
 <213> Homo sapiens

<400> 290  
 cccggcagcg ggggcagcgc gggggggccga gacggcagtg cctaccaggg cgcgctgttg 60  
 cctcgagaac agttcgcggc cccgcttggg cggcgggtgg ggacctcgta ctccgccacc 120  
 taccggcct acgtgagccc cgacgtggcc cagtcctgga ctgccggggc ctccgatggc 180  
 agcgtcctgc acggcctccc aggcgcgagg cccaccttcg tgtccgactt cttggaggag 240  
 ttcccggtg agggctcgtga gtgtgtcaac tgcggggccc tgtccacacc gctgtggcgc 300  
 cgagatggca cgggccacta cctgtgcaat gcctgcggcc tctaccacaa gatgaatgg 359

<210> 291  
 <211> 954  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 cccagatcat cgacatggtg cgttgtgtgtg gtggtacagc tgtggagtct tacctgtcac 60  
 agtgtcaaga aatgaagggg atgaacggaa ccagggtctg accctgtatc tgtggatacg 120  
 gcaggagtgg acagatgcct acctacgatg ggacccaat gcctatggtg gcctggatgc 180  
 catccgcac cccagcagtc ttgtgtggcg gccagacatc gtactctata acaagtactg 240  
 cctatctggg cccctcctct ctcttaccct tctctagact tgcccttagc tgtgggggtg 300  
 tagtgatccc ctctccctac cacataacct ggttgccacg ctgccctgga agcttttccc 360  
 caggaccctt ctaagctgcc aagcactcag cccctccatg gcacccccac tttaggctat 420  
 cccaggccag cccaggctga acgtctcctc ggaacctact gtgtggtcca gggcagatgt 480  
 ctgaatcaca agggcctctc tagggcacac ttttagctct aagtctctca gggctcccc 540  
 aagagcctgt ctaaggtctt ctttctccca ggacatagcc ctctggaaca ctgctttatg 600  
 tctccttgac cagttccgtg tctccagccc agcacatagc tctgcataat ttctctgggg 660  
 ccttctaca agttttgcag atgtccccc aggggaagtca ctgtgtgtcc cggagctacc 720  
 tctgggttct gcagaggcct ttttatacat cctctggcta cgtctgtgtc ccttctggcg 780  
 ccttcaggca ccaccccttc caggcctcga aaggcagcgg gtctctctag gtgcactcca 840  
 cctctgtgtg tgctttgttc tgaaaacaag aatcaaatta acgaaaaaaa aacaagcaca 900  
 agtttattta tttatttgag acacagcctg ggcaagagag tgagacttca tctc 954

<210> 292  
 <211> 595  
 <212> DNA  
 <213> Homo sapiens

<400> 292  
 tacgcactga ctggtgcggtt ggttattgtc accgggatgg tgatgggaaa tatcgccgat 60  
 tttttcaatc tgctgttttc cagtatgagt aataccttca ccttcctcaa cgcgcgcatt 120  
 ttaatctcta tcttcctcaa cgcctggctg atggaaatcg tcccgttgaa aacgcagtta 180  
 cgttttggct ttctcctgat ggtgctggcg gttgccggtt tgatgttcag ccacagcctg 240  
 gcgctgttct cggcggcgat gttcattctc ggggtggta gcggcatcac catgtcgatt 300  
 ggtacattcc tggtaacaca aatgtatgaa gggcgtcagc gcggttcccg cctgttattt 360  
 accgactcct tcttcagtat ggctgggatg attttcccaa tgatcgccgc gtttctactg 420  
 gcgcgcagca ttgagtggta ctgggtttat gcctgcatcg ggctggtgta tgtcgtctatt 480  
 tttattctga ccttcggctg tgagtcccg gcgctgtgca gccatgcgac taagtgggt 540  
 accgccagta gttatcccag tctggacggt gtacagctac ggacattgaa tgcgt 595

<210> 293  
 <211> 552  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(552)  
 <223> n = a,t,c or g

<400> 293  
 tcttgaagag ccgctgctga tcaacaccag cttaagcaaa gaacagcgtc gggaaaaagc 60  
 cctgtcgatg atggcgaaag tcggcctgaa aaccgagcac tatgaccgct atccgcatat 120  
 gttctccggc ggtcagcgtc agcgtatcgc catcgcccggt ggtctgatgc tcgaccgga 180  
 tgtggtgatt gccgatgaac cggtttccgc gctggatggt tcagtgcgcg cgcaggtgct 240  
 gaatctgatg atggatttgc agcaggagtt ggggctgtct tatgtcttta tctcccacga 300  
 cctgtcgggtg gtggagcaca ttgctgatga agtgatgggt atgtacctgg gccgctgcgt 360  
 ggagaaggga acgaaagacc aaatcttcaa taaccgcgcg catccgtaca ctcaggcgct 420  
 actttccgag acgccgcgcc tgaaccggga cgatcgccgc gagcgcatca agctcagcgg 480  
 tgaactacca agccactga atccaccgcc gggttgcgcc ttcaacgccg gctgttgtcg 540  
 gcgnttcggc cc 552

<210> 294  
 <211> 426  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 294

tagcgccacc	cttgaacggg	tactaaatca	ccctgacgaa	acgcaagccc	gacgcttaat	60
gacgctggaa	gatatcgtca	gtggttattc	caatgtgttg	atttccttg	cagatagtca	120
gggtaaaacg	gtgtatcact	cccccggtgc	gccggatatc	cgcgagttta	cgcgtgacgc	180
catacccgat	aaagacgctc	agggtggcga	ggtgtatctc	ctttccggcc	cgacgatgat	240
gatgccaggc	cacggtcacg	ggcatatgga	acacagcaac	tggcggatga	ttaacttgcc	300
ggttggcccg	ttggtggacg	gcaaaccgat	ttatacgctc	tacatcgcg	tttcgatcga	360
ttttcatctt	cattacataa	atgatttgat	gaataaactt	attatgaccg	catcggtaat	420
catcat						426

&lt;210&gt; 295

&lt;211&gt; 340

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

gggtgctggc	gtatccgggg	attaaagtct	cgacggcaga	agccagggct	attttaccgg	60
cgcagtatcg	ccgccaggat	tgcattgcgc	acgggcgaca	tctggcaggc	ttcattcacg	120
cctgctattc	ccgtcagcct	gagcttgccg	cgaagctgat	gaaagatgtt	atcgctgaac	180
cctaccgtga	acggttactg	ccaggcttcc	ggcaggcgcg	gcaggcggtc	gcggaaatcg	240
gcgcggtagc	gagcggtatc	tccggctccg	gcccgaacct	gttcgctctg	tgtgacaagc	300
cggaaccgc	ccagcgcggt	gccgactggt	tgggtaaaat			340

&lt;210&gt; 296

&lt;211&gt; 281

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

cgggcagcag	cagcgcgtgg	cgctggcccg	cgcgtgatc	ctcaagccga	aagtgctgct	60
gtttgatgag	ccgttgagta	acctcgacgc	caacctgcgt	cgcagcatgc	gcgacaagat	120
ccgcgagttg	caaaagcagt	ttgatatcac	ctcgtgtac	gtcaccacag	atcagagcga	180
agcctttgcg	gtttctgata	ctgtgctggt	gatgaacaag	gggcacatca	tgcatatcgg	240
ctcaccgcag	gatctccggg	tacggagatt	gaattggtaa	t		281

&lt;210&gt; 297

&lt;211&gt; 155

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 297

tggcggtgca	ttacctagag	cgggtgagaa	ttgccgaaca	tgcgcataag	tttcccgga	60
agatttcagg	tggtcagcag	caacgcgttg	ccattgcgcg	ttcgctgtgt	atgaagccga	120
aaattatggt	gtttgatgag	ccaacgctcg	cgctc			155

&lt;210&gt; 298

&lt;211&gt; 217

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 298

gctccctatg	acgccgaaaa	ttatTTTgat	tatgacaatc	tgaataacgg	acTTTcttTg	60
cagcactggT	ttggcgtcga	ttcactgggg	cgtgacattt	tcagccgtgt	cctggTtggT	120
gcgcaaatct	cgctggcggc	gggcgtgttt	gccgtgttta	tcggTgcggc	gatcggggac	180
ttgctgggct	tgctcgctgg	atattatgaa	ggctggT			217

&lt;210&gt; 299

&lt;211&gt; 568

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

aggTattctg	tctgatcgct	gaccttgacc	cgatcgatga	gcttgtggac	ttcccgatcg	60
tttacgcttc	tgcgctgaac	ggTatcgcg	gtctggacca	cgaagatatg	gcggaagaca	120
tgaccccgct	gtaccaggcg	attgttgacc	acgttctctg	gccggacgtt	gaccttgacg	180
gtccgttcca	gatgcagatt	tctcagctcg	attacaacag	ctatgttggc	gttatcggca	240
ttggccgcat	caagcgcggt	aaagtgaagc	cgaaccagca	ggTcactatc	atcgatagcg	300
aaggcaaaac	ccgcaacgcg	aaagtcggt	aagtgcTggg	ccacctcggt	ctggaacgta	360
tcgaaaccga	tctggcgga	gctggcgata	tcgttgcgat	cacgggcctt	ggcgaactga	420
acatttctga	caccgtttgc	gacacgcaaa	acgttgaagc	gctgccggca	ctctccgttg	480
atgagccgac	cgTttctatg	ttcttctgcg	ttaacacctc	gccgttctgc	ggtaaagaag	540
gtaagtctgt	aacgtctcgt	cagatcct				568

&lt;210&gt; 300

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

```

<400> 300
caaggcaccc gcgctgaatc tcaagggtcc tccaaagata aaaccctgtc tgccttcgct    60
ggcctgaaat tcggtgacta cggctccatc gattacggcc gtaactacgg tgtagcatac    120
gacatcggtg cgtggactga cgtcctgcc aatttcggtg gtgacacttg gactcaaacc    180
gacgtgttca tgactcaacg tgcaactggg gttgcaacct atcgtaacaa cgacttcttt    240
ggtctgggtg atggtctgaa ctttgcgtgc cagtaccaag gcaaaaacga tcgtagcgat    300
ttcgataact aactgaagg taacggccac ggcttcgggt tctctgtctac ctatgaatac    360
gaaggg

```

```

<210> 301
<211> 199
<212> DNA
<213> Homo sapiens

```

```

<400> 301
gcgataccta ttccgtttct attccgctgg gagccaccat caatatggcg ggcgcagcaa    60
tcactattac cgtgttgacg ctggctgcgg ttaatacgtc ggggtattccg gtcgatctgc    120
ccacggcgct gctgttgagc gtggtggcct ctctgtgtgc ctgtggcgca tccggcggtg    180
cggggggggtc tctgctgct

```

```

<210> 302
<211> 140
<212> DNA
<213> Homo sapiens

```

```

<400> 302
gccacgcgc agcaagggtc gccagtggt atcacctga agctaaataa ccttgtcgat    60
aaaggcctgg ttgatcgtct gtatgcggcc tccagctcgg gcgttcgggt taatctgctg    120
gttcgcggaa cgtgttcgct

```

```

<210> 303
<211> 441
<212> DNA
<213> Homo sapiens

```

```

<400> 303
cgcgcgaatg acgctcatcc ccggcacaca tctgctggaa aacatccaca acatctgggt    60
gaacggggta ggcacgaata gcgcgccgtt ctggcggtat ttgcttaaca gctttgtgat    120

```

```

ggcgttcagc attacgctcg gcaaaattac cgtctcgatg ctctcgccat ttgccattgt 180
ctggtttcgt tttccgctac gtaacctctt cttctggatg atttttatca ccctgatgct 240
gccggttgaa gtacgtatct tcccgacggt ggaagtcac gccaacctgc agatgctcga 300
cagctacgcc ggtttaacgc tgcgctgat ggcctcggcg accgctactt tcctgttcgc 360
caagttaa atgtcggggc cggacaaggt ggtgccagcc gcgcggatct ccgggtacgg 420
acctagagtt cgtaagcaag a 441

```

```

<210> 304
<211> 402
<212> DNA
<213> Homo sapiens

```

```

<400> 304
ctgtgcgaaa tgtttgctg atgcggatga atgcccctcc ggggcgtttg aacggattgg 60
tcgcgatata agccttgacg ctctggaacg ggaagtgatg aaagatgaca tttcttttcg 120
cacgtccggc ggccgctca cgctttctgg cggcgaagt ttaatgcagg cggagtttgc 180
taccggtttt ttacagcgac tgcggtctgt ggggtgtgtca tgcgccattg aaactgccgg 240
agacgcacca gccagcaagc tattaccgct ggcgaaattg tgcgatgaag tgttgttcga 300
tttaaaatt atggacgca ctcaggcgcg ggatgtggtg aagatgaacc tgccacgcgt 360
gctggagaat ctgcgtttgc tggtagtgga gggcgtaac gt 402

```

```

<210> 305
<211> 346
<212> DNA
<213> Homo sapiens

```

```

<400> 305
tacctgttat tgttgtctg ctcccttggt atgtctctgc tggttgggct ggtgtacaaa 60
tttacgcgcg aacgcgcggg caaacagtcg ctggatgatt tgatgaacag ttctgtgtat 120
ctgatgcgca gcgaattgcg tgagatcccc ccacacgact ggggtaaaac tctgaaagag 180
atggatttaa atctctctt cgatctcgt gtcgagccac tgagtaaata ccatcttgat 240
gatatttcca tgcaccgact gcgtggcggc gaaattgtcg ccctggacga tcagtacacg 300
tttttgcagc gtatcccgcg cagccactac gtgctggcag ttggtc 346

```

```

<210> 306
<211> 207
<212> DNA
<213> Homo sapiens

```

```

<400> 306

```

```

gttgaattat tcctcagcga tgaaggcgat gatgtggtga ttgaagtcgc cgatcagggc    60
tgcggcggttc cagagtctct acgagacaaa atatttgagc agggggtcag tacgcgtgct    120
gacgagccccg gtgaacatgg cattggggtg tacttgattg ccagctacgt aacgcgctgc    180
ggtggtgtta tcactctcga agataat                                     207

```

```

<210> 307
<211> 214
<212> DNA
<213> Homo sapiens

```

```

<400> 307
tcgacgccat tatcgcccc gatgccaacg ccttgcccgc tgccgcacaa gccgcagaaa    60
acttgaaaaa tgacaaaagta gcgattgtcg gattcagtag gccaaatgtg atgcgcccgt    120
atgtagagcg cggcacggtg aaagaatttg gcctgtggga tgtgggttcag caaggcaaaa    180
tatcagtgtg tgtggcgcat gcattacagt aaaa                               214

```

```

<210> 308
<211> 129
<212> DNA
<213> Homo sapiens

```

```

<400> 308
tacatcgtag tgacggggaa aacacattgc ggtacgccac ttactaccgt tacaggagac    60
gcaacgcaat cgggttatct gacgctgaac ctgcctgaaa tgtgggaagt gtcagggttat    120
aaccgtggtt                                     129

```

```

<210> 309
<211> 358
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(358)
<223> n = a,t,c or g

```

```

<400> 309
gccggttttg ccgcatcaat ggtgcttagc gatgactcaa cgtaccagtg cgccgactgc    60
aaatctgccc gccgggccag taaggagtag ccagttcat caagaagctg gcttgccact    120
ttcggcaacg cgaccggatt aagcttcaat gactttgtct ggttatttgt aagtgcgctt    180

```

aaccgtgcct	caataatfff	cattttcccc	gcgacatcgt	tgagctgctg	ccgggttttg	240
ctggcattaa	tatcgggttc	cacaccttca	actgaagaag	taatcccggt	ctgatatagc	300
tggcgatcgg	tcgcgataat	ggcgntctgc	tctttttcta	tttgcgtcaa	gaccgtgg	358

<210> 310  
 <211> 253  
 <212> DNA  
 <213> Homo sapiens

<400> 310						
tggcggcctt	cctgagagaa	tattgccgag	gagtacgcga	ctaaacgcta	tcgttctaac	60
gtcatcaact	gggggatggt	accgctgcaa	atggcggaag	taccaacctt	tgaagtgggg	120
gattacattt	acatccctgg	cattaaagcg	gcgctggata	atccgggtac	gacgtttaaa	180
ggttatgtga	tccatgaaga	tgccgcggta	acggaaatta	cgctctatat	ggaaagtcag	240
gaagccagaa	cag					253

<210> 311  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 311						
gctgcaaact	gaaattggca	gcatggtcta	tgccggtgaaa	ccaggcgatg	gttctgcgcg	60
tgaacaggcg	gcgagctgcc	agcgtgtgat	tggcgggtctg	gcgaatattg	ccgaggagta	120
cgcgactaaa	cgctatcggt	ctaactgcat	caactggggg	atgttaccgc	tgcaaatggc	180
ggaagtacca	acctttgaag	tgggggatta	catttacatc	cttggcttta	aagcggctaa	240
gtatagtcgg	ggcacggcgt	ttacagtcta	tgcgatctcc	gggtacggac	ctcgaatctg	300
ataa						304

<210> 312  
 <211> 344  
 <212> DNA  
 <213> Homo sapiens

<400> 312						
actctagagg	atctgctgat	ggcgtagat	ggagagcaac	atcttcagca	acaggtatcg	60
gaaaaagtat	tagccgataa	tgtgttaatt	gcccctgggt	ctgttaaacc	tgatgcgaca	120
ttctggtcgg	ccttaatcca	ggatcgctat	aacgtgatga	cctgtattga	aaaagacgcc	180
tgcgctcctgg	tcgagcaaga	tctgaatagt	gatggtcagg	cggagcggat	cctgtttgct	240
tttaatgatg	acagagtcac	tgtctatggc	tttgactcag	acagaaaaga	atgggacgcg	300

cttgatatga gtttacttcc gaacgaaata acgaaagaaa aatt

344

<210> 313  
 <211> 630  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 agagtcaaat agcagatgca ggaagatgcc aggtgaaaga tgccgggggtg gcccagctcg 60  
 gctgtccctg ctgcttgacc tgcccactcg ccctcttccc ccccccgac aggtgattga 120  
 cttcgatcc gccagcattt tcagcgaggt gcgctacgtg aaggagccat acatccagtc 180  
 gcgcttctac cgggcccctg agatcctgct ggggctgccc ttctgcgaga aggtggacgt 240  
 gtgggtccctg ggctgctgca tggatgagct gcacctgggc tggcctctct accccggcaa 300  
 caacgagtac gaccaggtgc gctacatctg cgaaaccag ggctgcccc agccacacct 360  
 gttgcacgcc gctgcaagg cccaccactt cttcaagcgc aacccccacc ctgacgtgc 420  
 caaccctgg cagctcaagt cctcggtga ctacctggcc gagacgaagg tgcgccatt 480  
 ggagcgccgc aagtatatgc tcaagtcgtt ggaccagatt gagacagtga atggtggcag 540  
 tgtggccagt cggctaacct tccctgaccg ggaggcgctg gcggagcacg ccgacctcaa 600  
 gagcatggtg gagctgataa ggcctgctc 630

<210> 314  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 314  
 cgccttgtaa agaaacgagt tgagtgtagg cagtgtggga aggccggcag gaaccagtca 60  
 acgctgaaga cgcacatgcg aagccacacg ggggagaaac cgtacgaatg cgatcactgt 120  
 ggtaaggcct tcagcatagg ctccaacctg aatgtgcaca ggcgatcca caccggggag 180  
 aagccctacg aatgccttgt ctgcggggaa gccttcagcg accactcatc cctcaggagc 240  
 cacgtgaaaa ctcaccgggg agagaagctc tttgtgtcat ccgtgtggaa aaggctccag 300  
 tgagcgcgcc tgctttagag acacaggatg attcagaccg gaaacagacc tcgtgggtgt 360  
 aagaggaagc ctctgtgagc tcgcacctta ctgggtgcaa aagaatccac ggaacttggg 420  
 agaagtccag ttctgtaaa aactgggaag acgaggcggt ctcatcccat aggaggttg 480  
 tgagaactca cgcgggggt gaaaatgtac gtctgtagca tggagaagcc ttcagggtac 540  
 attcagctct taacaaacac aggaggactt aatggcagct tggcatttaa tgtcaaaatc 600  
 caagcgtgg catttaatgt caaaatgact tcagaccact tctagccttc tgggcccag 660  
 agtaataatg agcactag ggagcatctc tgtaaacaca gtggctgggg aaacccttc 720  
 tagtctcact tgattcctca tgacggaaat cactactaaag agagaaatca gtgaagtaag 780  
 gaacgtggaa ggtcatgaat gggccgcaaa ccacggccag ctgcttgtct ttgtatggct 840  
 tgccagctaa caatagtggg tccatcttta aggaagaaga atgtttgatg gagaaaattt 900  
 gtggccaatg aagtctgaaa tacttcctgt catctgcccc ttccagaaa aacttggccg 960  
 acccttgggc tacagcacgg gttctcagtc gggcgacgat ttggctgtgt aggcgtcatt 1020  
 tggcaatgtc tagagacatt tttggtagtt agaattgggg gaagatactc ctgacttgta 1080  
 ataagaagac atcagagatg ctgctaagtc ggctccagca cacaggagcc cccacaacg 1140  
 aagagttagt gccccaaac gtcactgttg ctgaggttga aaataatcat gcagtcattc 1200  
 ctcaattact gcctccagca attcctccat ttttatgaat cttgtgagca cttacgctag 1260  
 gagaaatttc ttttcaaaa cttttaaaat acagttagtg ctgataattc ctatgtggaa 1320

atgattccag	ccatggtccc	ctcacttgag	catgtgaata	ttctcacgga	gagaagcccc	1380
agcgagattt	tccggtgaat	acgggattgc	acttactctt	tcatcacgga	aacagacccc	1440
cgagagaagc	cccaacgaga	ttttccggtg	aatacgggac	tgcacgtact	ctatcatcat	1500
gaaaacagag	ccccgttcat	aaatttttca	tctttatttt	taaggttata	ctcctctaaa	1560
taacccttaa	gcctcatcaa	gaaaggtttg	tttatagtat	ttttactata	gcttcatcct	1620
tgataacgtc	ctaattttct	tctggacaac	ctccttgacc	aatggcatat	tgagatctat	1680
gtgacatgag	gatatttctc	agtaccactt	gtttactggt	acctgatgca	cacggattgc	1740
gaccagagca	tgatgcctcc	atcaagtggg	aatatgtttg	cagcctgctg	tccagccaag	1800
agtgacagat	acttctagtg	acttccccgg	tatccactct	catcttcttc	caatatcaag	1860
agaatccagg	ttctgtcaga	ttagtaaggt	gtgctaattc	aaattttaaa	aaatctctta	1920
cagggttttct	tgcagctggg	accatccatg	tctcacagcc	ctggccactg	acagatcagc	1980
agatgtcacc	acatgggctt	ctgagaaagc	tcttgaatgg	ggatcgttct	taaacatgaa	2040
ttcctccctg	tatgttttgt	tctttgcttt	acttttcacc	ttgcaaagag	atccagtacc	2100
tagtatttgga	agatccacct	taacgaccgt	gcatatgaaa	accacagtct	aaggaagtga	2160
ctgcagaaa	ctcacagcga	ccctggcctc	ccctgtggcc	tctttgagtg	tctgcagcag	2220
ccctggactt	ccagacttct	atcacatgag	aaaaataaaa	actgattatt	ggtttaaaaa	2280
aaaaa						2285

```
<210> 315
<211> 1316
<212> DNA
<213> Homo sapiens
```

<400>	315					
ggctgtctat	cagtggataa	ggtgggggct	gtctatcagg	ggagaaggtg	ggggctgtct	60
atcagtggag	aaggtggggg	ctgtctgtca	gtggagatgg	tgggggctgt	ctgtcagtgg	120
agatggtggg	ggctgtctgt	cgggtggagat	ggtgggggct	gtctgtcgg	gtagatggtg	180
ggggctgtct	gtcgggtggag	atggtggggg	ctgtctgtcg	gtggagatgg	tgggggctgt	240
ctgtcgggtg	agaaggtgga	agcttgtact	cacagcaggg	gatatttaga	cttgaagggg	300
ccaggaggga	ggtactgggt	tctactaagc	cccatgttca	ctgggcagcc	actaagttag	360
ggaccgtgtg	tgtaccgagt	ggattccgac	aaagaagctg	tctcaggagc	cccagccagc	420
tgcagagggg	ggccaagct	ccaaggctgg	gtgtcaggtt	tgccaggtgc	tggtccgct	480
aggggcccga	ggctgcgctg	ggcgggactg	ggctgggctg	gtacctgtgc	ccggtgtcag	540
gccagctgta	gttcgacgg	tcagctgccg	ctctctggcc	ccatgcgaac	tgctgtgcca	600
ggtgcaccct	gggggaccag	gctgcctggg	cttcttgga	ctggtgaagc	tgccgccact	660
tctctatg	tgtctccagc	aggcaattct	gggtaaacga	tcttcatttg	cctataaagc	720
tgcacagctc	acaggccttg	gacgctttct	gccccagccc	cagcatttgc	cctttggaca	780
gactctgaaa	ccgtgcgcag	aacgcaccct	gtcattacaa	atgactctgc	gaggcagtc	840
ccgggggcct	ggcaggagca	cctgtgtttc	tgtggggctc	gaaaatgaca	gaccaatcgc	900
ttgaacccgg	gaggcggaag	ttgcagtgag	ccgagatcga	gacattgccc	tccagcctgg	960
gcaacaagag	caaaactcca	tctcaaaaaa	aagaaaaaag	tgccgagtgg	agtcgtcacg	1020
cccgtaatcc	tagcaactttg	ggaggcagag	gtgggcggat	cacctgaggt	cgggagttcg	1080
agaccagcct	gaccaacatg	gagaaaaccc	atctctacta	aaaacacaaa	aattagccgg	1140
gcgtgtgcat	gcctgtaatc	ccacctactc	aggaggctga	gggaggagaa	tgcgttgaaa	1200
ccggggagccg	gaggttgtag	tgagccgaga	tcgtgccatt	gcactccagc	ctgggcaaca	1260
agagcaaaaa	ctccatctca	aaaaaaaaaa	ggagagagag	aaaccgggac	cgaag	1316

```
<210> 316
<211> 2486
<212> DNA
<213> Homo sapiens
```



<400> 316

tttttttttt	ttaaacaaaa	ctttattggt	aatagttttc	aaatatgttt	acaacagcac	60
actgttcaag	aggaagtctc	gtccttcgca	gcacacaggt	tgaatcgccc	ccgcacccac	120
ccggggcccc	accccaggcc	tgagaactcc	tcttgggatg	gggagaagtt	atgagagggg	180
gaaatacggg	gatgaatggg	gtggctcccc	agcggctccc	cacttttcta	ttaogagaga	240
aaaaagcaca	aatgagaaa	tgggggagag	gtgatggaca	gctgacagct	aagctggagg	300
aggggcgccc	aggatggggg	aggcggaa	tgggtgggtga	gtaaaacagg	cagcccctcc	360
ccagcagctc	tagccttgaa	ccccgggcgg	tggcttgggg	ggacttgggc	tcttctgttc	420
ccttttgcag	ggatgccctc	cccactcagc	tgagggaagg	ctggacgtta	aaatctagcg	480
gagaataaaa	ttaaggagtt	ggggggaaac	gctgctggga	ggaaagactt	gggcttgggg	540
ctccccctct	gtctttttgg	gggatgactc	ctctttggca	gggagagggg	cagctgcttt	600
gtctggcttt	caaagcccaa	gggtgaagac	aggtctgttg	gggaaaaaga	gagcggaggc	660
ttcctaagg	ggcctagacc	ctcgcaggat	tggcagagag	gattccccgg	ggagggggccc	720
aggggagatt	agcagcgggg	aggttcaa	cccagcgct	ccctttccaa	agtcagtctg	780
cttctcttta	aaatggattt	gaggaatggg	gggacatggg	aggggtggga	gtagagggaag	840
gagggaggga	ggcactgggtg	gaacttaaat	aagattttta	attgttgttt	ttttaaaaaa	900
attctagcaa	gaacccact	gaacatgtca	ctaaaaatct	ctccttccca	ggcaggatta	960
ctccgaaaag	aaggttggcg	cttcgttcat	ttgcccttag	caagtggggc	ctgtgggttg	1020
gtgggatggg	ggtgtgggtg	ggggctggag	ttaagcgtga	gccccctctt	ccataccctg	1080
tccctggata	caccagcaag	acctggtctg	actggagtgt	agaaactcgt	ttaaaacagg	1140
cagaagtggg	ctgggagggc	tgagggctg	gggggctgtg	gggaaagaga	aagggaaaag	1200
tgggagaggg	ggcaggaggg	tgaaggggat	gagggggagc	agctgggtgt	tctgtccctc	1260
tgattatctg	ggcttctctg	tccccctacc	cctggagggt	gggggtgggg	tgaaattaga	1320
tgaaggaac	tctggggccc	tctggctgtt	caatccaacc	ctcccacccc	cccgacccaa	1380
aaaaagaaaa	aaagaaaaag	aaaaccatg	ggggcacagg	catgcccta	aaactagaa	1440
aactccttgc	ccaaacttct	cattgatgga	aaaccggat	ttcttcttcc	tcatagtcgt	1500
caaagttaac	tcgtatcccc	agggccttta	aactttggta	tgaagggagc	ttccaccttc	1560
ctctggtaga	tggcaatcca	gtcagttgtg	gcaaaccact	tgtggttctt	gatatcgttg	1620
accccatctc	tgaggttccc	aaagcgcttg	gtgagatcta	cctgcaggag	gttcgcgagc	1680
aggctccttca	agtacagagc	gaagtgggaa	gggaagcgca	ccttcccaga	gacgatcttc	1740
tcatagatct	ggatgggctg	gtctgcgaag	aagggcgggt	agccagcggc	catttcatag	1800
ataagaacct	ccaggggcca	ccagtccaag	gccttggtgt	agcctttgct	caggataatc	1860
tcagggggcca	ggtactcagg	ggtgccgcac	aaggtccaag	tgcggccctt	cacgcgcttg	1920
gcgaaaccga	agtctgtcac	ctgaatgtag	ccctgctggg	caatgagcag	attctccggc	1980
ttcaggtccc	tgtagatgag	atccagcgag	tgcagatact	caaaggtcag	gacgatctgg	2040
gccgcgtaga	aacgggcatg	gggctcactg	aaccttccga	tccgccgtag	gtgtgagaac	2100
atctccccgc	cgggcacgta	ctccatgacc	atgtataagt	ttgagtgtgc	cttgaaggag	2160
aactcgagtt	tgacgaggaa	cggaaagtgt	acagcttgca	ggatgcgctt	ttcattcagg	2220
gtgtgttcga	tctgtttcag	tttccccacc	ttctgttagt	cgaggatctt	catggcatag	2280
tggttcccg	tctccttggt	tttcaccagc	atcaccgcgc	cgaaggagcc	cgtgcgagg	2340
gtcttgattc	gttcaaaactg	atccaagtgg	gctgtgttct	gagcgggact	ttccattttt	2400
ttaagaaaat	cttctttggc	tttggctaa	aattctttca	cgctctctctg	ctcgtgcccc	2460
ttcttggcgg	cggcggcggt	gcccat				2486

&lt;210&gt; 317

&lt;211&gt; 867

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 317

tttttttttaa	gtttatataa	ctttattata	agtattaatt	tgtttgaatt	aagtttatat	60
aactttaata	taagcattaa	tttgtttgaa	atataaagta	ttataaaata	ttgtaattaa	120

gcttacagat	aatttttaaa	atatatacat	tatgactaat	ataccaaaat	tattttatatg	180
tacacattta	tatttaatac	ccaaagaaaa	tttactacca	cattgctaca	gtagatatta	240
acctgacatg	tttattaatt	gatcctatag	gtataattat	aggtcagcat	aatttttacag	300
tctattcttt	tattttacta	aattaggaat	gccactattc	cggacaaaat	aaatgcagggt	360
gatgtggcca	cccaagaatc	atagtagctc	ttcagttagc	tatcttgcaa	tctctgatat	420
aattctacta	tgtgaataga	gtgaattcca	attcttcac	aaaaagtgc	ggtggagggt	480
gtcagggtgtg	ttccagtata	gattcccaat	ccaacggccg	gcagatggga	gagcagcaga	540
gatggaaatt	gtgctcagaa	taagccctct	ttctcataat	acttgtattt	ctcatgctga	600
gagtagctgt	gcacttttgg	tgtttagaga	agaacttctt	tggaagaata	ttttctgggtc	660
aatttgacca	atgttacatg	taatctgaat	tagtctgtaa	gattctttca	acctcttttc	720
ttctctcaat	acgggttttac	tcagactgag	agctgtcttt	ctcttcaatg	ctttgggaat	780
tcagtgcctt	gtgtctaagc	ccctattagt	atcacatgg	gtctgtgagt	gaggggggct	840
gtcacctgga	gaactcctgg	agctgct				867

&lt;210&gt; 318

&lt;211&gt; 1683

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 318

ggcacgaggt	aggaaccagt	ggtctatgtc	ccgaccacta	cttggettga	tagggcttaa	60
tgaaaagggtg	agagagccag	ctccctgggtg	ccaaccaga	agcagtggca	accacgcact	120
tggtatcacc	aagccctggg	agaaatgtgt	atagaaacac	cccacgggtg	tgaaacagggt	180
aaaatgggtc	atttactgag	caagtcccat	ttgtgctttc	agtatcacat	aatcatttaa	240
ctgttagaag	tcagcatgtg	tggtagctca	cagacacagg	ataaaggagt	gtttccocta	300
ggcagtaaga	gaaacctttc	aaggaaataa	tgtacctggg	tatcagagga	cctaagacct	360
aagttctagt	tctagctctg	ctataaacia	gtcttgagat	tctggtaaaa	gaaaggctctg	420
gataagatga	cccttttaaa	gtgctttaca	atttaaaaaat	tcttgatatt	cttagtagga	480
tgaagccata	ttatcccaca	agtgccttgc	tgaatttctt	ttttaagggt	ccaatttttag	540
tagacattcc	attctctctt	agagaagaac	attcttcaac	cctgcagatg	acggagggtct	600
aatctgcctt	cccctgcttc	tctaaccctt	ctgtccactc	cttgccccac	agtatttttc	660
tgacctaaga	aacagtattg	tgaacagcca	gccaccggag	aagcagcagg	ccatgcacct	720
gtgttttgag	aacctgatgg	aaggcatcga	gcgaaatctt	cttacgaaaa	acagagacag	780
gtgagtataa	agcgtcctgc	ctagaaatct	cagacaattg	ctatttttca	aatcaacgaa	840
acaggcagtt	gctttaaagt	ctttgacatc	tgtgtttgga	ggccatctaa	agcaatgcaa	900
tccaatagaa	aagtgaacca	tgttaaacag	gcaaaattca	ttttaataat	atattttatt	960
taaccatttg	tatctaaaat	attgtatcag	tgtgtaatca	gtatttttaa	attgtgggtt	1020
ttcacattct	ttttgtacta	catttccaaa	atcctgtgta	ctttacattt	aacagcatat	1080
ctcagttcat	acgttttcat	cagaaatact	tgatctgtat	ttagatttca	taaatttaca	1140
gttgacaaaag	tagattcctg	taatacccag	attgtttcaa	acacacctag	ggactttcca	1200
gtaactgcat	tgagtatctg	ggctttgcaa	ttacttttta	aattttat	aatttttaatt	1260
aattttaa	aaggcatttt	aattttaa	taagatgcag	ttggggagct	gaatgtttaa	1320
ttgtatttaa	tttgatttca	tgttctcagt	cacactggcc	ataattcagg	ggcacggtag	1380
ccatatgtgg	ttaggcagcc	gccctattgg	gacaggcata	gcactgcacc	acctgggtct	1440
tgctggcatt	aaggaaatga	ggatgggctt	tactgggctt	tactggccct	tcacgtgtga	1500
gggcaacttc	ctacttctgt	cagtgaattt	tctttgtg	tgccatgagc	ccaaggtagc	1560
cctcaggggc	ccagatttga	ccagatctct	aagccaactt	ttctcttaga	gtcttaagac	1620
tgaattaa	tgatctttga	aacagaacct	atcaattcat	acattctact	tcccatgctt	1680
taa						1683

&lt;210&gt; 319

&lt;211&gt; 1606

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 319

tttttttttt	ttcgtatttc	aagggttttt	attctgagca	gtaggtacaa	aaaataatga	60
catagtgttg	tctaattctg	tatagttcag	gcacctcca	caggctgtca	atctctgatt	120
tgatctactt	ttaccagatt	taacagatcc	ttgaatttac	tttactgtat	atacttcctt	180
cttgctcaca	ttgggaatca	aactaatgct	ggaaacatgc	atcttcagac	ttcattgagg	240
aattccagat	tgagacacgc	tgggatgtgg	attgagtgca	tggttagaga	agatggatta	300
aatggaaaaca	aaacaggaaa	catgtgcttg	gcatctaata	gcagttgctg	agggtcattc	360
cgetcttgta	gttgtgcctg	gattgttcgt	ataaaggcca	ctgttacccg	ttcttcaaat	420
tcattcaggg	gagtataaag	gtttaaaatt	ttgacaatct	gctgggtgct	gaggggaggta	480
cacagggagc	agatagcctc	tgcgtectcc	tgggttttct	tctttaattg	caggagctgg	540
gctgcttggg	tcagaggttc	catggtctga	actgctccac	tctggtgaag	gtttcttccc	600
cgaagccact	cctcaagctg	acttatattg	tacctgagtt	gcattgcctgt	gctccaagag	660
cagacgtcct	tccgcaggag	caggtcatta	agagtcactg	cgttgatcat	gtagaagagc	720
tgtttgaata	cctgcaggat	gatctcaggg	tccaagccct	ggtcacacat	gactgtatga	780
aaggcattca	tctggcggat	gatagcttcc	aggcgggatg	agttatcctc	atctgccatg	840
ctggaggagt	gcttctggga	gccagtgggc	ttcacaccag	atagaccctg	aatgctctaa	900
ttttccaaca	tggcagaaac	tatcatcggc	tgtaacacac	cctcggcaat	tttaatgagc	960
tgtctgtaga	tctgaatgga	aaggtcacgt	caggcacctg	acggatttcg	gtgagggtcaa	1020
aattcttaag	acagtgttca	attctgcttt	gcagtgttct	gagtcatgaa	gccctcatcc	1080
ccgctgtact	gcttcagaca	gtgaagaagg	cgggcagggtg	ttggataacc	agaatgacgt	1140
catctcaaag	tcattcattgt	gctttttcag	gactttctta	atgccgttga	tgggtggagg	1200
cagcagggag	tgcaccttga	gatcgctcgt	gggtgtagtcc	cgcgtgccgg	atgcacatgt	1260
agaggatgta	ggcggggaga	cagggcactg	tgcccgacag	catctggggc	ttcaagtctg	1320
tcaccagggt	cgggatgagg	agggcctcgt	cctctttgtg	gtactccagc	atgccctgga	1380
aatccttctc	tttccgctgg	accgtgacct	gcctgttgag	ctcatggcgc	ttcctctcac	1440
tctggggcaa	tgcctgggca	gcttctaggt	cctgggcttt	cttcatgtaa	atcttcagtt	1500
gctttttgag	cttctctca	tctttttcca	gcttttctac	cagttcttta	agggtccagat	1560
tctcgttggt	cagccgggat	atttctctgt	gaacgccgct	cgtgcc		1606

&lt;210&gt; 320

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 320

ggcacgagga	gaatactatt	cttaaagctg	ctgaagtgca	gggtccacca	aaatgagtag	60
taacacctga	agcaaaggcg	tttatttgac	gatgtttggc	ctaccaaag	gaggactgca	120
ttgatgccca	gcaactggcc	tgtgaccccc	tacttgctgc	attatatcca	aaaattggtc	180
tttgtgagta	gcctgtctgg	ggctgctatt	gcatcaacct	ttggggtgtc	caacagctgt	240
tcttcgaatt	gagactgact	ccaaggccac	aaactgttca	acacacacaa	agtggacaaa	300
tagcatttag	cagcagggtt	ggaacgtaga	gaatctgaat	ggatctgatg	aaacctgaac	360
cagggtgctta	ttttgttgct	tttttcccat	ccactgagca	tgacagcatg	gattctcttt	420
aaggagaaac	catgggcagc	tccagccagg	cctcatagga	aaaggcccgg	catgaggttc	480
tggcgtcaat	ggccactgtg	tatggctgct	ctgagtgagg	aaaaaactaa	aaagaaaaac	540
tggttccatg	tactgtgaac	ttgaaaacat	gcagactcac	gggggttcct	gatgcaatgc	600
ttcagatgaa	gattgtggac	ttgaaaatac	agactagaag	gccgggcaca	gtgggtcatg	660
cctgtaatct	cagcac					676

<210> 321  
 <211> 1502  
 <212> DNA  
 <213> Homo sapiens

<400> 321  
 tttttttttt ttttctattg cttaatagaa aacatatttt tattccgtac tttaaaaata 60  
 tagactttct agcaacttat aaattttctat tataataata aattgatact ttgagccaag 120  
 aaaacaatat aaccaaaaat tcattttgttc cttttgttta ggggtgtttt acattttatgc 180  
 ataattttgc ttttataaaa gatgattggt acaatcaggt atacaactac ttgggttatgt 240  
 ctaagtctctg tctcttaaaa tatgttcttt tagagaattc atttaatcat cttattcttt 300  
 tcttcaattt tctccaaaca gtggtagaag tactatttga tagacagaat aaagaaaatt 360  
 gtttttggcc acaccagat cactactgata tctacagcat agtcctggct acaggggagc 420  
 tcaactctaa ctggtgaagc gggcctgggt tagaaaagtaa caatgaggta gtaactcatg 480  
 atagtgtctag ctgttatcaa aaattaacaa ctttaggtat ttttgttttg gggttttgcg 540  
 gtttaggtac atccaaaatt tcttcatagt ctgcactcat tccctttgcc cagcgaccaa 600  
 ctgtgaccat tcgctctgaa ttctgacttt cagggcaatc tttctttaaa tgttccacag 660  
 agccacaaaag tttgcaaccg ccaccatcag catagagtcc tttgggatta tcaggacaag 720  
 atctagacag gtgccccatt tctccacaaa caaacatttt tgcaaaaagga aattcgccaa 780  
 gagccgggtc tacttttagcc ttacacttgg ttatttcgtg ctctgtggac ccacacctgt 840  
 aacatatccc agtcccctg tcttgatttt caagggcggc ggggcaatct gcaattccat 900  
 gaccaggttt tctacaatgg aaacacacca ttgcattttt ctttgccgct tgtcttttta 960  
 atcttcttcc ttcccgctga ctgtctttct ttaaagcaac tgcaatttct tcccttactt 1020  
 cctcactgtc tgttgcata atttgcccat tgtgaaccat ctgtgaattc tgtcttaggt 1080  
 attccatgaa tccattcaca tcttcattta agtactcttt tttctttttg ttctttttat 1140  
 gttttgcttg ggggtgcata tttttgaggg atagcctatt ggcttcaagt tgtttacgct 1200  
 ttggttaggt ttggttggt cctcaaagg atccttctt catgtcctcc catgatgttg 1260  
 caggcaagg tctcttggt tatgtggtac taactcgggc ccacctggtc ataatttcat 1320  
 cagtgggtacc ttatcaattt ttaagacaag caggggtggt tagccatcaa caacaaaac 1380  
 aacaaaacta aagagacatg ctatatcact atatgtcaca tatgccata tgttaaaact 1440  
 ttaattatta aaacactttt tatttcagtt agatatctgt atacatattt aatggctata 1500  
 at 1502

<210> 322  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 322  
 gttgggggtct cactctgtcg cctaggctgg agtgcagtg cgtggatctc tgctcactgc 60  
 aagctccgcc tcccgggttc atgccattct cctgactcag cctccggagt agcggggact 120  
 acaggcgcac gccaccaggc ccggctaatt tttttttttt gtatttttag tagaaacggg 180  
 gtttcaccgc gtttagccaga atggtttcta tctcctgacc tcatgatccg ccacctcgg 240  
 cctcccaagg tgctgggatt acaggcgtga gccactgtgc ctggccaaac gctggttagt 300  
 ttgggagtga gaccacatta catttaaata tatttacaat gttttctgct ctattcttta 360  
 gtagactttt cctcacgtgg tcctacgcat ttctttctaa gtttattttc atatagccta 420  
 tccctgtcta caatttaaat tgggatcttc tatattctag ttattatttg taaataagaa 480  
 aactactgac ttttttctag tatattttct cagaatagga ttttctattt ttctataaaa 540  
 tgaccaatgt tatgaagctt cgtaagtttt gtcaaagtga tacacacata cagcaaaaaa 600

tcaaatagta	cagaagtata	aaagcaacaa	cctctgcctt	gcccccttctc	caccttcagg	660
tccccctccc	agatacaata	atTTTTtagct	ttttatTTTT	aattattctg	gttggtacct	720
acataactct	gggcaatatg	gaaaagttat	tgattttgta	tattaatttc	ataatcagtt	780
accttgatga	attctcttgt	ttctagtagt	ttttcttttag	ggtttttaaag	ggatacaatc	840
ataccatttg	cagttagtaa	ccattttatc	tcctcttatt	tccaacttcg	tactgttttc	900
tcttgtctaa	tttgttttta	attgggtgggt	acttctagaa	caaggttaaa	taaaagtggg	960
gttggtgggc	gtccttattt	ctgatatta				989

&lt;210&gt; 323

&lt;211&gt; 1106

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 323

tgggacgcgt	ggggggacgc	gtgggctcgg	tcgcttagtg	tgtctcctag	ttcctatcct	60
gaactacaca	ctgaagttcc	actgtctgtc	ttaattctgg	gattgcttgt	tgttttcatc	120
ttatctgtct	gttttggggc	tggtttattc	gtctttgtct	tgaaacgccg	aaagggagtg	180
ccgagcgttc	ccaggaatac	caacaactta	gacgtaagct	cctttcaatt	acagtatggg	240
tcttacaaca	ctgagactca	cgataaaaaca	gacggccatg	tctacaacta	tatcccccca	300
cctgtggtac	agatgtgcca	aaaccccatc	tacatggcag	gaagggaagg	gagacccagt	360
agcctattac	cgaaacctgg	caaggagttt	cagctattag	gcaacctgga	ggagaaaaaa	420
gaagagccag	ccacacctgc	ttacacaata	agtgccactg	agctgctaga	aaagcaggcc	480
acaccaagag	agcctgagct	gctgtatcaa	aatattgctg	agcgagtcaa	ggaacttccc	540
agcgcaggcc	tagtccacta	taacttttgt	accttaccta	aaagggcagt	ttgccccttc	600
ctatgaatct	cgacgccaaa	accaagacag	aatcaataaa	accgttttat	atggaaactcc	660
caggaaatgc	tttgtggggc	agtcaaaacc	caaccacctt	ttactgcaag	ctaagccgca	720
atcagaaccg	gactacctcg	aagtcttgga	aaaacaaaact	gcaatcagtc	agctgtgaag	780
ggaaatcatt	tacaacctta	aggcatcaga	ggatgctgct	ccgaactggt	ggaaacaagg	840
acattagctt	ttgtgtttgt	ttttgttctc	cctttcccag	tgtaaatggg	ggactttgaa	900
aatgtttggg	agataggatg	aagtcctgat	tttgcttttg	caagttttcc	tttaaattat	960
ttctctctcg	ctctcctctt	cccactccca	cactgaaaaa	caaagaagaa	aaaagaaaca	1020
aaaccataaa	caaaatctat	gaagaaatgc	attgtagaaa	cattcatgtc	cactgatggg	1080
tcctaagaag	agaagggaaa	aagaaa				1106

&lt;210&gt; 324

&lt;211&gt; 2366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 324

gcactatgtc	acattgccgt	ggggcagcag	atgaacctgc	actggctgca	caagatcggg	60
ctgggtggta	tcctggcttc	cacggtgggtg	gccatgtcgg	ccgtggccca	gctgtgggag	120
gacgagtggg	agggtgctgt	gatctccctg	cagggcacag	cgccattcct	gcatgtgggg	180
gctgtggcag	cagtcacat	gctctcctgg	atcgtggcag	gacagtctgc	ccgtgcagag	240
cggacctcct	cccaggtgac	cattctctgt	accttcttca	ccgtgggtgt	tgcctcttac	300
ctggccccctc	tcaccatctc	ctctccctgc	atcatggaga	agaaagacct	cggcccccaag	360
cctgctctca	ttggccaccg	cggggccccc	atgctggctc	cagagcacac	gctcatgtcc	420
ttccggaagg	ccctcgagca	gaagctgtac	gggctccagg	ctgacattac	catcagcctg	480

gacggcgtgc	ccttcctcat	gcattgacacc	accctgcggc	gcaccaccaa	cgtggaggag	540
gagttcccg	agctggcccg	caggcctgcc	tccatgctta	actggaccac	cctgcagaga	600
ctcaacgctg	gccagtgggt	cctgaagact	gaccccttct	ggacagccag	ctccctgtca	660
ccctccgacc	acagagagge	ccagaaccag	tccatctgca	gcctggcaga	gctcctggag	720
ctggccaagg	gcaatgccac	actgctgctc	aacctgcgtg	acccgccccg	ggagcaccce	780
taccgcagca	gttttatcaa	cgtgactctg	gaggccgtgc	tgcactccgg	cttccccag	840
caccaggtca	tgtggctgcc	tagcaggcag	aggcccctgg	tgcggaaggt	ggctcccggc	900
ttccaacaga	catcaggctc	caaggaggca	gtcgccagcc	tgcggagagg	ccacatccag	960
cggtgaacc	tgcgtacac	tcagggtgcc	cgccaggagc	tcagggacta	cgcgctcctg	1020
aacctgagtg	tgaacctcta	cacagtcaac	gcaccgtggc	tcttctccct	gctgtggtgt	1080
gcgggggtcc	catccgtcac	ctctgacaac	tcccacaccc	tgtcccaggt	gccttcccc	1140
ctctggatca	tgcccccgga	cgagtactgt	ctcatgtggg	tcactgccga	cctggtctcc	1200
ttcaccctca	tcgtgggcat	cttcgtgctc	cagaagtggc	gcctgggtgg	catacggagc	1260
tacaacctg	agcagatcat	gctgagtgtc	gcgggtgcgc	ggaccagccg	ggacgtcagc	1320
atcatgaagg	agaagcttat	tttctcagag	atcagcgatg	gtgtagaggt	ctccgatgtg	1380
ctctccgtat	gttcagacaa	cagttatgac	acatatgcca	acagcaccgc	caccctgtg	1440
ggcccccgag	gggtggcgag	ccacaccaag	accctcatag	agcggagtgg	gcgttagctg	1500
aagacatgtc	tgtccacact	gtacctgaca	cagaagctgg	ggagcctagg	agagctggtg	1560
gaagtgtgtc	tgaactcgga	gtgctctggg	agcgggctcc	acagcctcct	tgtgggctcc	1620
agcccttgt	cagccgcagc	ctctcttgag	ggggactccc	tgtctcctga	ggcccagctg	1680
ggccaggact	ccatcctttc	agatgcccct	gcaggcctgg	ggctccttct	gggaagtatg	1740
gggcctaggg	cttgggtcccc	ctcttctgag	gccctctcct	gtatcccgc	ctggaagctt	1800
tgatgggtca	tgggcatgc	catacccct	gtggcaatgg	agtgtgtgga	tgtcacctg	1860
tgccatctgt	cctcctgtct	gtgccaggag	gcacctgagt	tctctgctgt	tatcctgccc	1920
caagggcctg	ggccgagcct	ctacctgaag	caactctgct	cttctgtca	gtctcaaagc	1980
acaaggaggt	tcagcccagg	aggaagccag	ctgcaatgtg	gagacacgtc	ctcctcccca	2040
accacactca	tgccaccgcc	aacccctgc	cccaggagcg	ggcctgagcc	acgtccccta	2100
ggagcagctg	gagatggcca	aaagagtga	ctcaggacta	ctggatccca	tgcccagggtg	2160
tccagcagac	ctcaaggcag	aagggtcacc	taaccagga	gttccacaga	ctgatgtgac	2220
ctcaggttcc	cacatcagtg	gccaccaggc	agggcccacc	tggtagaagt	gttctggata	2280
tggcccaggg	tgggtgtgtg	gctaagtggg	cctgaacaga	gggaacccta	gggcccctgg	2340
ccaatgtgat	taaagctgcc	atcttg				2366

&lt;210&gt; 325

&lt;211&gt; 1925

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1925)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 325

ttttttgaaa	tctgggtccca	aagtttcaaa	agaataactaa	tgcaacaaaa	agaaataacc	60
tctctgtata	aagtgtattat	agagatgtgt	gttgaggtaa	acagcttcat	aaaaaccgtt	120
gagcagggaa	gcacagccac	tgtatagaa	attttttaggt	aagtctgggtg	ctagcattat	180
tctacaaaac	tgtttacacc	cattataaat	aggggacagt	tcttattgct	cctggagctt	240
gtagctccaa	tctgttccag	ctccactgaa	aatgattttt	tctcaacaat	tggtagcaaa	300
gatttccaaa	tttacaaaaa	gtcattacca	atgcatact	ttttgattaa	tttctgattg	360
ccatatagat	atggactaca	gtatgcatgt	ccttgacacc	aagtacagaa	aaaaagctta	420
gaaaagtctg	tttatcaaag	ttcagttcaa	tgagaaacat	gaaaaagtgc	aaaatatgta	480
caattcctgg	cagttctcac	acgggatttt	tttgactaca	gaccataaaa	gtttacattt	540
gtgtaaatgaa	atgacgatgg	atttcacatc	actgttaata	tacaagtttt	tgtttcaaag	600
tgcttacttt	atttataaaa	gagaagatca	agagggttgc	aggaattttt	tttttttaac	660
aacaaatcaa	tggtatgtgt	cccaatctcc	ttcttctct	tccttttagtg	caacatggcg	720

cagcagcctc	atggataagg	tctgatttca	aaagacattc	ctgaaacctc	acctacagca	780
gcactctagg	gggtcccatta	gggggtggctc	tcttttttctt	ctgcagccga	ttctgaacct	840
ttcgagattt	tactactttc	attctcacct	caaaaacttc	atgaatggcc	ttccggaagc	900
aatgaaaatt	atagtcaatt	agcccttttc	tttcaaagct	ttcctctctg	acaagcaaaa	960
cgagagccag	gaactttgtc	acctctttta	aataaagcac	ggttgtatta	ttaagcttta	1020
tgatggctgt	ggattccttg	tcataggggg	ttcctgctcc	atcttctttg	agaccataaa	1080
tacaagagat	gtcaataacc	acatctatca	tatcacagca	gagctcatag	gtttgcatat	1140
ccaccggagt	actatcagtt	gcaatataaa	ttttactgac	cacatcaaatt	agaaatgcct	1200
tttcaattcc	agaatttgag	ataaagatgt	tcagcaaatt	ctccagagtt	gggagttgtg	1260
gaatcagttt	ctgaacaact	ttgctaaaag	cttcaaatat	tgaatgatca	tatatgcttg	1320
tcagataaaa	gctgaggtga	atTTTTTcta	atccagcatc	tgcaagggtca	tcgtttgccc	1380
tctgggtgaat	atctctttgg	gtttcaattt	tgtgggtcatc	tgacagacca	tccactttat	1440
gaataaacac	ctcgaagttg	atgtcagtat	tcactttgta	ggccctgggtc	accgtgaggt	1500
ggagcctggc	cagggcttcc	atgtaatcat	cctgtgagtc	aatgacaaat	atcagtgctc	1560
ctgttccccg	gaagatcatc	tcatagtcaa	atgtagggtc	aaaaaagtca	atctgtcctg	1620
ggaagtccca	aatctgaaaa	ttgacaaaag	agctgttgga	aacatcttcc	cggcatatct	1680
tattagtgtc	ctccaagaac	agagtttcgt	tgggagacat	tttgtgaaag	acaactttct	1740
gaatagacga	cttgccgctt	ctcctcaggc	ccatgagcag	gattctcggc	ttcacttcag	1800
tgctgaaggg	gtcactgaag	tccagaactc	cctcctctgt	gccgctgtcc	ggatcggcgt	1860
cggagagtc	gggcccgtct	ccgtagtcgg	ctgaattccn	ccgngtgac	tgagtctcat	1920
tccca						1925

&lt;210&gt; 326

&lt;211&gt; 1181

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 326

tttttttttt	ttgagatttc	ccaggactgg	ctttaatttg	aaaaatctga	ttgggggtctc	60
ttcccgatc	agagaaggaa	cagcccaagc	tatgacccca	gggccaggga	attcagtccc	120
caccagaccc	tgtcattcca	tcactagggg	gtaattccag	gtctcccctg	ccagccctga	180
gacaggagga	cggatgtgaa	gttgcccagg	actagattct	gtctctccaa	agtggcccaa	240
gcctgtttct	ctgtactagg	gaagccagct	gtgtcttttc	gaggacagtt	gggtccagcca	300
gcaggctcag	ttcagatacc	agacaacat	tccagcacga	gggctcagcg	ccctggcccc	360
ggcggtcgct	ccagtgcctg	tgtgcccacc	agcacatcca	tgaggtagtc	caattcggcc	420
tcgtccagct	ccggagcttc	ctccttgccc	ggcccatcct	cagggcctgg	tttgaggccc	480
tcagaggctg	gtgccc aaag	ttcattgtca	tacatagagg	tgtcaatatc	ctcaaacagg	540
ccctcaagcc	catcgtccag	tagacagcca	gtggctgggc	ccagcaggtc	caaggcaccq	600
aggctgggcg	ctgctcccc	gatgctacgg	cctgggtggc	cctcgtctgc	caaggggttg	660
ggagcctgac	tcaggccctc	aatgtggctg	aggtcctcca	ggaggctggc	catggaggct	720
gaaagggcag	cgtccgagct	tgccagtaag	ttgtcagcca	cactgggggc	tgcagggtggg	780
ctaggcacag	gtggcagggc	agccgcgggt	gccatggacg	cctggatgcg	ccgcagagtg	840
ttcacgacca	gcaccaggtg	ccgcaggtcc	ggctcactct	gctgcaggct	gtggtggagc	900
ttgagcactg	agagggtcaaa	gagggaagcta	gaggccacgg	ccgggggtgc	ctgtgccacc	960
gctgcgtggc	caggatctag	ccaccaggag	tcgactgcca	gagggttcctt	ctcctcctcc	1020
tctctccgtt	tccgttccag	acccttgctc	agcatcttgc	tcactagcgg	ccaatcagaa	1080
cgaagaggta	gccaccacac	accaatcagg	aaacggcggc	ggcagcatcg	cttgttggtc	1140
gtcctccgga	aaccgcgcgc	tgggtcgcgc	ccacgcgtcc	g		1181

&lt;210&gt; 327

&lt;211&gt; 1842

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 327

```

aagtacaaaa taatatttta ataacatagg aacatgaaca tgaaaaacaat gtaaacagggt      60
tagaattttt ggatatgata cctaccaaac gtgatttgga accgtaccgc aactgggtaa      120
aattttctatg gcaaaaggat taaccaaggc atatcatagg aaatccactt tgcccaatat      180
aagcagttct cagcacatac tcaaatgcac acaaacatga aaatcggaaa taaagggaatg      240
ttaaaaaaat aacttaggca gacacaaata aaaccacccc actagtgtat gaatgatgcc      300
acgtttctta tgatcttaat tacatttaag gatttaaaaa atgccactga tctcacagtt      360
tacaatatcc aaatcttcaa acctgctgga agaagtccca cagcacagcc tggaaattcg      420
catccgttgc attctctcgt gcagttacct gcttatgggc tgtaccttct gccttgatat      480
gtagtcagtt cttcctgaag gatggaagct ctcttttgca gaaaattaac ctgtgatatt      540
agggaggaaa tgggtgtctt aagttcttgt cttagggatg ctggcatcaa tcctttcaat      600
tttgtttcat attcttgtcg tatgtaagtt atctgttccct gtgactccaa ttcttttgtgt      660
tgtaattttt tctctgcaca tcgcacctga ttagaacggg tttctaattc atcttgtaaa      720
accttgattg cttggtcatt atctctaata agctgcttct tctcatcttc aaacttttgt      780
ctaacatcct ggagccgctt ttctgcagca agctgctgct ggctgttctc ttctttcaga      840
gaggaaatgg ttgtctgaag ttctgctatg atctgtgaag atttggcaag cttctgagtg      900
tattccttct caatctgctt cagcttgctg ttggcctttt ccagtgtcat ctctgtctca      960
gcagcatgag tctttttcag ctctattttc atcttttctg attcagcctt cagtattatt      1020
acgacaatct catgttccct tgtagccctt tgcttttctt cttcacgaag aagaccaagc      1080
tctaccagct gctgtttccg ctgtgagttc acattgatca attcttctct caacttgatg      1140
acctgggctt ccatgtcggc aataacctgt gcatctcggt tcttgaactc ctgaatttga      1200
ttttcgtgct ccatattggc agcgcgaagc tgtttttcca ggttttcaat ttcccgttca      1260
tggctctgga ctaggctatc cttctctgct ttatgctgct gtaatagggt cgtcttctcc      1320
tgttcatgct ccagcttcag ctctactatc tgttgttcac accgctgtct gatgtcctcc      1380
agttgccata aaaactcctt tgattgtttc tcacgaagag atttggatct agttagatct      1440
gcctccactt ttccatttcc aaagcttccct caaatttatg aattttcttt tgagtatctt      1500
cttttccctt atcaagttca ctctgcaagt catgagcctt tttttcatag atgtgtttta      1560
gatgactttt ctccatctga aacttatatt cttgatccct tagttgttgc tttctttgaa      1620
gttctgattc ctgtaactgc tgttttaatt gacagacatt ctgctctaata tcttcaatca      1680
tactagatgc cttagaagct gaaagagcat gttcttgttt tagaagggtt atatcagcat      1740
catatttggg ttgtaacagt ttcatgtttt gctcataatc atttacaaga tggtccttct      1800
ctttatgcag tgtgttaacg cttgccttta cttcttgtaa tt                                1842

```

&lt;210&gt; 328

&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1293)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 328

```

tttttttttt ttgacgcggg gagagattta atttacatag cagccacttg ggggtccagtc      60
agagctgggg cagtggggga atctataacc ccagagggtg ccccccagac ccccccaccc      120
gggagaccag tcctcaccaa cccttggatg ggctcccaag gttgtgcaga agatgtctca      180
gtcaaaagga tagagacatt tgggaaataa aggcgtgtcc caaagttggg gggaangtcc      240
acggcctggg agtggatagc ctacatggtg gccccagggg gtctgagaga ccagtcccat      300
gtccctgggc gagtccttca gcctgggtgg ccctagagga aagccttcgc gggcggaaac      360

```



tgttccctgg	aggagggcgc	ggtactggtc	aaaatccttc	ctttccacac	gggtgacgcc	420
gccttcctta	gcatacccac	aacttcccgg	cacaccagcc	ttgataaagc	gcttcattcg	480
tgggacacca	gaatcacacc	aacccttgaa	attgtttgaa	ggcaaggccc	cagagcctca	540
atggctctcc	catgtccaag	gtgggtttgt	gggttcaccc	cagaatgtag	aaagtggggg	600
cagggcaata	gtccatctga	gcaaaaggcc	acttcggctt	ctttctggcc	cccaagacag	660
gctggcaaaag	aggacgcatg	gcccagttct	ccggagatgc	ccataccgaa	cccaagctgg	720
tgacnggtac	tcctcctcag	gccgccccag	gaaaacttgc	gtgcccagca	agttcccaca	780
agcactgaac	gttttaggtcc	cagctgctcc	cacatgggtgc	tggctgaaat	agccaatctt	840
cagattcctg	tgagcgtgtc	tgatgccccg	aacagggtgcc	aggtccccc	aaagcagctt	900
cagcatggta	gacttcccag	ccccattctc	tccaaccaca	cagatgcgag	actcgagatc	960
agcagacaca	gagaggcgac	tgaagatgac	gtgcttcgga	tcgtagtaga	aatccacctc	1020
atctagctgc	agaattggcg	gcgagaactt	ctcaaacc	tcagggaact	tcattacgac	1080
ctctgattcc	ttgtccacag	gcttcagctc	aggcctggga	gaagagatga	ggtagactag	1140
atttattact	taaaaaata	acttctaca	cgagtaatat	atgttcagag	aaaacttaga	1200
aagggttgt	actcctacca	ctcaggtatc	attactttag	agtcattctt	tctcatctac	1260
tgtatgctaa	aaaatagaat	taggcttttt	gtg			1293

<210> 329  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<400> 329						
aaatttgtat	ttcgataacc	attagtgcag	tgcggtggaa	gtcaagatgg	cggcgcggac	60
agcgttcggg	gctgtgtgcc	ggcgccctctg	gcagggattg	gggaattttt	ctgtaaacc	120
ttctaagggc	aatacagcca	aaaatgggtg	cttgcttctc	agtaccaata	tgaagtgggt	180
acagttttca	aacctacacg	ttgatgttcc	aaaggatttg	accaaaccctg	tggttaacaat	240
ctctgatgaa	ccagacatat	tatataagcg	cctctcggtt	ttggtgaaag	gtcacgataa	300
ggctgtattg	gacagttatg	aatattttgc	tgtgcttgct	gctaaagaac	ttggtatctc	360
tattaaagta	catgaacctc	caaggaaaat	agagcgattt	actcttctcc	aatcagtgca	420
tatttacaag	aagcacagag	ttcagtatga	aatgagaaca	ctttacagat	gttttagagtt	480
agaacatcta	actggaagca	cagcagatgt	ctacttggaa	tatattcagc	gaaacttacc	540
tgaaggggtt	gccatggaag	taacaaagtt	ttgtttcttt	atTTTTTTtag	acacaattag	600
aacagttacc	agaacacatc	aaggagccaa	tctgggaaac	actatcagaa	gaaaaagaag	660
aaagcaagtc	ataaagcctc	agggaggcca	tttttgccta	aatttgaaat	gaggggtggc	720
cagatgagta	tgtttaagtg	gagagtgcct	ccagctgaga	tgatttgagt	ctgtcctaac	780
tgctccattg	agttctcgtg	ccctcatcag	ctgagggcag	ggaatggaac	tttaatggaa	840
gaaccacttt	tatctattct	ttttattcat	tgtttcagtt	ctgatttcag	caaacatgag	900
caaaccactt	tgactgaaag	cagaaagagt	gaaaattcta	ttttgttacg	ctactgggtg	960
tcaattatta	gtttgtacca	tttttaattt	atgtcagttg	atgcatctga	aaataagtgc	1020
ttggagtgtt	cgtaccctta	ttttttttta	agattcctag	aaggaatctt	tggttaattc	1080
agattgagca	gttaaagttt	ttgctattta	cctttgtgca	ggctggcata	tgctaatttg	1140
ggggtggtaa	ccaaccgatt	ttatctcatg	taagcattac	atTTTgaaga	ctgaatatac	1200
ttcacagcag	atcaaacaca	tttatggcat	gcactgacct	cttcttggag	cccagaactt	1260
tatagagttg	cctaccaggg	ttactgtaat	ggaatttatg	atcttaagaa	attactagtt	1320
gtattattta	tcctatgatt	cattcattca	ataagctttt	actgcataaa	ctttacatcc	1380
agcactgtag	ttaagtaccc	aaaattgaat	agaaataatg	gcttttgaaa	attgcacaaa	1440
gcaggccagg	cacggtggct	cacgcctgta	atcccagcac	tttgggaggc	cgaggcaggc	1500
ggatcacgag	gtcaagagat	ccagaccatc	ctggctaaca	cggtgaaacc	cogtctctaa	1560
taaaaatata	aaaattagct	ggacatgggtg	gcacgtgcct	gtaatcccag	ctactcagga	1620
ggctgaggca	ggagaatcgc	gtgaaccggg	gcccggtgga	ggctgcagtg	agacgagatc	1680
gcgccactgc	actccagcct	ggcgacagag	cgagacaccg	tctcaaaaaa	aaaa	1734

<210> 330  
 <211> 2105  
 <212> DNA  
 <213> Homo sapiens

<400> 330  
 tttttttttt ttatgtcatt cagcctttac tgtaaaaaag gaaacaataa aaacaaaacc 60  
 ctattaataa acacaatgca aacaatgccc gagattatca taaaaacata ctagcaagcc 120  
 acaagtacca gagaggggtg aacaggcata tctgctagct ctctctttgc agtcttcagc 180  
 ctcccacagg aggcacaagg tccaaactat tctcAAAA aaaggacagc ctctttatgc 240  
 tgaaatagga actttaaagg aagctcttct tgtagtccaa atggacgtac cttgtggtat 300  
 ggctgtaagg actcgatttt acggcttggtg tattcctaac tatagctagg cctgtcacct 360  
 gctgttctctg tgatctcagc tttaacctaga agagctcctg aaacagaatg ggtacacgaa 420  
 aatctggaat gaatagctat ctgctcaaaa acgattgttt aaaaacagat gattggggcc 480  
 gggcgcggtg gctcatgcct gtaatccag cactttggga ggccgaggcg ggcggatcac 540  
 gaggtgagga gatcgagacc atcctgggca acatggtgaa acccgtctc tactaaaaat 600  
 acaaaaatta gctgggctg gtgatgccag ccactcgga ggctgaggca ggagaatcgt 660  
 ttgaaccagg gagttagagg ttgcagcag ccgagactgc gccactgcac tccagcctgg 720  
 cgacagagcg agactccgtc tcagaacgaa caaagaaaca acaaaaccag atgactggga 780  
 gactgaagag gaaaaaagat gggagaaaaac gtagggaagg gatggggcct cacagactca 840  
 gctgtgggtg ggggggtaaa tcattacctc aggagaagcc caaggaattg tccccagggt 900  
 gagctttgga aagaaaacaa aaacaaaaac aaaaacacca aaaaacacct aaatttcctg 960  
 tattaagtg acacataatc atgttttctg attctcttca ctgtctgct gcggggagg 1020  
 ggtggggaag gtgttaatga tgctgatccc tacttctgct tcaaggagat ctggtgggga 1080  
 attctccac cagtccagag ttgctgggtg ctgacctcat ccctgtatca cgggcctaga 1140  
 atgtgggagg ctaataggat ggggtgggtg caggaggtag aagaggggat ggcctagaga 1200  
 gtttctccat tcagagctgg agagtgttg aaggggaagg tattttaaaa gggctccacc 1260  
 caccctagc cccagccctc cagctgtggg gagaggccac ctctctgat ggggtctcga 1320  
 tgctgtgct ctgttcctgg tctggcacgt cctctcttc ctgctccaag ctgaagtct 1380  
 cgagctctg aaaaatctca tccatgaagt cctgggagtt ctgtttgtaa gacacagcta 1440  
 atcgaattgc atcattgaag agcttcacaa catttggtacc atcagcagcc gagacgaaat 1500  
 acaggggcag ggagaacttc ttggcaaaat tgaagctttt ttgggtcacg tttatgtctg 1560  
 ctgtagagag aaggtaggac attggtctgt ctgtcaaggg aaggggaaga ggtttggagg 1620  
 ggggggccac tggaggcctt cattccagaa agtgggatag gcagggatga ttgggaaaca 1680  
 ggtcctagaa agagctcagt taatagggat ctgtgtcttg gaaagagggc aggtcggctt 1740  
 agctggcttc tttataagggt gggaagaatg caagcaacca accaagggtt gtatcttctc 1800  
 gtgggaggga ggaccaatca ctgaagggtt cctgcccggg gaatggagga ggaaatgtat 1860  
 gagggcaggt cccagtgaa ttgctaacac ccaggtgcag ggatggcccc accatcaatt 1920  
 ttattggcca ccacgatgca tgggatctct ggctgaact cccgaagctc tgtataaccag 1980  
 gtgctcaggt tctatgggt gactttctc tggacatcaa acaccatgat gcaagcgtgg 2040  
 gtctgtggt agtaggagc atgcatgctc tggaaaccgt cctggcctgc cgtgtccaa 2100  
 aagtc 2105

<210> 331  
 <211> 5654  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ggagcgagc cgtcgggtc agtcggcggc cggactggga agatggagc agctactctg 60  
 acctacgaca ctctccggtt tgctgagttt gaagattttc ctgagacctc agagccggtt 120

tggatactgg	gtagaaaata	cagcattttc	acagaaaagg	acgagatctt	gtctgatgtg	180
gcatctagac	tttggtttac	atacaggaaa	aactttccag	ccattggggg	gacaggcccc	240
acctcggaca	caggctgggg	ctgcatgctg	cgggtgtggac	agatgatctt	tgccccagcc	300
ctgggtgtgc	ggcacctagg	ccgagattgg	agggtggacac	aaaggaagag	gcagccagac	360
agctacttca	gcgtcctcaa	cgcattcatc	gacaggaagg	acagttacta	ctccattcac	420
cagatagcgc	aaatgggagt	tggcgaaggc	aagtccatag	gccagtggta	cgggccccaac	480
actgtcgccc	aggtcctgaa	gaagcttgct	gtcttcgata	cgtggagctc	cttggcgggtc	540
cacattgcaa	tggacaacac	tgttgtgatg	gaggaaatca	gaaggttgtg	caggaccagc	600
gttccctgtg	caggcgccac	tgcgtttcct	gcagattccg	accggcactg	caacggattc	660
cctgcgggag	ctgaggtcac	caacaggccg	tgcctatgga	gacccctggt	acttctcatt	720
cccctgcgcc	tggggctcac	ggacatcaac	gaggcctacg	tggagacgct	gaagcactgc	780
ttcatggatg	cccagtcgcc	tgggcgtcat	cggagggaag	ccaacacagc	ccaacttatt	840
tcatcggcta	agttgggtga	ggagctcate	tacctggacc	cccacaccac	gcagccagcc	900
gtggagccca	ctgatggctg	cttcatcccg	gacgagagct	tccactgcca	gcacccgccg	960
tgcgcgatga	gcatcgcgga	gcttgaccgg	tccatcgctg	tggtagctgg	cggccacctg	1020
agcacacagg	catttggtgc	tgaatgctgt	ttgggaatga	cgaggaaaac	tttcggattt	1080
ttgcgttttt	ttttcagcat	gttgggataa	gtactgtgtt	cacgtggttg	ggaatctgaa	1140
gggtataaga	gccggaactg	tgtccttgca	ccctcacgtc	cctccccag	gcaccacctc	1200
ctgtgcagcc	ttcatggcct	tcgagtggcc	cagagagcgt	gtgtctggat	gtgagcgtgt	1260
gtgggcgcgt	ctgagtgctg	catggatgag	tgtgaccat	ggtgagtggt	tccccctcac	1320
acctacatct	aaacacacgg	gcggcccttc	caccaccccc	tgcaccacct	tcgtcacacc	1380
cacatttaaa	cacgggcggc	ccctccaccc	acccactcct	gcaccacctt	ttgttttccg	1440
gaggctctga	cttgacctct	ctgggggatt	tcctaagaag	gagcttccct	gtttttccat	1500
tttgattacc	tagttgtgat	ttttggtgtg	tgatttatgc	agacctgcct	gcctccaaat	1560
atatttgatg	gggaaagagg	ccaaaaaacc	cccctagaaa	tcatgaatga	cggtgacatg	1620
ctcaggggaag	cagttaaccg	aatcgggggc	tctgttgttg	atgctccgcc	ccatttagga	1680
ggaagaaggc	agatctgggc	ctgaaatggg	acggtctctg	agctgtggcg	cagccccaga	1740
gtgcacacca	gcctccatgc	acctcctggg	cagggtggca	gtagtgggga	acatgggctg	1800
gagctctgtg	gctcacactt	tttgtttgtt	tgtttggttt	tgagacggag	tctcactctg	1860
tcgcccaggc	tggagtgcag	tggcgcgac	tcggctcact	gcaagctccg	cctcccagggt	1920
tcacgccatt	ctcctgcctc	agcctctgga	ttagctggga	ctacaggcac	cgcgccaccac	1980
gcctggctaa	ttttctgtat	ttttaataga	gacgggtttt	cactgtgtta	gccaggatgg	2040
tcttgatctc	ctgacctcat	gatccaccca	cctcggcctc	ccaaagtgtc	gggattacag	2100
gogtgagcca	ctgcgcgcag	cctggcgcac	acttcttacc	agaacctagt	cacgaattcc	2160
tcgtcgaaat	agaattaggt	atgtttgtta	ctgtaaacgc	agcttggtgg	cttacagtga	2220
ttggcactct	aacagtcagg	tcaggctaga	gagccagcca	cgcagacag	aggagtggac	2280
gcgtgaacgt	tgagttgaga	ccaaaggggc	cacctgggtg	gataactgtc	ctcaccctgt	2340
aggaggagga	atgtccctcg	tccccggggg	agagtgtctc	tacaccagcg	cagaggcggc	2400
agaatgggtg	cttcagggga	agagagtgcc	cagtttgagc	ttctcccccc	atttcgtttc	2460
tttttgtgtt	aacatctgcg	catctggcag	cgttgagaat	tcctagtgc	tgctattaca	2520
ggcggcagct	ttaaggatgt	gattgcgggt	gaccttggtc	cgggtccctg	tctcctggct	2580
cctcagcagg	aggctccctg	tgtcacgggt	tccttgggca	gttctcggtg	gcctttgccg	2640
ccaagcttcc	agggagctgc	tgggcgaagg	ctgagaccca	gcggccctgt	ctcacagtca	2700
cagagagaag	agctccccac	ttggccctaa	ctcataacct	gccccaatcc	cggaaacactc	2760
ggtgaggttt	gagagatgca	caccacgtaa	catctcgtgg	gcgaatcaag	gcacagcaac	2820
gcagtggagc	ctgaggggag	ccgggcactg	gtgcagggga	ccatgcacag	ggcaccctcg	2880
gagctccatt	cccggccaca	ggagccaagg	caggctggaa	tgtccagcac	ctgcatgctg	2940
ggggcctctg	ctgcgccact	ggcagtggga	atggaagccc	ccacctctta	tccgactgca	3000
gatgggggtg	tcgtgttctg	ctcatcgtca	tttctgttta	gggttttttc	tgtaagactg	3060
aagatgactt	cagtgtattg	tgccagcaag	tcaaaaagct	gtctctgctt	ggaggtgccc	3120
tgcccattgt	tgagctgggtg	gagcagcagc	cttcacatct	ggcctgcccc	gacgtctctga	3180
acctgtccct	aggtgagagc	tgccaagtcc	aggtgggggtc	cctcggagggt	acgatctgtg	3240
cccttgcttc	cccagtcctg	gcccccttgg	ttttgaccat	taagggtgtg	gtgagcctga	3300
gccgtgagca	cttggcagtg	gttcgcctgt	gagaccagggt	atggagtggga	gcgtcccttc	3360
ctccaagctt	gcgccccagca	gcccaggacc	cacctcgtct	tccccaccag	cgctgcctgc	3420
cggggcgctg	tggagctggg	cgtgctacca	tggagtccctc	aggggtcttg	agcagacaga	3480
acatgcaggc	tctgtggtga	cgcagtcctg	ggtggggggac	tggttcactt	gggcaccact	3540
ggccatgggt	ggcgtagacc	cctcggacca	tggccagcgt	gccgcaggag	cgggcctggg	3600
ctcgtgcagt	gaagtgcgtg	gcctgtgagc	gcctcctctc	atctctgtct	ccctgtggga	3660
aactctacaa	acaaggcaat	ggcaatggaa	ccactcctga	tgaccacgag	ggtcacagcg	3720
gggacagagg	ccctcaggc	ctgagattgt	gcgggcccgc	ccctgccttc	ctcaccctgc	3780
cctgtccttc	ttctctgctc	cctcccccca	tattcgcagg	tctgcacaac	ccccggacct	3840
gttcacaccc	gcatggggac	agctgtctgt	gggctgcaga	gcaggcactg	ctcagtcctgc	3900
cccacgceaa	gggccccttga	ctcacaccca	ggtggcccac	ccaagatgcc	tgatgcgcta	3960

tgctctgttc	cttctagatt	cttctgatgt	agagcgactg	gaaagattct	tcgactcaga	4020
agatgaagac	tttgaaatcc	tgcccccttg	aaaatccctg	ggtcgggggt	ggcacctgtg	4080
agagcctggg	gtcctcggtg	ccgctgcgtt	tcatccatcc	cgcccgcctg	cctgcccagg	4140
gctgcgcccc	gtgtgcctc	ccccagagg	gccacccgct	gtgtcgtgg	actgaggctg	4200
cgctgcccgg	gaggccttac	tgcttggtgt	cagactgccc	agctcagagt	gcccgtcagg	4260
gcctgtgcat	ccgcacgcgg	agccgtctgt	taggagcttc	cagagcgctc	tctcgacact	4320
gccagccccg	tgtagcacc	tgggcctcag	tcccacttgc	tcccaggcgc	cggttctgtg	4380
gttggtttgg	aattaaagtc	ctgtttgaag	ttgtcagaca	cagacatgaa	tttctggggc	4440
gctccctgag	tcagtctcag	aagacctgtg	caggctggcg	tgagaggagc	ggcagccaca	4500
ctgcggcccc	acgccaagg	actgggctgc	tctcgagggg	ggcgcgcca	ccgctgtgtc	4560
ctctctgccc	agcctggctt	accaagggct	acctcagtgg	gagatgaggt	tggaggaaacg	4620
aaggcgaggt	tcctccttgc	tttggggaga	aaagtattca	ggaagtgggt	gtgtgggaaa	4680
cctgaagatg	gcgtgcacag	gacacagcgt	ggtcggcctg	ggcagaaggg	cggctggctg	4740
tcttgagct	gctgctggag	cctgcctca	gagtgtccct	ttccagtgtc	gtggcattct	4800
gtggcagctt	ccccagggtg	ggtagcgggg	ggggggcggg	gcctccacct	gtgacagcca	4860
ggcttgaggg	tggacggcgt	gcctctccca	ggagccttcc	ccatgtcctt	gccttgtctga	4920
gaattgccct	cccatgcgc	tgagggtgtta	ggtaggtttg	ggccaaaagg	ggaaaaccac	4980
ttgagtcttg	tggtgtgtgg	tgggcagaca	ccacagggtg	gcacacactg	gtggcatttc	5040
cagaacctca	gccccgattc	cagcacccac	caccgcctga	ccctgtgtaa	cctgctgtcc	5100
cgggtcccag	agtgcactct	gccccactgc	tctgctgcct	gtcctgggaa	agtagctttg	5160
ccccactagg	aaatgtaaac	aggagggtct	ggggagcgtg	ggcacttttc	tcatgagcag	5220
ctactgcggc	gttggcagga	ctcgtgctg	ctgctgctgc	tgcttgtgta	ggtcggggag	5280
ccggagatcc	ccgaggacgc	gcgcgggaca	gtcggcactg	accggcccat	ctggtagcag	5340
aggacacccc	cagcccccca	agcattgaag	acatagtgtg	tttccctcgt	tcctttctcc	5400
cttgggtgta	gttgggtggt	ggaagcaggg	aaggctgggt	cgatctccat	tccttgggct	5460
ccgcgtccga	gttcatgggt	cgccgctgtg	ctgggagctg	cagtgggaat	gtgtgggaca	5520
ccttgaccaa	aggggagctt	tgtctcgtgt	gttttgaaaa	aggcttaagt	aagagaatgt	5580
tgttcattct	tagtagtata	gtttgcaatt	cttaattggca	aataataagt	ttcagtagaa	5640
acccaaaaaa	aaaa					5654

<210> 332  
 <211> 283  
 <212> DNA  
 <213> Homo sapiens

<400> 332						
ggagccaccg	cgccccccgc	caaatttaga	ctttttgagc	tctgtgcgtt	gtgcctttca	60
acacttttca	caatggattt	tctgtctctt	gataaggaag	gcacccttga	tcctgtcatg	120
gattcattta	gcacacattg	gaccacgata	ggcctgctg	acatgttttt	ttcattgtag	180
acagcattat	aagaacttta	aatctcacgg	cacaaacccc	tcgaagtctg	tctgggcaca	240
tgccacatgc	caatcttgtg	cctttcccaa	ccttcttggt	tgg		283

<210> 333  
 <211> 1759  
 <212> DNA  
 <213> Homo sapiens

<400> 333

gaccgcctt	gcggaattcg	gcacgagga	ccctgtgcc	caggctccgt	gcgagcagca	60
gtgtgagccc	ggtgggccac	aaggctacag	ctgccactgt	cgcctgggtt	tccggccagc	120
ggaggatgat	cgcaccgct	gtgtggacac	agatgagtgc	cagattgccg	gtgtgtgcca	180
gcagatgtgt	gtcaactacg	ttggtggctt	cgagtgttat	tgtagcgagg	gacatgagct	240
ggaggctgat	ggcatcagct	gcagccctgc	aggggccatg	ggtgcccagg	cttcccagga	300
cctcggagat	gagttgctgg	atgacgggga	ggatgaggaa	gatgaagacg	aggcctggaa	360
ggccttcaac	ggtggctgga	cggagatgcc	tgggatcctg	tggatggagc	ctacgcagcc	420
gcctgacttt	gccctggcct	atagaccgag	cttcccagag	gacagagagc	cacagatacc	480
ctaccgggag	cccacctggc	cacccccgct	cagtgcctcc	agggctcccct	accactcctc	540
agtgtctctc	gtcaccggc	ctgtgggtgt	ctctgccacg	catcccacac	tgccttctgc	600
ccaccagcct	cctgtgatcc	ctgccacaca	cccagctttg	tcccgtgacc	accagatccc	660
cgtgatcgca	gccaactatc	cagatctgcc	ttctgcctac	caaccggta	ttctctctgt	720
ctctcattca	gcacagcctc	ctgcccacca	gcccctatg	atctcaacca	aatatccgga	780
gctcttccct	gcccaccagt	cccccatgtt	tcagacacc	cgggtcgtg	gcacccagac	840
caccactcat	ttgctggaa	tcccacctaa	ccatgcccct	ctggtcacca	ccctcgggtg	900
ccagctaccc	cctcaagccc	cagatgccct	tgtcctcaga	accaggcca	cccagcttcc	960
cattatccca	actgcccagc	cctctctgac	caccacctcc	aggtcccctg	tgtctcctgc	1020
ccatcaaate	tctgtgcctg	ctgccaccca	gcccgcagcc	ctccccaccc	tcctgcccctc	1080
tcagagcccc	actaaccaga	cctcacccat	cagccctaca	catccccatt	ccaaagcccc	1140
ccaaatccca	agggaaagatg	gccccagtc	caagtggcc	ctgtggctgc	cctcaccagc	1200
tcccacagca	gcccacaacag	cctgggggga	ggctgggtctt	gccgagcaca	gccagaggga	1260
tgaccggtgg	ctgctgggtg	cactcctggt	gccaacgtgt	gtctttttgg	tggctcgtct	1320
tgcactgggc	atcgtgtact	gcacccgctg	tggcccccat	gcacccaaca	agcgcacac	1380
tgactgctat	cgtgggtca	tccatgctgg	gagcaagagc	ccaacagaac	ccatgcccc	1440
caggggcagc	ctcacagggg	tgcagacctg	cagaaccagc	gtgtgatggg	gtgcagaccc	1500
ccctcatgga	gtatggggcg	ctggacacat	ggccggggct	gcaccaggga	cccatggggg	1560
ctgcccagct	ggacagatgg	cttctctgctc	cccaggccca	gccagggtcc	tctctcaacc	1620
actagacttg	gctctcagga	actctgcttc	ctggcccagc	gctcgtgacc	aaggatacac	1680
caaagccctt	aagacctcag	ggggcggggtg	ctggggtctt	ctccaataaa	tggggtgtca	1740
accttaccca	aaaaaaaaa					1759

<210> 334  
 <211> 2852  
 <212> DNA  
 <213> Homo sapiens

<400> 334						
ctacgagtac	gtcggcgccc	gcacctcccc	gcaccgcccg	cgtcgcgcg	ccggaggagc	60
gaccgcccga	gttctcgagc	tccagctgca	ttccctccgc	gtccgcccc	cgttctctcc	120
gtccggggcc	ccgcaatggc	ccaggcagtg	tggtcgcgcc	tccgcccagc	cctctggctt	180
gcctgcctcc	tgccttgggc	cccggcaggg	gtggccgcag	gcctgtatga	actcaatctc	240
accaccgata	gccctgccac	cacgggagcg	gtggtgacca	tctcggccag	cctggtggcc	300
aaggacaacg	gcagcctggc	cctgcccgtc	gacgcccacc	tctaccgctt	ccactggatc	360
cacaccccg	tgggtgcttac	tggcaagatg	gagaagggtc	tcagctccac	catccgtgtt	420
gtcggccacg	tgcggggga	attcccggtc	tctgtctggg	tactgcgcg	tgactgctgg	480
atgtgccagc	ctgtggccag	gggctttgtg	gtcctcccca	tcacagagtt	cctcgtgggg	540
gaccttggtg	tcacccagaa	cacttcocct	ccctggccca	gctcctatct	cactaagacc	600
gtcctgaaag	tctccttctc	cctccacgac	ccgagcaact	tcctcaagac	cgccttggtt	660
ctctacagct	gggacttcgg	ggacgggacc	cagatggtga	ctgaagactc	cgtggtctat	720
tataactatt	ccatcatcgg	gaccttcacc	gtgaagctca	aagtgggtgg	ggagtgggaa	780
gaggtggagc	cggatgccac	gagggctgtg	aagcagaaga	ccggggactt	ctccgctcg	840
ctgaagctgc	aggaaacctt	tcgaggcatc	caagtgttgg	ggcccaccct	aattcagacc	900
ttccaaaaga	tgaccgtgac	cttgaacttc	ctggggagcc	ctcctctgac	tgtgtgctgg	960
cgtctcaagc	ctgagtgcct	cccgtgggag	gaaggggagt	gccacctgt	gtccgtggcc	1020
agcacagcgt	acaacctgac	ccacaccttc	agggaccctg	gggactactg	cttcagcatc	1080
ggggccgaga	atatcatcag	caagacacat	cagtaccaca	agatccaggt	gtggccctcc	1140

agaatccagc	cggtgtgtctt	tgttttccca	tgtgtctacac	ttatcaetgt	gatgttggcc	1200
ttcatcatgt	acatgaccct	gcggaatgcc	actcagcaaa	aggacatggt	ggagaacccg	1260
gagccaccct	ctggggtcag	gtgctgctgc	cagatgtgct	gtgggccttt	cttgcctggag	1320
actccatctg	agtacctgga	aattgttctg	gagaaccacg	ggctgctccc	gcccctctat	1380
aagtctgtca	aaacttacac	cgtgtgagca	ctccccctcc	ccaccccatc	tcagtgttaa	1440
ctgactgctg	acttggagtt	tccagcaggg	tgggtgtgcac	cactgaccag	gaggggttca	1500
tttgctggg	gctgttggcc	tggatcatcc	atccatctgt	acagttcagc	cactgccaca	1560
agcccctccc	tctctgtcac	ccctgacccc	agccattcac	ccatctgtac	agtcacagcca	1620
ctgacataag	ccccactcgg	ttaccacccc	cttgaccccc	tacctttgaa	gaggcttcgt	1680
gcaggacttt	gatgcttggg	gtgttccgtg	ttgactccca	ggtgggcctg	gctgcccact	1740
gcccatttct	ctcatattgg	cacatctgct	gtccattggg	ggttctcagt	ttcctcccc	1800
agacagccct	acctgtgcca	gagagctaga	aagaaggcca	taaagggtta	aaaatccata	1860
actaaagggt	gtacacatag	atgggcacac	tcacagagag	aagtgtgcat	gtacacacac	1920
cacacacaca	cacacacaca	cacacagaga	aataataaca	catgcgtcac	atgggcattt	1980
cagatgatca	gctctgtatc	tgggttaagtc	ggttgctggg	atgcaccctg	cactagagct	2040
gaaaggaaat	ttgacctcca	agcagccctg	acaggttctg	ggcccggggc	ctccctttgt	2100
gctttgtctc	tgcagttctt	gogcccttta	taaggccatc	ctagtccctg	ctggctggca	2160
gggggctgga	tggggggcag	gactaatact	gagtgtattg	agagtgcctt	ataaataatca	2220
ccttatttta	tcgaaaccca	tctgtgaaac	tttcaactgag	gaaaaggcct	tgcagcggta	2280
gaagagggtg	agtcaaggcc	gggcgcggtg	gctcacgcct	gtaatcccag	cactttggga	2340
ggccgaggcg	ggtggatcac	gagatcagga	gatcgagacc	accctggcta	acacggtgaa	2400
accccgctct	tactaaaaaa	atacaaaaag	ttagccgggc	gtggtgggtg	gtgcctgtag	2460
tcccagctac	tcgggaggct	gaggcaggag	aatggtgcga	accggggagg	cggagcttgc	2520
agtgagccca	gatggcgcca	ctgcactcca	gcctgagtga	cagagcgaga	ctctgtctcc	2580
aaaaaaaaaa	aggccggggc	cgggtggctca	cgtttgtaat	cccagcactt	tgggaggccg	2640
aggcggggcg	atcacgaggt	caggagatcg	agaccatcct	ggctaacacg	gtgaaacccc	2700
gtctctacta	aaaatacaaa	aaaaattagc	cgggcgtgat	ggtggggcgc	tgtagtccca	2760
tctactcggg	aggctgaggc	aggagaatgg	cgtgaacccg	ggagggtggag	gttgcaagtga	2820
gccgagattg	cgccactgca	ctcccgctcg	gg			2852

<210> 335  
 <211> 865  
 <212> DNA  
 <213> Homo sapiens

<400> 335						
gtcgtggaat	tcgccttcca	gctgtcttct	gtgagtgtct	gcctgacagt	ttcctttggc	60
tggcagctag	gcactgtgtc	ttcctgtctc	tctagggact	ggttcttgaa	gggaaacctc	120
ctcatcatca	tcgtcagtgt	gttaatcatc	ctgcccctcg	ccctcatgaa	acacttgggc	180
tacctggggt	acaccagtgg	tctctctctg	acctgcatgc	tgtttttcct	tgtttcggtc	240
atctacaaga	agttccaact	tggctgtgct	ataggccaca	atgaaacagc	aatggagagt	300
gaagctctcg	tgggactccc	cagccaagga	ctcaacagca	gctgtgaggc	ccagatgttc	360
acagttgact	cacagatgtc	ctacacagtg	ccattatgg	cttttgcttt	tgtctgccac	420
cctgagggtc	tgcccatcta	tacggagctc	tgcgggccct	ccaagcgcag	gatgcaggcc	480
gtggccaacg	gttccattgg	ggccatgttc	tgcatgtatg	ggctcacagc	aacctttgga	540
tacctcacct	tctacagcag	tgtgaaggcg	gagatgtctc	acatgtacag	ccagaaggac	600
ccgctcatcc	tctgtgtgcg	cctggccgtg	ctgctcgccg	gtgacctca	ctgtgccagt	660
cgtgctgttc	cctatccgcc	gggccctgca	gcagctgctt	ttcccaggca	aggccttcag	720
ctggccacga	catgtggcca	tagctctgat	cctgcttggt	ttggtcaatg	tccttgtcat	780
ctgtgtgcca	accatccggg	atatctttgg	agttatcggg	tccacctcag	ccccagcct	840
catcttcate	ctccccagct	gtatt				865

<210> 336  
 <211> 1126  
 <212> DNA  
 <213> Homo sapiens

<400> 336  
 gtggcgccgg gagcaaaagc agcatgatgc agctcatgca cctggagtc ttttatgaaa 60  
 aaacctcctc ctgggcttat caaggaagat gacactaagc cagaagactg cataccagat 120  
 gtaccaggca atgaacatgc cagggaatth ctggctcaca caccaactaa aggactttgg 180  
 atgccactgg agaaagaagt caaagttaag cacttacttt tcattggatt gcttcataat 240  
 ttcttgggtga tggaaaattc attcctaaag caacaagatt aaaggatgtt tgggtaagca 300  
 attagtttac ctgtcttttc tgggacctta cacggttcat ccatgattgc attttctttt 360  
 agaattggag tttaatgaat aaaaacttta atataatcta ctgattcttt atctcactaa 420  
 ggtgaaacac tcttatctta cagaaatatt tccccctttc tttgctttta ggttggcatt 480  
 gcaaatggta cggtcaccga acaggctaca aagaatgcc tttctttatc aaagacaacc 540  
 aaaagttaca acagttcaga gtagcacatg aggatttcat gtatgacatc atacgagaca 600  
 ataaacaaca tgaagaaga gtaaggatac agcagttaaa acagttactg gaggattcta 660  
 cctcagggtga agataggagc agctccagtt cctctgaagg taaagagaaa cacaagaaaa 720  
 agaagaagaa agaaaagcat aagaaaagga agaaagaaaa gaaaaagaag aaaaaacgga 780  
 agcacaaatc ttccaagtca aatgagggtt ctgactcaga gtgacaagga tgtgacttgt 840  
 tcaacattct cttctcaaac actgaccaag gaacagagga agatgcagtc agagaaagca 900  
 gcaggataga gacgccgaga gaggagtata tgtgggtcac agcagtgagc tcccacccgc 960  
 cttgcagtga agatgtgacc ccaggagagg gagtgtctcc ttccagggtc tagctctgga 1020  
 cagcagctga ttttaggcag gaaagtttct tcatcggtgt cctccctgct ggtcacatga 1080  
 gtttacgatt cctttgaagt gtctcccaca ggggtggcagg actggg 1126

<210> 337  
 <211> 4280  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1) ... (4280)  
 <223> n = a,t,c or g

<400> 337  
 aagaaattgc aggtgctgca gcagagaaca tgttaggcag tttgctgtgc ctcccagggt 60  
 cagggtcagt gcttcttgac ccctgcactg gttctacat atcagagaca acaagtgaag 120  
 cttggagtgt agagggtatt ccaagtgact cagaggcccc agacctaaag caggaggagc 180  
 gtctgcaaga actggagagc tgttctggac tgggtagcac atctgatgat acggatgtca 240  
 gggagggtcag ttcccgcccc agcacaccag gcctcagtg tgtgtccggc ataagtgcaa 300  
 cctctgagga tattcccaat aagattgaag acctgagatc tgagtgcagc tctgattttg 360  
 ggggttaaaga ttctgtcact agtccagaca tggatgaaat aactcacgat tttctttata 420  
 tacttcagcc aaaacaacat tttcaacaca ttgaagcaga agcagacatg agaatccagc 480  
 tgtcttctag tgcccaccag ctgacctctc ctctctctca gtcagagtct ctgctggcca 540  
 tgtttgatcc actgtcttca catgaagggg ctctctgtgt ggtaaggcca aaggttctact 600  
 atgctaggcc atcgcatcca ccaccagatc ccccaatcct ggaaggagct gtgggaggaa 660  
 atgaggccag gttgccaaac tttggttccc ccatgtttta actcccagct gaaatggagg 720  
 cattcaagca aaggcattcc ttacccttga gagactagtt cgaagcagga gctctgaata 780  
 tagtatcttc tgtccggaga cccatgagtg accccagctg gaaccggcgt ccagggaaat 840  
 gaagagcgag aactccctcc agctgcagcc attggtgcta cttctttggt ggctgcacct 900

cattcatcat	cttcatcccc	gagtaaggac	tectcaagag	gagagactga	agaacgcaaa	960
gatagc gatg	atgagaaatc	agacaggaac	agaccttggt	ggagaaaacg	ttttgtttca	1020
gccatgccta	aagctcctat	accattttaga	aagaagaaaa	aacaagaaaa	agacaaaagat	1080
gatctggggc	ctgacagatt	ctcaaacactc	acagatgato	ccagccctag	actcagtgc	1140
caagctcagg	tggttgagga	tattctggac	aaatacagga	atgccattaa	acggaccagc	1200
cccagtgatg	gagcaatggc	aaactatgaa	agtacagagg	ttatgggtga	tggtgaaagt	1260
gcacatgatt	ctccccgtga	cgaagcactg	cagaacatct	cggctgatga	tctcccagac	1320
tctgcaagcc	aagcagccca	cccgcaggat	tcagctttct	cttacagaga	tgcaaaaaag	1380
aaactgaggc	ttgctctttg	ctctgcggac	tctgttgctt	tcccagtgtt	gaccccatte	1440
aacaaggaat	ggttttaccag	accacacaga	cccagaagac	aatgaaattg	tatgtctctt	1500
aaaagttcaa	atagctgaag	caattaatatt	acaagataag	aatctaattg	ctcaacttca	1560
agaaacaatg	cgctgtgtgt	gccgttttga	taataggact	tgtaggaaac	tgctggcttc	1620
gattgtctgag	gactacagaa	aaagagcccc	atatattgct	tatctcactc	gttgtcgaca	1680
aggatcagag	accacacagg	ctcacctgga	aaggctattg	caaagagttt	tcgaggacaa	1740
agaagtggcc	aatcgatact	ttaccactgt	ctgtgtgaga	ttactgcttg	agagcaaaag	1800
aaagaagatc	agggaattca	ttcaagactt	tcagaaactc	accgcagctg	acgataaaac	1860
tgctcaggta	gaagattttc	tcagattttc	ttatgggtga	atggcccagg	atgtcatatg	1920
gcaaaacgcg	agtgaagaac	agcttcaaga	tgacacagct	gccattgagc	gaagcgtgat	1980
gaaccggatt	ttcaagctcg	ccttctaccc	taatcaagat	ggggacatac	ttcgcgacca	2040
ggttcttcat	gaacatatcc	agagattgtc	ttaaagtagtg	actgcaaato	acagagctct	2100
tcagatacca	gaggtttatc	ttcgagaagc	accattggcca	tctgcacaat	cagaaatcag	2160
gacaataagt	gcttataaaa	ccccccggga	caaagtgcag	tgcatcctga	gaattgtgctc	2220
tacgattatg	aacctcctga	gcctggccaa	tgaggactct	gtccctggag	cggatgaactt	2280
tgttcctgtg	ttgggtgttg	tggtgataaa	ggcaaatcca	ccctgtttgc	tgtctactgt	2340
gcagtatatc	agtagctttt	atgctagctg	tctgtctgga	gaggagtcct	attggtggat	2400
gcagttcaca	gcagcagtag	aattcattaa	aacctatgat	gaccgaaagt	gaccaagacc	2460
aaggcccacc	aaggcagcag	actgttaatc	agacaaacag	atctctgaga	aggtgcatca	2520
gctgctttga	aggetgaaga	ttgtttttga	tgatactgca	cagcatcagg	catttttaaag	2580
cagatcttta	ctaaacaggt	taatgagcta	acaagcaggt	tctctcgtct	ttgggctctt	2640
tcctttcttg	gttgcatatt	ctattttctt	gtccccaagt	agagactagt	actacaaaaa	2700
gggaccacat	ttttcaagta	tttctaagta	taaaaaacaa	aacaaaaatc	tcttaggaaa	2760
tgtctagacc	tccattcttg	gattcccttt	ctttcccttt	atttttaaaa	agaacagtac	2820
ccctctttta	agatgctgtc	ttacattaat	gagcatctaa	tggaagaag	gtatgagttg	2880
cactgaggat	tagaatagtg	gtgcgttagt	ggcattatct	ataaaatacac	tcacctaaat	2940
tgaaagctaa	gaaggaaatg	taaatataat	atatatttat	atttgatgta	atatggacat	3000
ctgcagattc	taataaacaa	ggactattgc	tgatagtagg	ctgtgacata	ctgtcttggt	3060
aaattgtttc	cttgacaaaa	tttaagctga	gcttaaaagc	aaaaaaacaa	aaagtacaca	3120
gaaatatatta	ttaaaatgta	atacagttta	ttgaactttc	taggtatgga	gtttgatgga	3180
cagggctgcc	tttaatgagt	gtgaagggtc	ctaagtcact	tagacatctc	accgtggaag	3240
tttgtgagcc	tgcattagga	gatagactga	ttaccataca	tgacataaaa	aggaacagtg	3300
gatagctcat	actttatggt	ggttcttctc	ctccgaaata	atatactgca	gaaatcccag	3360
acagagctcc	ttacaaacct	ttaatgttaa	tatatTTTTT	atgattattc	acattgaaatg	3420
cacagaccaa	gaattcagtg	aatgtcattt	tttaaaaaac	taattttgat	tgtctgctct	3480
agtatacaca	gttttactag	tgataaaacta	ttttaatcaa	ccatactatt	cttatggaaa	3540
aaaatatcta	ttttggcagg	tttctgtgcc	tttatttccc	tcttctgaaa	aaaagtctgt	3600
gttttcatag	tttgggtttg	attgtatatc	aataattaat	caggaatggg	ttttggtgcc	3660
tgaaaaattg	gccatggagg	cacaccaaag	cttcaagcac	aagtcttgta	catgggccat	3720
cactgtctgg	tttcacttcg	tgtgtttcct	aaacacattt	agctgctttt	ttaacaaact	3780
cagccccata	cttgagtccc	ttgttggttg	gagcatttcc	aggcatcttt	taagggaact	3840
gtgacaaaaca	gcctcgggca	gatgaacacg	gaggctctct	gttgtctgtc	tctgagatct	3900
tttgtctctg	gaatgcctaa	agattttatt	tttttttctt	tggtttttatt	ttattttatt	3960
ttattttttt	gagacagagt	ctcacctgtt	tgcccaggct	ggagtgcaat	ggtgcgactc	4020
tggtcactcg	caacctccac	ctcccagttc	aagtgtattcc	cctgcctcag	cctcccgagt	4080
agctagggac	tacaggcgca	tgtaacccaa	gcccggttaa	atttttgtat	ttttagtagg	4140
aaacgggggt	tttcaccatg	ttggggccagg	gtggatcctc	aatctcctga	acctcggtga	4200
tccaccgcc	ttngggcttc	ccaaagtgcc	gggatttaca	agcgtggaac	cacctgnccc	4260
agccagaaat	taggattttt					4280

&lt;210&gt; 338

&lt;211&gt; 1796



<212> DNA  
<213> Homo sapiens

<400> 338

tggccatctt	tactgtgggc	tgaagcctgt	gcgcttactc	gcgcatgtgc	aagccttccc	60
tcgctttcct	cttccaagta	gccttgcccta	gagcggagcc	tcccgcgccca	tttctgtgcg	120
cctgcgtagc	gtgacccctgc	gcagcctggg	aggcgggtct	tagctccagg	tgcgtaacggc	180
atctgacttg	acgtggccca	caactgaaaag	gtctggggag	aaggcgccgt	gtccgggtgt	240
ggagaggggc	gtcgtggaag	cgagaagagt	ggcccgtccc	tctcctcccc	ctttccctct	300
ttcggaaaagt	ggttttctgcg	ggggccggga	gcctcggagt	accgaacctc	gatctccggg	360
gcggggtcct	tgggtggggac	tgagcgcccc	ctcccgggga	cgggcgggtct	ggccgcggag	420
ttcccctgcgg	gagcgtgatt	ggctggaaac	ggctcccgaac	ccccagggga	gcccgatccc	480
tgggggaccc	tggcttcgga	ctccagtatc	tgctcgtcgca	gggtccctgc	cctagtggcc	540
tatgtccctt	gctcggggcc	atggagacac	tgccggccagt	acggcggcgc	ctctgtctga	600
agaaggggaa	gtgacctccg	gcctccaggc	tctggccgtg	gaggataccg	gaggccccctc	660
tgccctcggcc	ggtaaggccg	aggacgaggc	ggaaggaggc	cgagaggaga	ccgagcgtga	720
gggggtccggg	ggcgaggagg	cgaggggaga	agtcctccagc	gctgggggag	aagagcctgc	780
cgaggaggac	tcgaggact	ggtgcgtgcc	ctgcagcgac	gaggagggtgg	agctgcctgc	840
ggatgggcag	ccctggatgc	ccccgccctc	cgaaatccag	cggctctatg	aactgctggc	900
tgcccacggg	actctggagc	tgcaagccga	gatcctgccc	cgccggcctc	ccacgcggga	960
ggcccagagc	gaagaggaga	gatccgatga	ggagccggag	gccaaagaag	aggaagagga	1020
aaaaccacac	atgcccacgg	aatttgattt	tgatgatgag	ccagtgcac	caaaggactc	1080
cctgattgac	cgagacgca	ccccaggaag	ctcagcccgg	agccagaaac	gggaggccccg	1140
cctggacaag	gtgctgtcgg	acatgaagag	acacaagaag	ctggaggagc	agatccttcg	1200
taccgggagg	gacctcttca	gcctggactc	ggaggacccc	agccccgccca	gccccccact	1260
ccgatcctcc	gggagtagtc	tcttccctcg	gcagcggaaa	tactgattcc	cactgtctct	1320
gcctctaggg	tgacgtgtcc	gtacctgctg	gagcctgggc	cctccttccc	cagcccagac	1380
attgagaaac	ttgggaagaa	gagagaaacc	tcaagctccc	aaacagcacg	ttgcgggaaa	1440
gaggaagaga	gagtgtgagt	gtgtgtgtgt	gttttttcta	ttgaacacct	gtagagtgtg	1500
tgtgtgtgtt	ttctattgaa	cacctataga	gagagtgtgt	gtgttttcta	ttgaacatct	1560
atatagagag	agtgtgtgag	tgtgtgtttt	ctattgaaca	cctattcaga	gacctggact	1620
gaattttctg	agtctgaaat	aaaagatgca	gagctatcat	ctcttaaaaag	gaggggctgt	1680
agctgtagct	caacagttag	gccccacttg	aaggagagg	cagaattgta	ctcaccacaga	1740
ttggaaaatg	aaagccagat	gggtagaggt	gcctcagtt	agcacctgtc	ccatct	1796

<210> 339  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 339

cttggggccga	gggacgtttg	ggcaagtggg	ttagtgctgg	aaacggggca	ccaatgagat	60
cgtagccatc	aagatccctga	agaaccaccc	atcctatgcc	cgacaagggtc	agattgaagt	120
gagcatcctg	gcccggttga	gcacggagag	tgccgatgac	tataacttcg	tccgggccta	180
cgaatgcttc	cagcacaaga	accacacgtg	cttgggtcttc	gagatgttgg	agcagaacct	240
ctatgacttt	ctgaagcaaa	acaagttag	ccccttgccc	ctcaaatata	ttcgccaggt	300
tctccagcag	gtagccacag	ccctgatgaa	actcaaaagc	ctaggtctta	tccacgtga	360
cctcaaacca	gaaaacatca	tgctgggtgga	tccatctaga	caaccataca	gagtcaaggt	420
catcgacttt	ggttcagcca	gccacgtctc	caaggctgtg	tgctccacct	acttgacgtc	480
cagatattac	agggcccctg	agatcatcct	tggtttacca	ttttgtgagg	caattgacat	540
gtggteccctg	ggctgtgtta	ttgcagaatt	gttcctgggt	tggccgttat	atccaggagc	600
ttctgagtat	gatcagattc	gtatatttca	caaacacagg	gtttgcctgc	tgaatattta	660

ttaagcgccg	ggacaaagac	aactaggttt	ttcaaccgtg	acacggactc	accatatcct	720
ttgtggagac	tgaagacacc	agatgaccat	gaagcagaga	cagggattaa	gtcaaaagaa	780
gcaagaaagt	acattttcaa	ctgttttagat	gatatggccc	aggtgaacat	gacgacagat	840
ttggaaggga	gcgacatggt	ggtagaaaag	gctgtccggc	gggagttcat	tgacctgttg	900
aagaagatgc	tgtccattga	ttctgtcaag	agattctctc	cagtcggatc	cctgaaccat	960
ccctttgtca	ccatgtcact	ctttctcgat	tttccccaca	gcacacacgt	caaatacatgt	1020
ttccagaaca	tggagatctg	caagcgtcgg	gtgaatatgt	atgacacggg	gaaccagagc	1080
aaaacccctt	tcatcacgca	cgtggccccc	agcacgtcca	ccaacctgac	catgaccttt	1140
aacaaccagc	tgaccactgt	ccacaaccag	ccctcagcgg	catccatggc	tgacgtggcc	1200
cagcggagca	tgcccttgca	gacaggaaca	gcccagattt	gtgcccggcc	tgacccgttc	1260
cagcaagctc	tcatcgtgtg	tccccccggc	ttccaaggct	tgacggcctc	tccctctaag	1320
cacgctggct	actcgggtgcg	aatggaaaat	gcagttccca	tcgtcactca	agccccagga	1380
gctcagcctc	ttcagatcca	accaggtctg	cttgcccagc	aggcttggcc	aagtgggacc	1440
cagcagatcc	tgcttcccc	agcatggcag	caactgactg	gagtgggcac	ccacacatca	1500
gtgcagcatg	ccgccgtgat	tcccgagacc	atggcaggca	cccagcagct	ggcggactgg	1560
agaaatacgc	atgctcacgg	aagccattat	aatcccatca	tgacgacgcc	tgactatttg	1620
accggtcatg	tgacccttcc	agcagcacag	cccttaaatg	tgggtgtggc	ccacgtgatg	1680
cggcagcagc	caaccagcac	cacctcctcc	cggaaagagta	agcagcacct	gtattgcggc	1740
cgcgctagag	tatccaagat	tgctgtctgc	t			1771

&lt;210&gt; 340

&lt;211&gt; 2725

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 340

ggaattcgct	atatgccgct	atcctctggg	catgtcagga	ggccagattc	cagatgagga	60
catcacagct	tccagtcagt	ggtcagagtc	cacagctgcc	aaatatggaa	ggctggactc	120
agaagaagg	gatggagcct	ggtgccctga	gattccagt	gaacctgatg	acctgaagga	180
gtttctgcag	attgacttgc	acaccctcca	ttttatcact	ctggtgggga	cccaggggag	240
ccatgcagga	ggtcatggca	tcgagtttgc	ccccatgtac	aagatcaatt	acagtcggga	300
tggcactcgc	tggatctctt	ggcggaaccg	tcattggaaa	caggtgctgg	atggaaatag	360
taacccttat	gacattttcc	taaaaggactt	ggagccgccc	attgtagcca	gatttgtccg	420
gttcattcca	gtcacccgacc	actccatgaa	tgtgtgtatg	agagtggagc	tttacggctg	480
tgtctggcta	gatggcttgg	tgtcttaca	tgctccagct	gggcagcagt	ttgtactccc	540
tggaggttcc	atcattttatc	tgaatgattc	tgtctatgat	ggagctgttg	gatacagcat	600
gacagaagg	ctaggccaat	tgaccgatgg	tgtgtctggc	ctggacgatt	tcaccagac	660
ccatgaatac	cacgtgtggc	ccggctatga	ctatgtgggc	tggcggaaag	agagtggcac	720
caatggctac	attgagatca	tgtttgaatt	tgaccgcata	aggaatttca	ctaccatgaa	780
ggtccactgc	aacaacatgt	ttgctaaagg	tgtgaagatc	tttaaggagg	tacagtgtcta	840
cttcgcgtct	gaagccagt	agtgggaacc	taatgccatt	tccttcccc	ttgtcctgga	900
tgacgtcaac	cccagtgtc	ggtttgtcac	ggtgcctctc	caccaccgaa	tggccagtgc	960
catcaagtgt	caataccatt	ttgcagatac	ctggatgatg	ttcagtgaga	tcaccttcca	1020
atcagatgct	gcaatgtaca	acaactctga	agccctgccc	acctctccta	tggcaccac	1080
aacctatgat	ccaatgctta	aagttgatga	cagcaaacct	cggatcctga	ttggctgctt	1140
ggtggccatc	atctttatcc	tcctggccat	cattgtcatc	atcctctgga	ggcagttctg	1200
gcagaaaatg	ctggagaagg	cttctcggag	gatgctggat	gatgaaatga	cagtcagcct	1260
ttccctgcc	agtgattcta	gcatgttcaa	caataaccgc	tcctcatcac	ctagtgaaca	1320
agggccaac	tcgacttacg	atcgcatctt	tccccttcgc	cctgactacc	aggagccatc	1380
caggctgata	cgaataactcc	cagaatttgc	tcagggggag	gaggagtcag	gctgcagcgg	1440
tgttgtgaag	ccagtcagc	ccagtggccc	tgaggggggtg	cccactatg	cagaggctga	1500
catagtgaac	ctccaaggag	tgacaggagg	caacacatac	tcagtgcctg	ccgtcaccat	1560
ggacctgtc	tcagggaaaa	gatgtggctg	tgggaggagg	tttccccag	ggaaactcct	1620
aactttcaaa	gagaagctgg	gagaaggaca	gtttggggag	gttcatctct	gtgaagtggg	1680
gggaatggaa	aaattcaaag	acaaagattt	tgccctagat	gtcagtgcca	accagcctgt	1740
cctggtggct	gtgaaaatgc	tccgagcaga	tgccaacaag	aatgccagga	atgattttct	1800

taaggagata	aagatcatgt	ctcggctcaa	ggacccaaac	atcatccatc	tattatctgt	1860
gtgtatcact	gatgaccctc	tctgtatgat	cactgaatac	atggagaatg	gagatctcaa	1920
tcagtttctt	tcccgccacg	agccccctaa	ttcttcctcc	agcgatgtac	gcactgtcag	1980
ttacaccaat	ctgaagttta	tggctaccca	aattgcctct	ggcatgaagt	acctttcctc	2040
tcttaatttt	gttcaccgag	atctggccac	acgaaactgt	ttagtgggta	agaactacac	2100
aatcaagata	gctgactttg	gaatgagcag	gaacctgtac	agtggtgact	attaccggat	2160
ccagggccgg	gcagtgtctc	ctatccgctg	gatgtcttgg	gagagtatct	tgctgggcaa	2220
gttcactaca	gcaagtgatg	tgtgggcctt	tgggggttac	tttgtgggaa	aactttcacc	2280
ttttgtcaaa	gaaaaggccc	ctattcccca	gctgtccaga	tgaacagggt	tattgaagaa	2340
atactggaga	gttcttcccg	agacccaagg	gagggcagac	ttacctcccc	tcaaccagcc	2400
catttgtccc	tgactcctgt	gtaataaagc	tgatgtctcag	ctgctggaga	agagatacga	2460
agaaccgtcc	ctcattccaa	gaaatccacc	ttctgtctct	tcaacaaggc	gacgagcgat	2520
gctgtcagtg	cctggccatg	ttcctacggc	tcaggtcctc	cctacaagac	ctaccactca	2580
cccattgccta	tgccactcca	tctggacatt	taatgaaact	gagagacaga	ggcttgtttg	2640
ctttgccctc	ttttcctggt	cacccccact	ccctaccctt	gactcatata	tacttttttt	2700
tttttacatt	aaagaactaa	aaaaa				2725

<210> 341  
 <211> 916  
 <212> DNA  
 <213> Homo sapiens

<400> 341						
cgtccaggga	gcactgcca	caggccgagc	cggggcctcc	cgcaagagga	aggaggtgcc	60
ctcaaggcta	cggacctggg	gtcccgggtg	tggacgcccc	atggggctca	ggcctaaaga	120
ggccgagagg	gcctcgggga	cccagtgcac	gccccacgct	gagcagcaca	ggctgcccc	180
ccgtgggctc	cccgatctct	ctctggatca	ccgagacctc	gcagggaggg	tcacagggg	240
cgcaggcccc	agggccacca	cagtgggaag	tctcccttc	cccaggcacg	taatcttcca	300
ggtcagccag	tgtcagcatg	cggccgttgt	gcgtgaggat	cttgggggtca	cgatcccca	360
ggctgtgtgt	gtcctgggac	tcttcctca	caaaggcgtc	tccgtcttcc	ccctcttctc	420
ctccgcctc	ctccatggtg	ccctcctcct	ccaggctgcc	catgccagaa	gcagcccagt	480
ccacactgcc	tctggcatcc	acgcggaaga	caaggggctc	tctgacgccg	accatggctg	540
tgccttgggc	ccaggcctcc	tgggccagca	gcttgttgtt	ggagttgttg	gaattggggg	600
ccctccggg	ggtcgcaacc	ggcagtgtga	agagatgccc	cgatgagctc	ctgggcacct	660
ctgtgggtgg	agacacaccc	tgcgggccca	tcttcttcac	ccggacttca	atggtctcct	720
ccacctccac	ccacttgggc	tggggccccc	agagtcgggg	cagagctgga	gagtgggcct	780
cggcctccgt	cacatacagt	gtgggcacca	cgggcttctg	gcctggttct	gcctccggcc	840
tgcggggctg	gccagcacct	ggcaggtaca	gcaggtcggg	ggccagtagg	cctggcctca	900
gcgggctggc	agagca					916

<210> 342  
 <211> 860  
 <212> DNA  
 <213> Homo sapiens

<400> 342						
caagatcccc	acaggcttaa	tcgtccctt	aaggaaaaag	ttattccttg	catccgcggt	60
aaacttgggc	ccccccaagg	atcctttaaa	cgggcccggc	cttttttttt	ttttcaattt	120

cttcaacagg	tcatgttcaa	tttcttcaaa	gttttaacat	aaaaataatg	agagccagga	180
gtggggccgg	ggcctggggg	gacgaaggtg	gtatgtgaaa	caagggttggc	acacaggcct	240
cacctcctc	tgctcagat	tcccaagtgg	gcaggtgggg	gtgaatgggg	ctccgggtag	300
cacctcagct	cctctcagct	ccccctcagcc	tgttctcctt	ccagacccag	agagctgaga	360
agagtagctg	tgaggctcag	ggcagaggct	ctctgccttt	caggaacagc	ccttaaccct	420
gctccccctg	cttgggcctc	aggaaggtgc	cgcagctct	cctgccgtcc	ctgggcccgc	480
ctggctctgc	tgtgtccaga	tggtcaggct	actgccagct	ggggccttgc	tgctctgaag	540
tcccaggaag	ccagggtct	gcaggagcct	cttgcctcca	ggctgggttg	ggaagacgtc	600
ctccaggaag	tagtagatat	ggcccaccgc	aatccccagc	aggtccacga	ggatggagtt	660
gcccagcagc	agcgagaagc	ccatgagcgc	ccaaggcagg	aacgggtgct	ggaacttccg	720
gaacacaagg	tgcggttgga	agtagagttg	aaaggggctg	aggagctcca	gctgcaccgc	780
ggcggtggtg	aggacacagg	ctgcggtgta	agccccgctc	accgccggca	cctgcaggaa	840
ctcgcccgct	agtccctgcc					860

&lt;210&gt; 343

&lt;211&gt; 3658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (3658)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 343

tttttttttt	tttaagatag	aaatctatgc	actttaatga	ttgccagaat	tgcccagcat	60
agcttcagta	aaatagagaa	ttgtctagaa	aatacaatct	ccaaaatgtg	tgcaagtact	120
gcaaaccgga	cagaccgggg	cagggcaagg	cccttgaaac	caagtcctcc	ttgagcacct	180
ttcccagggt	agaaaccctt	cttcagcctg	tgcttcgcac	gtttccttca	gcgtgccgcc	240
cattccagact	gcgccaaact	acgtccccag	tgcccacgcc	tgngtggatc	aagtgtccaa	300
cgggaaagta	tgagttaggg	caagcgcttt	ttttttaagc	tgtaaacgct	tcacatgact	360
ggggccccgt	aggaaattgt	ggggagctta	ggatgagcct	gggagctttt	tcagggaactt	420
ggatgaggac	tctgtacaca	aatgtgtact	ggcagagagt	ctgcaccagc	atcattctct	480
gttgccctca	gcatgtccag	cactctcggg	atgtccagca	cctcattgtg	ttccaggcag	540
gcgatcatga	tctccgacaa	aatcaccacg	ccagtccttc	ctaccccagc	actgcagtgg	600
accaacaacg	gaggggttgg	gctttgggga	tcacttgtgc	tatttgtatg	gcgtcgaaac	660
gactggatct	cttcaagata	tgataaaaat	cccttgaggt	cttctggaca	gccatgttca	720
ggccagtctg	tgtattggag	gtgccagacg	gtcctctctt	gcccggtaag	gaggtgcttc	780
atcttcaggc	ctgtggtggc	atagcagcca	gagtctgtgc	ggaaccgggt	cgtgatctta	840
aaccttccat	aggtgacagt	gttgtgcctg	gaaccaagtc	gtggccagta	cctaaagctc	900
ttctcccttc	cacctcctc	ttctgctgtc	accattgcta	taattgcaat	tccctgttcc	960
cataccatct	gccaaaaatc	ttgacaggta	ttctgtaatg	gtccctgtgt	ggcaatataa	1020
tcccattcga	ttccactgac	agagacctta	atatgtgatg	cgttgatgta	accagtgttg	1080
ttttcttttag	ttgggaccaa	ctccactctc	acatcatcat	aaggaagaac	atcttggaa	1140
cgatttctct	ctgcattttc	agggagtcgt	gctgttgagc	actccccatc	aactagccgt	1200
ttcttaagaa	ttctttcata	ttctgtgaat	accattcctt	gttctaatac	ttgttcagaa	1260
attttacacc	tttcatcatt	cgttgctctg	gtagccactt	cctttccttc	atcaggcaga	1320
ggcactcgag	atagggagag	tccatttagg	gcagccagtt	taagaggacc	aatttttttt	1380
gcatctactc	gagtcctttt	cattccccct	agaggcggga	gcccttccac	gatgttcttc	1440
ttcccagaga	gaaggtcoga	caccggcctt	ttcttcagag	agtcctcccg	ggctcggtag	1500
cggcctgaag	tgggtgaggtc	ggactccgac	atggagggca	tcagcagccc	gtctctccag	1560
ggcgcgtggg	cctctgcggt	cgtgoggacg	gggctgetgt	ccatcatcct	cttctccgcg	1620
ttcgggacgt	gggccttggg	ctccaggatg	tgcagggggc	cggcgagcag	gacgcagggg	1680
cagccagggtg	ggtcctgggc	cagggcgggc	cgaggctcgc	gcgcacgtgc	agggggcgcc	1740
cgggccccgc	tctcctcctc	gaagtcctcg	tcctcctcct	cctcgtctgt	gtggattagc	1800
atgggtggcgt	ccgacaggga	cttcttatgg	ccgtacctca	agccctccgc	ctcctccggc	1860

ccttctcgc	gtgtcctctc	ggtgaaaacg	ctggggctgg	gagcccaccg	agacggctcg	1920
cggcgccac	ctctgcgcgc	gacgcggata	gggtgcgctc	cttgagccgc	agggccctcca	1980
ggcgtggct	gagcccgcc	acctcgatgc	tggtccggtt	gtgcagctgc	gcgtggcgcg	2040
cggcggtgag	gggtcgctg	acctcctgca	gcgagtgcgc	cacgggcagg	ctgtcctcct	2100
ggaacgtttg	caccgagtgg	tgacgcgcgc	gcgtgatgag	gtcggggttg	ctgctgctga	2160
tgtaaagggtg	gcgggacagg	tctggcgctgc	tggtggcggg	cctggggggc	gggtagggtg	2220
ggggtggccg	gtacacctgc	gtccgcatga	tggtgggaga	cgggtagtcc	tgccgctgca	2280
gctgcgcatt	ggtcagctcc	ggcacgctga	ccgcgcccac	cacgggcgcg	cgctcggcag	2340
ggtaggggta	gggagacggg	ctgtggaagc	tgtagctcag	gctgaacggg	cagtgtgcgg	2400
ccgctggcga	ggggagctgt	gcgtgctcgc	ggatctcggg	ctggctgtag	accagcgccg	2460
cgggcctgct	gtaggcgtag	gagctgcgca	tggtgaggtt	tcgcagcgag	tggtctctgc	2520
gttccgcatg	caccaggccc	ctgttgagct	gcttcacac	agtctcatag	tctggggtgg	2580
ggcggtagga	cgggggtatc	acggcgctgt	gccgatggga	cgggaggtag	tcaggcctca	2640
tgacgtcact	cccgggtgatg	ctagggttgg	acgacatcgg	cgagggtgc	aagtagggct	2700
gaggattatt	taaggagtgg	gtgctgtgtg	cactgtagac	actggcattt	acggatccga	2760
ccgttgaagt	caatctgggc	tctattcaag	cttgtctgaa	attgaccata	gtatcccttc	2820
ctggttgggc	acaaagaggt	tatcttggga	agaagcata	ggttctgtat	aatgtccatt	2880
atagtgaac	tggcggtggg	ggaggcatca	cgtagggtctg	gggttttaggc	agagacatcc	2940
ttgaagaaga	cctcctcctg	attgggttca	ctgtgacagt	ctgagtttgc	aggttacact	3000
ggtttagtct	gtaaaacttg	tgtcgcgcaa	cacagagtct	ccaaatgtat	tttgctgttt	3060
ccatgtcttc	agtttgaaat	tgaatggtct	cctctttatt	tgccagctct	aatgcaaaaa	3120
aggacttggt	gtgggacatg	ttggcaatgt	catgccacct	aaataccaca	ggatgccttc	3180
cattcttgtg	ttcacaaaag	ataccttcaa	gacacgctcc	aatggatatg	tcacttcctt	3240
ggctatcctt	agcagggtag	ctctcttctc	catagccatc	cattctctct	acctcctgca	3300
tgtacagcat	ttcagcatca	ggagctgtga	gccctctgta	tttctgatgt	agtaaggcca	3360
ctttttgggt	tgcttcttcc	aatacttttt	catcttgtaa	ccatcccaca	ggaaacaagg	3420
caaatttctg	aagaaagtcc	tgggattcat	actgatcaaa	gtcaccaaaa	atcgcttgaa	3480
cagctaagcc	tgctaggtga	attggctgtt	ccaagggtaca	agggatacct	tcttcccaga	3540
tatccttcct	cagttgcaga	taatactggg	acccggtaat	cctctgctgg	aagcgaggaa	3600
cctgaggcgc	ttaaaccccc	attccaaaat	agacggtagg	ttccaaggcg	tttttttc	3658

&lt;210&gt; 344

&lt;211&gt; 419

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 344

aataaagaaa	gaaacagaag	ctggccgagg	agtgagttga	gctttccaag	ttagctgacc	60
ttaaagatgc	tgaagctgtc	cagaaattct	tcctggaaga	gatatagctt	tggtgaagag	120
atcctagcta	aaggtgtaga	ccacctgaca	aatccaagtg	ctgtgtgtgg	acagccacag	180
tggttactgc	aagtgttaca	acaaactctt	ccactaccag	tgatccagat	gcttctgaca	240
aagcccctac	cagttaatca	gagacttgta	agtgtctggc	cttgccaaa	gacgatgtgg	300
aatgagaaac	aaatgtcaac	ataataaaat	ctcagttaaa	atacttgaaa	aattcttaac	360
ttggtagttg	agcagaaggg	caaatatgct	tgttatgaac	tattctacat	tgaaatcta	419

&lt;210&gt; 345

&lt;211&gt; 1253

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 345

ggaattcctc	tgtcccgcc	tacacaggg	gggacgggg	agggcgggca	ttgagctttg	60
tgtcctgggg	tcaggggtg	tcccctgcc	gcctcacc	accaagcgg	tctcatggg	120
ctcctctggc	tgggcccacc	cgcagtggta	tccttctggg	ggcccttatg	ggagcctgcc	180
gggggtgcag	atcctgccgg	gggtgcagag	cctgctgggg	gtgcagatga	tttctgggtc	240
ccaggaccat	gagggggctg	ctctacacac	agccggaaga	tgctgcggac	ccaaaactggc	300
cctttccctc	ccacaccacc	ccaggacc	tggtctggct	ggaggccacc	catgctaaaa	360
taggctcaag	ggcctacttt	agcttctggg	caaagggtctt	ggcctggggc	tgactctgtg	420
gccttcctga	gctgcctccc	cagtaggcct	cagtgcctggg	ctacaggcct	cctccattcc	480
ctccattcat	gtgacccccc	ccctcccagc	agaaactctc	ttccgtagcc	caggagcagc	540
tggtgaggg	ttcacctgcc	catgccccag	cctaaggccg	gcttccccag	agcagacggg	600
ttgcactctc	ctgccccctca	ggcccaactct	gtcatccaac	aagctcactg	caactggccc	660
atcttaaaaa	caacaccggc	tggtcacgct	ggctcacacc	tgtaatccca	gcgctgtggg	720
aggccggggc	ggggggatca	cttaaagtca	ggagtttaag	accagcctgg	gcaacatgg	780
gaaacccgag	ctccactaaa	aacacaaaaa	caaattaagg	caccctgagt	ggtggtgggt	840
gcctgtggtc	ccagcgactc	gggaggctga	ggcagaattg	cttgagccca	ggaggtggag	900
gctgcagtga	gccacgatcg	catcacgcac	tccagcccgg	gcaacctggc	aagaccctga	960
ctctaaaaag	aaaaaaacaa	caaaaaaaa	aagcccacgt	tcaagggcag	cactattcaa	1020
aagagggaag	caactcagga	atccaaacgc	gcaggaggga	acacatcggg	gttcatccac	1080
aggggaacac	gattcaccca	aaaaaaggaa	ggaaaccggc	ccggccccgg	gacttgaatg	1140
cactggagg	agactgtgat	gaacaaaagc	acccaaacc	aaaagggcag	ggacgggggtg	1200
atctgactga	ggtgaggacc	ccagccagcc	aaattcatgg	agacagaaag	aag	1253

<210> 346  
 <211> 807  
 <212> DNA  
 <213> Homo sapiens

<400> 346

tttcgtcgga	ggcgggcgcg	ggcgcgtccc	tgtggccagt	cacccgagg	agttggtcgc	60
acaattatga	aagactcggc	ttctgctgct	agcgccggag	ctgagttagt	tctgagaagg	120
tttccttggg	cgttccttgt	ccggcgccct	ctgctgccgc	ctccggagac	gcttcccgat	180
agatggctac	aggccgcgga	ggaggaggag	gtggagtgtc	tgcccttccg	gagtcggccc	240
cgtgaggaga	atgtcccaga	aatcctggat	agaaagcact	ttgaccaaga	gggaatgtgt	300
atatattata	ccaagttcca	aggaccctca	cagatgcctt	ccaggatgtc	aaatttgtca	360
gcaactcgtc	agacgggggt	tcactgtgtt	agccaggatg	gtctcgatct	cctgacctcg	420
tgatccaccc	gcctcggttt	cccaaagtgc	tgggattaca	ggcgtgagcc	accacgccc	480
gccaatattt	tgtaattttt	agtagagatg	gggtttcact	atgttggcca	ggctagtctt	540
aaactcctgt	cctcgtgatc	ctcccacctc	ggcctcccaa	agtgcctgaga	ttacaggtgt	600
gagccactgc	atccagccaa	taatatgctc	tttaacaaac	aatggatcaa	aggagaaatc	660
acaagggaaa	tagaaaaata	cttaaaaatg	aatgaacatg	aaagaaaaca	taccaaactg	720
atgggaaaca	gtgaaaacag	tgcaaacgag	gcaatttata	gctatacacc	attaaattta	780
aagataagaa	agacgtcaaa	ccaacaa				807

<210> 347  
 <211> 918  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 347

tttttttttt	ttagaatata	tttcatttta	ttataaagca	gtgctcccaa	acttttcaca	60
gcgtacacct	cgaggggtga	gaactaacat	ccaagcacac	ctggatggtg	gatgggaccc	120
acttctgggt	aacctgatga	ggaagctcta	gtgaagaaat	tcaggacgcg	gtcttcagag	180
cagagggctt	ggttcaagtc	cctgttctgc	cacttactaa	ctgcatgacc	ttgagcaagc	240
cacttaattt	ctctgctcct	tctctgtgaa	atgggtacaa	tgtggtcagc	agtaaaggaa	300
ctaatacatg	tacagcactc	agcacaaaagc	ctggcacaca	gcaggctctc	accagggtgcc	360
attctcagca	caactgcttg	gttgagctac	tgtggcagtg	gcaggttgtg	ccccaaagggg	420
gtgggctcag	gagcccgtgc	agcaagaggc	agtgaaccaag	gaggcagggg	acaatagccc	480
tatcttttca	ggatctctgc	cttggacctg	gagaatggag	agactttgct	cctatcacgt	540
cccaagttgg	gaaaactaag	gacgaagccg	gtgactgaca	tctgaaatgg	aatcctctgc	600
atctccaagt	ggccctatac	ctgacaatat	cattactagt	gaaaaccaag	tgacaaacac	660
actcctcgac	cccaagttct	tccacatgtc	ccattgagga	gagcacagcc	aataacgcag	720
agtgtattta	tgcgacgggc	tggctaaaca	ggctggctac	gagtccggaa	cagtgtcagg	780
atctggcttc	ccattggccg	acatgacaga	atccttctcg	cggtgctctc	tgatgtactg	840
gtccaacagg	gtggtcagct	ggaggggctg	gtgctggagc	agggagtggg	tctgggctgt	900
gaggcaggtg	gagttctg					918

&lt;210&gt; 348

&lt;211&gt; 1893

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 348

ctgaatccat	ggaaaaacgc	tttacaggac	ttctgcttac	cttttctcag	aatcaccagc	60
cttcttcagc	accacctttt	tggggaagat	ttacctagct	gccaggaaga	agaagaattt	120
tcagttcttg	ccagctgcct	gggacttctg	ccaacgtttt	accaaacaga	acatccattc	180
atcagtgcc	cctgtctgga	ttggccagtt	ccagcatttg	atattataac	tcattgggtg	240
tttgagataa	aatcattttac	tgaaagacat	gcagaacaag	gaaaggcctt	gcttatccaa	300
gagtcaaaat	ggaaattacc	acacctacta	cagttgcctg	agaattataa	caccattttt	360
cagtactacc	acagaaaaac	ctgtagtgtc	tgaccaaagg	ttcctaaaga	tcctgctgtt	420
tgccttgtgt	gtggtacttt	tgtatgcctg	aaaggacttt	gctgcaagca	acaaagttac	480
tgtgaatgtg	tactgcactc	tcagaactgt	gggtgcaggaa	caggtatttt	ccttttgatc	540
aatgcatcgg	taattatcat	cattcgaggt	caccgcttct	gcctctgggg	ttcctgtgat	600
ttggatgctc	atggagagga	agaccgggat	cttaggcgag	gcaaacctct	ctacatttgt	660
aaggaaagat	acaaagttct	tgagcaacag	tggatttctc	atacttttga	tcacatcaat	720
aaaagatggg	gtccacatta	caatgggctg	tgactctcca	cctcagcatt	gcacgtatc	780
atcattttcg	ctacgaattt	atttttcaac	aataagcttt	aacttaattt	gggggattaa	840
cacttttgct	gagggagaaa	aagaaaacat	acattatgaa	gcctttccaa	aattaggtgc	900
ttggtaatca	cgttaatggg	ataatttttt	ttttttaata	tctggagaac	attaataaca	960
agttaaatta	ttcttttagtg	gtcatttttt	aagtgcacaa	ttaataagaa	gcacaacttg	1020
ttcacaaact	cattcagaaa	tgattctccc	aacaatgcat	atcagctatt	cattgatact	1080
tagagtgggt	gtgatttatt	tgacatttta	ctgcttcttt	ctgtctgtgt	gttttaattt	1140
gcacctgcca	agcataatgc	atcttttttc	ctctgccatt	cctgtgttga	ttggagaatt	1200
tttctgtatg	taattagaaa	aaaatgtaaa	acatgattta	tgtgaataac	tgatatagtaa	1260
aagttggctc	aatagtagaa	ctttaaaatt	ttttcttatt	gtgaggaatc	tgttaaaagt	1320
ttaaagcttt	gctgaaaact	gaattcattc	tcaggaaatt	cataaatctt	ctccccaggt	1380
aaataattga	aatagctgta	aaataagtag	atagctgctg	ttaatatata	acagtacatt	1440
ttgggggggca	tatgtgtggg	tgggggggtcc	ttaaaaaatca	aaatttgcca	tttcagttgg	1500
atgaattact	agaggtaata	acaaatctta	ctataaaaatc	aagaggttta	agaacataca	1560
ctgggcagat	gttgattccg	tgcatgccca	cctttttatta	ccaaacaagg	ttttgtttat	1620
atgattgtat	tagaaatgct	cagacttccc	cagaaatgaa	ccataaattt	tggaacttcc	1680
tttcagctca	agaggttcag	ctatattgta	tttgtgcagt	ggtaatcact	acctattttct	1740

ggctcggggtt	tcctctaaaag	gaaaaaaaag	gcggcagtg	gtgatgacct	tcatggaatg	1800
agccacgctt	cctgcattcc	tccttaggaa	ctggctgtgg	aaaaccaatt	tatggtttgc	1860
aggggtttta	aaatccagta	aaaatggggg	atg			1893

<210> 349  
 <211> 1433  
 <212> DNA  
 <213> Homo sapiens

<400> 349						
gcaaggggca	gttggtgaac	ttgctgcctc	cagagaattt	tccttggtgt	ggaggcagcc	60
agggacccag	gatgctccgg	acctgttacg	tgctctgttc	ccaagctggt	cccgcctcca	120
ggggctggca	gtccctgagc	tttgatggcg	gggccttcca	ccttaagggc	acaggagagc	180
tgacacgggc	cttgctggtt	ctccggctgt	gtgcctggcc	cccactcgtc	actcacgggc	240
tgttgctcca	ggcctggtct	cggcgactcc	tgggctcccc	gctctcaggc	gcatttctcc	300
gagcatccgt	ctatgggcag	tttggtggctg	gtgagacagc	agaggaggtg	aagggtctgc	360
tgacagcagc	gcggaccctc	agcctccgac	cactgctggc	agtggccact	gaggaggagc	420
cggactctgc	tgccaagagt	ggtgaggcgt	ggtatgaggg	gaacctcggt	gctatgctgc	480
ggtgtgtgga	cctgtcacgg	ggcctcctgg	agccccccag	cctggctgag	gccagcctca	540
tgacagctga	ggtgacggcg	ctgaccagta	ctcggctctg	taaggagcta	gcctcggtgg	600
tcagaaggcc	aggagcctcc	ttggagctga	gccccgagag	gctggctgaa	gctatggact	660
ctgggcagaa	cctccaggtc	tcctgcctca	atgctgagca	gaaccagcac	ctccgggcct	720
ccctcagccg	cctgcacggg	gtggcacagt	atgcccgggc	ccagcacgtg	cggctcctgg	780
tggtatcgga	gtacacctca	ctgaaccctg	cgtctctcgt	gctgggtggc	gccttggtgc	840
tgcgctggaa	cagcccggtg	gaaggcgggc	cctgggtgtg	gaacacctac	caggcctgtc	900
ttaaaggacac	attcgagcgg	ctggggaggg	atgcagaggg	tgcgcacagg	gccggcctgg	960
ccttcggagt	gaagctggtg	cgaggtgcat	atctggacaa	ggagagagcg	gtggcccagc	1020
tcccatggaa	atggaagacc	ccccactca	ggctgactat	gaggccacca	gttcagagtt	1080
acagcccgct	gcctggaact	gatgctgacg	cagtggtggc	gccatggccc	catgtgccac	1140
ctcatgggtg	cttcccacaa	tgaggaatct	gttcgccagg	caaccaagcg	ggcaggccgg	1200
ctatgtagtg	tataagtcca	ttccctatgg	ctccttgagg	gaggtaatcc	cctacctgat	1260
ccggagggcc	caggagaacc	ggagcgtgct	tcaggggtgc	cgcagggaac	aggagctgct	1320
cagccaaaaa	ctgtggcggc	ggctgctgcc	aggatgccga	aggatacccc	actagcacc	1380
ctgagggggg	catgtggtca	ataaaagtcc	ttaggtgctg	cctaaaaaaa	aaa	1433

<210> 350  
 <211> 1062  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1062)  
 <223> n = a,t,c or g

<400> 350						
tttttttttt	ttccagtcac	taatgatctg	tccttttgag	atcttttact	tcagaggaag	60
atttaggcaa	gagagcaaca	tataatagtc	agtatacaaa	agaagggcat	ggaacatttg	120



gggaacacag	gggtttggag	ggcctgaagc	acaggggtgg	tggatttaga	aatgtgggaa	180
atatgggcca	tgagcctccg	gacagaatgg	ggtccaggaa	ggacagcatc	acacactggt	240
gctggaatth	ggggatcctt	ctgtgggcaa	cctcagcagt	ctggttattg	gccctttttt	300
cttacagcct	ggaaaactgg	accaagtthc	tattgatctc	agcgaccgac	cggcagcctg	360
taaggggcca	tggaagtgtg	gaactcattt	gttaaaatgt	tcaaaacttc	cttaacacca	420
tgttcacccct	tgaggcaag	gccccatagg	attggtctcc	caagaaaaat	gcacttagct	480
ccaagggcca	gagccttctg	cacatcattg	ccagttctga	ccccggcatc	caggtagtac	540
ttcatgttcc	cctattcagc	agctcctact	tctgtcaaag	catcaattga	agcaagaacc	600
tcatcaagct	gcctcccacc	atggttggaa	acaatgatac	cctggacatt	gtgcttcaca	660
gctaactctg	catcctcttt	tgtcaaaatc	cctttcagga	tgatgggcaa	tcgagttatg	720
ctctgaaacc	aggagagatc	attccagcag	agagaagtgc	tgataggagt	catctggaaa	780
taaggtattg	catttccctt	tttaggtgat	tgaagatctg	ttagtggtta	gttcctcctc	840
aactggtttc	gaatgtcatg	tcgcctgttg	ccacatacag	gtgtatccaa	agttattacc	900
aaagcctttga	aacctagggg	ttctaccctc	tggatcaact	gtttgttcag	ctgcaggtct	960
ggatgcacat	agagttggaa	ccatcggagg	ccttcgggag	ctcttgctgt	gtcattttcc	1020
ccgaattcca	ccacnctgga	ctagtgttct	caaaannntc	ga		1062

<210> 351  
 <211> 1227  
 <212> DNA  
 <213> Homo sapiens

<400> 351	
cagttttttt	ttttttttt
tgctgcatga	ttttattact
ataaatatac	agtaaaaacg
60	
aaccaacgat	gagcccatct
gagcacatca	gacggcagca
catgggagtc	ccagcggggc
120	
actctgcggc	ccgaacttca
cgcaaaagctc	tggcaccagg
actgatggcc	agaggctggg
180	
gccttggtgg	gggcgggggg
cgggcgggtgc	agggggctgt
gtgtgttgtt	ggggagaggt
240	
gcatgggggg	agagaggtgc
ttgggggtggg	gtagaggtgc
gtgggagatg	ctcgggccga
300	
gtgcacacac	atgcatggga
acatgtgcag	gagtatgtgc
gtgtgtgtat	gcgtgacagc
360	
atgtgtgagc	gtgagtgtgc
atgtgtgaac	gtgtgcgtga
gcatgtgcaa	gtgggcgtgc
420	
atttgtgtgt	gtgtacgtgt
gagcgcacat	gcgtgcctgt
gcacgagcgg	gaggggtggc
480	
tggcctgggt	gtgcagggag
ctgggtgtga	ggaccgtgct
gtccactgct	gggtctcgcc
540	
caggaggcag	agctcatgct
cggagccacc	gtgagcctca
gggaggggtac	tgagctgccc
600	
cacagccgac	ctgtccccag
gccccactg	cagggcagcc
ctccagagcc	aggtgagcag
660	
cagacacctt	gcctggccca
aggctccgca	gggggtggatc
catgccctgg	gtcaccacgg
720	
cccaggcact	ccctttgcca
tctgcggccc	caggaggttt
acctataaaa	aaaacaaaca
780	
aaacaaacaaa	caaaacagga
cgaggtcgcc	cagaggccaa
gcctccccgg	ccgggacccc
840	
attccccagg	tgtgctgctg
gcttctcctc	ccctgggccc
agcctgccac	agaaagcctg
900	
agacagaaca	aaccaaatac
gagagaactg	caagggggcc
gggcgcggag	gtcacgcct
960	
gtaatctcag	cactctggga
ggccgaggca	ggtggatgac
cttaggagtt	tgagaccagc
1020	
ccggccaaca	tggtgaaatc
ccttctctac	taaaaataca
aaaaaattag	ccgagcatgc
1080	
tggtaggcac	ctgtaatccc
cagctactca	ggagcctaag
gcaggacgat	cacttgaacc
1140	
cgggaggcgg	aggttgagct
gacccgagat	tgagccactg
cactccagcc	tgggcagcaa
1200	
gagtgaact	ccatctcaaa
aaaaaaa	
1227	

<210> 352  
 <211> 1194  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 352

tttttttttt	ttatgatttt	aatatacttt	atatttttaa	aaagtaacaca	gttttaaatt	60
ggtttcaata	ggtttcaagc	agaagggaca	ctgcctacca	cttgcggtcc	catttctgat	120
gaagggatg	tatcatgttg	caaactcaca	tttgcacgac	tggcaaagta	aaaagataga	180
taactttttg	tcaacataac	tttaagagtt	tatatcacgc	acagtttaaa	atcatgacga	240
gatgctgatg	gttggtactat	attcatgtct	cgtatgttgc	accataattt	ggttcacagt	300
ttatccatga	tttagcatgc	caagagaaca	tctcagtcag	taagagaaca	tctcagtcag	360
tgtcaccttg	agaagagcat	caaaagcaga	gggagcagaa	ggaggaccgt	ctgggccttg	420
agactcggcg	cacccccaca	ctccctcgca	ttctcctcag	gatggaagcc	atgacaagat	480
tctgggcgccc	ttctgatctt	ctgggccttt	agacgttcac	acttaaggga	ttcattatgt	540
tgactgtagt	taaggcatgt	ttccaaggat	tgcttttttc	tactctgcat	ttcagagggtc	600
aaaatttggc	aatgacaact	ctcttaacta	ctctctctct	ccaacagtgg	aaaggatgta	660
atcttccctc	tctaataatt	ctccccagg	tttcccttacc	actgataccc	cttactggtt	720
tccgtggtag	tgagtggacc	tgacacacaa	aggatatacc	tgatttcaat	gggtgccatg	780
gtgatggggg	ccacagattc	acagaggcag	ctgctgtcca	ccaccacat	gaacaggttg	840
ctgcttggga	tttgctggat	gacaaaggac	ctggttgaac	aagaggtagc	gaggcagtca	900
tttaccatcc	gtcaattaaa	gagccatgag	gaagacttct	ctcctgggtg	gtagcaacta	960
ccatattttg	taaagcaaat	tttgagagact	atcttactac	taatgttacc	ttctttctcc	1020
atgaggctct	tactttacaa	atacctagct	tactaggaa	aacaacaata	gctatgacga	1080
catgcggctc	atacaactca	ccttggaag	actgaagtgc	tgtatgtaca	aaacacaaga	1140
gtcagagttg	gctgaatcac	ctgttcccaa	ggtttaagag	gtcagacttt	caaa	1194

&lt;210&gt; 353

&lt;211&gt; 1140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 353

actctcacaa	ttaaaacatt	tgaaaaggaa	ttaatgggtg	atctccatta	gggaaagtgc	60
tgacaagccg	caagggatcc	cttgatgggt	ctgggcacag	gcgcccagcc	tgggtctctg	120
ctttgggagc	agcgagggga	atgtgtctct	cacccctagg	cctcctgggt	tgggtcctgc	180
tcaggccaca	cggcgacccc	acccccagcg	cgcctcagtc	caggctcactg	ggcaggggtg	240
ttactgctgc	gctccaaccc	aagcatgtag	atttcagaag	gggactagga	ccccggcgag	300
gtgtttgaga	ccaccggctc	ccaagtgcgt	cgccttgggg	gtttgcatcg	gctcctcagc	360
ctccccaggc	aatctctgtg	tagggctggg	agcgggaggt	ctgagttgag	ccgggtgcct	420
gagatctcgc	gtgcaggtcg	ggggagggga	gccccctcgc	ggctgtgggt	agagcgggag	480
aggaacttcc	cagactagct	ggcacagagc	ctcgggaagg	cggcgggcac	tgacgggtgt	540
ttacgggaag	tgctgcagcc	ttgggggtgg	gacagcgtgg	ccagaccac	cgcctcatct	600
gcacacctgg	gctcaagcgc	taatgacgac	aggggactga	gtgaatggga	cccccatgga	660
cccgcgcgcc	tgccccacgc	catggcctgg	gtttcgggag	ccttgcttta	ttctgcctcg	720
ggtcggaggc	tgggggagcg	agacctccag	tgcccgtgcg	gctgggggag	aggggtggag	780
ggccacttag	atgtaggagt	catcaccacc	gggcgcacgc	tagggacccc	cacccctccc	840
cgcgcctcgc	ccctcatcgc	cgtgcgcgga	gtcactggcg	ccatccacgt	ccaggggtgg	900
cgcgttgaga	acgaccacgt	ctgcctccgt	ccgatgtcc	tgcgcaaac	agacagcctt	960
gtaccgcgcc	tctggccgcc	gctccttggt	caggatggac	ctcaccgcgc	tggggcttcc	1020
gccagctcgc	gccgctgcgc	ggggctcaag	ggcaccgcct	ggggagggag	ggccgggggg	1080
tgccggctat	gcgggcatcg	gtgcctccgc	gggcttgggg	tcgtgcgtgg	ggctggggac	1140

&lt;210&gt; 354

&lt;211&gt; 2401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

```

agttaatctc tttggctggg cctacagatg acatacagag tacaggcccc caggttcctg      60
ctttaaatat ccttagagca ttgttcagag atacgcgcct gggagaaaat attattcctt    120
atgttgctga tggagctaag gctgcaattc tgggttttac atcaccgggc tgggcagtg      180
gaaattcatc cacacttctc tttagtgcct tgatcacaag aatttttggg gttaaaaggg      240
caaaggatga acattccaaa acaaatagaa tgacagggag agagttttcc tctcgtttcc      300
cagaactcta tccttttctt ctcaaacagt tggaaactgt agccaatata gttagacagt      360
atatggggaga accaaatcgt catccaagca tgtttctctt acttttgggt ttggagagac      420
tctacgcttc ccgatggat ggtacttctt ctgctctcag catgggacct tttgttccct      480
tcattatgag gtgtgggtcac tcacctgtct accactcccg tgaaatggca gctcgtgcct      540
tgggccattt tgttatgata gatcacattc ctaataccat tcgaactctg ttgtccacac      600
tccccagctg cactgaccag tgtttccggc aaaaccacat tcatgggaca cttctccagg      660
tttttcattt ggtgcaagcc tactcagact ccaaacacgg aacgaattca gacttccagc      720
acgagctgac tgacatcact gtttgtaaca aagccaaact ctggctggcc aagaggcaaa      780
atccatgttt ggtgaccaga gctgtatata ttgatattct cttcctattg acttgctgcc      840
tcaacagatc tgcaaaggac aaccagccag ttctggagag tcttggcttc tgggagggaag      900
tcagagggat tatctcagga tcagagctga taacgggatt cccttgggcc ttcaaggtgc      960
caggcctgcc ccagtacctc cagagcctca ccagactagc cattgctgca gtgtgggccg    1020
cggcagccaa gagtggagag cgggagacga atgtcccatc ctctttctct cagctgttag    1080
aatctgcctt ccctgaagtg cgctcactaa cactggaagc cctcttgga aagttcttag    1140
cagcagcctt tggacttggg gagaagggcg tgccaccctt gctgtgcaac atgggagaga    1200
agttcttatt gttggccatg aaggaaaatc acccagaatg cttctgcaag atactgaaaa    1260
ttctccactg catggaccct ggtgagtggc ttcccagac ggagcactgt gtccatctga    1320
ccccaaagga gttcttgatc tggacgatgg atattgcttc caatgaaaga tctgaaattc    1380
agagtgtagc tctgagactt gcttccaaag tcatttccca ccacatgcag acatgtgtgg    1440
agaacaggga attgatagct gctgagctga agcagtgggt tcagctgggc atcttgtcat    1500
gtgaagacca tcttctctca gagtctaggg tggccgtcgt tgaagtcctc accagtacta    1560
caccactttt cctcaccac ccccatccta ttcttgagtt gcaggatata cttgctctct    1620
ggaagtgtgt ccttacctt ctgcagagtg aggagcaagc tgtagagat gcagccacgg    1680
aaaccgtgac aactgccatg tcacaagaaa atacctgcca gtcaacagag tttgccttct    1740
gccaggtgga tgccctcatc gctctggccc tggccctggc cgtcctgtgt gatctgtctc    1800
agcagtggga ccagtggcc cctggactgc ccactctgct gggatggctg ttgggagaga    1860
gtgatgacct cgtggcctgt gtggagagca tgcacaggtt ggaagaagac tacctgtttg    1920
aaaaagcaga agtcaacttt tgggcccaga cctgatctt tgtgaaatac ctctgcaagc    1980
acctcttctg tctcctctca aagtccggct ggcgtccccc aagccctgag atgctctgtc    2040
accttcaaag gatggtgtca gagcagtgcc cacctcctgt ctcagttctt cagagagctt    2100
ccaccagctg ctgagtttgt gaagacagtg gagtccaca gactacgcat tcaagaggaa    2160
aggactttgg cttgcttgag gctgctggcc tttttggaag gaaagggaagg ggaagacacc    2220
ctagttctca gtgtttggga ctcttatgca gaatcgaggc agttaactct tccaagaaca    2280
gaagcggcat gttgaagaaa atctggggga ttgggatggg ggtatgtgtg gatttttctt    2340
ccactaaatc tgcaggaaac atgttgaaca taaattcaaa aattttatcc caaaaaaaaa    2400
a

```

&lt;210&gt; 355

&lt;211&gt; 2186

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

cggataaaga	cgctgggaga	ttgacatgca	tttcgaccaa	tagcattgca	gagagggcgt	60
tcatttcgcg	gatgttccaa	tcagtacgca	gagagtcgcc	gtctccaagg	tgaaagcgga	120
agtagggcct	tcgcgcacct	catggaatcc	cttctgcagc	acctggatcg	cttttccgag	180
cttctggcgg	tctcaagcac	tacctacgtc	agcacctggg	accccgccac	cgtagcgccg	240
gccttgcaagt	gggcgcgcta	cctgcgccac	atccatcggc	gctttggctg	gcatggcccc	300
attcgcacgg	ctctggagcg	gcggtgcac	aaccagtgga	ggcaagagg	cggttttggg	360
cgggggtccag	ttccgggatt	agcgaacttc	caggccctcg	gtcactgtga	cgtcctgtc	420
tctctgcgcc	tgctggagaa	cggggccctc	ggggatgcag	ctcgttacca	cctgggtcag	480
caactctttc	cgggcccggg	cgcccgggac	gccgatgagg	agacactcca	agagagcctg	540
gcccgccttg	cccgcggcg	gtctgcggtg	cacatgctgc	gcttcaatgg	ctatagagag	600
aacccaaatc	tccaggagga	ctctctgatg	aagaccagg	cggagctgct	gctggagcgt	660
ctgcaggagg	tggggaaggc	cgaagcggag	cgcccgcca	ggtttctcag	cagcctgttg	720
gagcgcttgc	ctcagaaaca	cttctgaag	gtgatagcgg	tggcgctgtt	gcagccgcct	780
ttgtctcgtc	ggcccaaga	agagttgga	cccggcatcc	acaaatcacc	tggagagggg	840
agccaagtgc	tagtccactg	gcttctgggg	aattcggaa	tctttgctgc	cttttgtcgc	900
gccctccag	cggggtttt	gactttagt	actagccgcc	acccagcgt	gtctcctgtc	960
tatctgggtc	tgctaacaga	ctgggtcaa	cgtttgact	atgaccttca	gaaaggcatt	1020
tgggttggaa	ctgagtccca	agatgtgcc	tgggaggagt	tgcaaatag	gtttcaaagc	1080
ctctgtcagg	cccctccacc	tctgaaagat	aaagtctaa	ctgccctgga	gacctgtaa	1140
gcgcaggatg	gagattttga	agaacctggt	cttagcatct	ggacagacct	cttattagct	1200
cttcgtagtg	gtgcatttag	gaaaagacaa	gttttgggtc	tcagcgcagg	cctcagttct	1260
gtataggcaa	tgctgtgtta	ttacttgaat	atagaatata	tagtttaca	aatgaaaatt	1320
ccaatgttct	caccaaata	atgccttcgt	gtgtccaaag	tataattatt	ttagatgcta	1380
attttgaata	gtttattaaa	cagttataaa	tatgcaaagt	agctggcatg	tagtgtcacg	1440
gattttcttg	atagaggaag	tgattggaag	tattccactt	aaagccatgg	aattagcaat	1500
agtttgcttt	ttaatagaag	gccattttgt	aagaatgttg	aaaatatgtg	taccgtttaa	1560
agaaaaagca	gctttaaagt	gacaaacaaa	ataccctttt	tcttttagta	tgggttattt	1620
ttctaggttt	tctgtccctc	cctcagtagt	gaagagtttt	ctttattcct	ggcagtgcta	1680
ggaatattgg	tttgaagaagc	tggtggccta	tctggagttt	ggccttggtt	acctagtatt	1740
ctaaccagtt	aaccagcctt	agtatgcatt	aaaattgtat	tgttcagaaa	gtttgtttct	1800
cattttctgc	aaattcttac	tttgaaaatg	aatcaccaca	tagtatgtcc	ctttaaagca	1860
ttgacgcaca	gacaaatgtt	taaagcacag	taaatacaaa	tatatgcctt	tggatattaa	1920
attaatgctt	gatgataaaa	gaatcaaact	tttttttttt	tgaaagggag	tctcgctttg	1980
tcacccaaac	tggagggcag	gggggggatc	actgttaagg	gcaacctttg	cctcccagga	2040
tcaagcaatt	ttgactcacc	ctcccaagta	gctgggatta	caggggcagg	ccaccatgcc	2100
cggctaattt	tttgtatttt	tagtaaaaac	ggggtttaac	catgctggcc	aggctggtct	2160
caaacacctg	accttgggat	cgtcc				2186

&lt;210&gt; 356

&lt;211&gt; 1142

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 356

attcacatct	tattcagcat	caaagaattc	acacatgaga	gtaagcacat	gaatgtaatg	60
aatgtggaaa	agctttcagt	caaacctcat	gccttattca	gcatcacaaa	atgcatagga	120
aagagaaatc	gtatgaatgt	aatgagtatg	agggcagttt	cagtcatagc	tcagatctta	180
tcctgcaaca	agaagtcctc	accagacaga	aagcctttga	ttgtgatgta	tgggaaaaga	240
actccagtc	gagagcacat	ctagttcaac	atcagagcat	tcataccaaa	gagaactcat	300
gaatgtaatg	aagatgggaa	gatattttatc	aaattcaggc	ttcattcagc	atctgagagt	360
tcacaccagg	gagaaatcat	gtatgtactg	catgtggtaa	agccttcagt	catagctcag	420
ccattgctca	gcatcagata	attcacacca	gagagaaacc	ctctgaatgt	gacgaatgaa	480
gaaaagggtat	tagtggttaa	ctcttaatcg	actoctgcaa	atctatacca	gtgagaaatc	540
ttacaaatgt	attgaatgtg	gcaaatTTTT	catgctatta	gtattttcat	accttagtca	600
catttgagg	attcacatgg	gaataaaatt	ccattgctgc	aatgaatgtg	aaaaagccat	660
cagtcaaaga	aactaccttg	tttagtatca	aattcacgcc	atgcaaaaag	attataaatg	720

taataagcat	gtatgtgtgt	gaggagattc	agtcataacc	caacgctcat	tcaacatcaa	780
agaatttata	cctaagagaa	cttatttggg	tgtagtaa	ggcagatctt	tcaataggag	840
tttaactagt	ctttgtcata	tcagaatatc	catagtagac	aagaatttga	tgtaacgcaa	900
atggaaaaac	tcgacaccac	atttcaggct	ttacccaaca	tcgaaataat	ggagagaaaa	960
ttgttgatta	tttgtttatg	aaattgttaa	tacatagtcc	caatcttttt	cattgcacaa	1020
aaatctaggg	ttgacttggg	aaatgcagtg	acattttctc	atggagtcc	tttattta	1080
atgtattcta	agtaggtacg	tttattttta	cttttttatt	ataattttga	tattaaaaag	1140
aa						1142

&lt;210&gt; 357

&lt;211&gt; 3167

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3167)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 357

ggaattcgcg	agcgagggc	gcatgactgg	caggcagctc	cacctgcagc	cctggtgccc	60
gatccactag	gtgaagccag	ctgggctcct	gagtctggtg	gggacgtgga	gagtctttat	120
atctagctca	gggattataa	acacaccaat	cagcaccctg	tgtctagctc	aaggttttgtg	180
agtgcaccaa	tcgacactgt	atctagctgc	tctggtgggg	ccttgagaga	cctttatgcc	240
tagctcaggg	attgtaaata	caccaatcag	cacctgtgtg	ttagctcaag	gtttgtgaat	300
gcaccaatcg	acactctgta	tctagctgcc	ctgatgggga	cgtggagaa	ccttgatatct	360
agctcagggg	ttggaaacgc	accaatcagc	gccctgacga	aacaggccac	tcggctctac	420
caatcagcag	gatgtaggtg	gggocagata	agagaataaa	agcgggctgc	cagagccagc	480
attggcaacc	cgctcgggtc	cccttccaca	ctgtggaagc	tttgttcttt	cgctctttgc	540
aataaatctt	gctactgttc	actctttggg	tccacactgc	ttttatgagc	tataaacactc	600
accgcaaagg	tctgcagctt	cactcctgaa	gccagcgaga	ccacaagccc	actgggagga	660
acgaacaact	ccaggcgcgc	aatgaacaac	tcaggcgcgc	ccgccttaag	agctgtaaca	720
ctcacccgga	aggtctgcag	tttcaactcct	aagccagcga	gaccacgaac	ccaccagaag	780
gaagaaactc	caaacacatc	tgaacattag	aaggaacaaa	ctccagatgc	gccaccttaa	840
gagctgtaac	actcacccgc	agggctccag	gcttcattct	tgaagtcagt	gagagaccaa	900
gaaccacaca	attccggaca	cattttggcg	accatgaagg	gactttcgcc	tattgccaag	960
cggtgagaca	atcgctgagc	agttagacca	tcacctattg	ccgagcgggtg	agaccattgc	1020
ctatcgccaa	gcaaactgag	gccatcaagc	tacagatggt	cttacaatg	gaaccccaaa	1080
tgagtcaaac	taacaacttc	taccgaggac	ccctggactg	accagctggt	cctggcactt	1140
cccctggcct	agagagttcc	cctctgaagg	acactacaac	tgcaaagccc	cttcttcgcc	1200
cctatccagc	aggaagtagc	tagagcagtc	atcgccaaa	ttcccaacag	cagttgggggt	1260
gtcctgttga	ttgaggggtg	acagcatgct	ggcagtcctc	acagccctca	ctcgctcgct	1320
cactctcggc	acctcctctg	cctgggctcc	cactttggca	gcacttgagg	agcccttcag	1380
ctctgtatct	agctactctg	atgggtcctt	ggagaacctt	tatgtctagc	tcagggattg	1440
taatacacca	tcagcacctc	gtgtctagct	caggttttgtg	aatgcaccaa	tggacactct	1500
gtatctagct	actctggtgg	ggccttgagg	aaccttgtgt	caacactctg	tatctaacta	1560
acctggtggg	gatgtggaga	accttgtgtc	tagctcaggg	atgtaaacgc	accaatcagt	1620
gccctgtcaa	accactcggc	tctaccaatc	agcaggatgt	gggtggggcc	agataagaga	1680
ataaaagcag	gctgcccag	ccagcagtg	caaccgcctc	aggtcccctt	ccacactgtg	1740
gaagctttgt	tcttttgctc	tttgcaataa	atcttgtact	gctcaactctt	tgggtcccca	1800
ctgcttttat	gagctgtaac	actcactgcg	aaggctctga	gcttcaactcc	tgagccagtg	1860
aaaccatgaa	cccaccagaa	ggaagaaacg	ctgaacacac	ctgaacatca	gaagaaacaa	1920
actccagacg	cgccacctta	agagctggaa	cacttacccg	aagggtccgt	ggcttcattc	1980
ttgaagtcag	tgagaccaag	aaccccccaa	ttccggatac	aatatcgaca	aaacatgcat	2040
ctttgatgtc	tgatagttac	agagagaaga	aattagttcc	tgtgggtttac	ceccattcta	2100
gcactccctc	cttcagtaaa	ttcctggaag	gagggagtg	accaatcgac	actctgtatc	2160

tatctactct	gggtggggcct	tggagaacct	ttatgtctag	ctcagggatt	gtaaatgcac	2220
caattggcac	tctgtatcta	gctcaagggt	tgtaaacaca	ccaatcagca	ccctgtgtct	2280
agctcagggt	ttgtgaatgc	accaattgac	actctgtatc	tagctgctct	gggtggggcct	2340
tggagaacct	ttatgtcgac	actctgtatc	tagctaatac	ggaggggatg	tggagaaact	2400
ttgtgtctag	ctcagggatt	gtaaacgcac	caatcagcgc	cctgtcaaaa	caggccactc	2460
agctctacca	atcagcagga	tgtgggtggg	gccagataag	agaataaaaag	caggctgccc	2520
caaccagcat	tggcaacccc	gctcgggtcc	ccttgccacac	tgtggaagct	ttgttctttc	2580
gctctttgca	ataaatcttg	caactgctca	ctctttgggt	ccacgctgct	tttatgagct	2640
gtaaacactca	ccgcgaagat	ctgcagcttc	actcctgagc	ccagcgagac	catgagccca	2700
ccggcaggaa	cgaacaactc	cagacacgct	gccttaagag	ctgtaacact	ccccgtgaag	2760
gtctgcagct	tcactcctga	gccagcgaga	tcacgaaccc	accagaagga	agaaactccg	2820
aacacatccg	aacatcagaa	ggaacaaaact	ccggaggcgc	caccttaaaa	gctgtagcac	2880
tcactgcgag	ggtcgcgggc	ttcattcttg	aagtcagtga	gaccaagaac	ccaccaattc	2940
cggacacaaa	accctgtctc	tactaaaaaa	tacaaaaaaa	ttagcgcggt	ggggtggccg	3000
gcgctgtag	tcgggtact	cangaggctg	aggcaggaga	atggcgggaa	cccgggaggc	3060
ggagcttgca	gtgagccaag	atggcaccac	tgcactccag	cctggtggag	agagtgcac	3120
tctgtctcan	aaaaaaaaag	aaaaaaaccc	attggttaaa	aacaaaa		3167

<210> 358  
 <211> 4747  
 <212> DNA  
 <213> Homo sapiens

<400> 358						
tttttttttt	ttgaattaat	tgatgagggt	tatttgattg	tctttcttat	aaaatacatt	60
aaaaataactg	cttttaactg	taggcacaca	attaaaacaa	atgtaaacct	atgtttaatt	120
taaaatatat	taaaatgatt	taataaagggt	cttttattat	tttacacatc	aaatttcag	180
caatcagtag	tccactgaag	gagaaaagga	ttatgaaaaa	acaatgaaag	cacagggtag	240
gaaaataaac	aacacaaaag	actaattctg	gatttttttt	ctgtgtcctt	aataccctgt	300
gctgtctttg	acaacaaaag	tgccttactt	atgtgattca	gaggcccgga	agtgaaaaaa	360
atacaagtag	ttaatgaata	atgcatatgt	tcatagcaat	ggtaaaatta	tactgtttcc	420
taatggatac	catttttctt	tatcgagtgg	gacactacag	agtcggatgt	taattgctcc	480
cacaaataca	gttttactct	tcacaataag	cattaagaca	tgtccttgga	gctctgtgac	540
ttcatcatat	actacaattt	cattgtaagt	ggggtcogta	catttttgaa	cagattttgt	600
tttctctcta	cgaacttcac	tgggatattg	taaaagataa	aattcaacat	gtgcactggg	660
cgcagagcca	tctgggagat	gaatgttttt	catgtgtttc	actagtagtg	tcagcttcac	720
atcctcgtag	gatatgacta	actgcacctt	aggcttcttg	tctggaaact	tctcacctag	780
gtacacaggt	gatgattctt	caactgtttg	tgtccagcc	tcagagagga	aaaagctaag	840
tacacaatca	ctgtttgtaa	cttcatgtga	tacatttaat	atctgttcca	tgtaatgatt	900
tagatctctg	aatcttctgt	gatctgaatt	tgtaaaagggt	aggtgccacc	aatgaggaaa	960
ctctgggaga	gtcagtgatg	caaactgctt	ctgaagttgg	ctgtgaagtt	ttgaaaactg	1020
ctcaaatgat	ttttctgtca	ggcttggttc	gttgtgtctg	tgtgtcacct	ggatcagata	1080
cagattactg	gatttcttgc	tgaaccctaa	aattgttgct	ctttcaatcg	acctagtgtg	1140
actcagcaaa	caggattcct	gaggaaaagt	ctgtgaagta	gatttggcag	ggcttatggc	1200
tgacatttgt	gcaagtgtgt	ggatcaagtt	attcaattta	acagggaaac	actccagact	1260
ttcctttatt	tctttggtaa	aatgacttgt	tgttccagg	tctgtgtctt	gtggacgaag	1320
attattatac	acataatttc	ggtcttgaaa	tcccacttag	ctcaggcagt	ccctgcatac	1380
agcatcattt	cccagcaggt	tccaagagca	gttggtctgt	ctttctgata	atattataag	1440
cacgacagca	aagttccac	aaaatcttga	aaatgctgtg	ggtttttccc	cacctctgt	1500
aataaagtat	tcccatctct	gaagtaaaaa	tgaaggagc	tcggtccctt	tttatccctc	1560
caaagtgttg	tgcagacact	aagaattttc	caaagtcaat	atgaaacatg	tggcccgaact	1620
ttgtcagcat	gatattatca	ttgtgacggg	cacatactcc	caggatgaat	gttaccacac	1680
accagccagc	acaggagtag	aaaaagttcc	tcaaggcctt	ttcataatct	gcctttaagt	1740
ggttgtgctg	actgaaccac	tttttaattg	tattttcttt	caatggctct	atcagtcag	1800
aatggcgatg	aatctttgct	agggtcacag	catcaggtag	catctgcacc	aatcgttggt	1860
cttttctgtg	ggatagacat	ctataaatga	tcatttgcac	atccaagcct	tcctgcagcc	1920

aaatattgtc	catcacttga	ataagctgca	gaacaagcat	atcctgacga	agatcatctc	1980
cagccttaaa	aataatgctg	atgtttttgc	ccatcagatt	agcattgatg	aaagtaatct	2040
tcaatggcaa	agcattagat	gtaaaatatg	aacatgcatc	gtgatcaatc	cctttttatac	2100
atagggcagg	gttcagagga	agatgacaag	tattttacatc	ttgaaagaac	tcttctagtc	2160
tgccaatttc	tttcttcagt	acctcctgtc	tttgatggtc	actggcagac	ttgactcctt	2220
ccccaatatc	tcccagaatt	ttgataagtt	tctgctcctt	ggaaaactca	tcaattcaagg	2280
ctttacctgc	acagaattgg	agagcagcta	gtagcttctg	ataccagctt	ttaaaataag	2340
cttcattttc	tgcatTTTTT	agcagccagt	aaagacgatg	ggcaacctgg	atgctctgca	2400
aggagcgggtg	gagtagaagt	tgacttaaag	gactctcaag	gttccattca	aacttgacag	2460
cctgaactag	ctgtgggaga	tattccagta	gttcatcatt	caagagggtg	tctaattggt	2520
gaactgccac	tttacgaatt	tcttgatctg	gaaaactgga	agtcaaaagc	ccaagagcct	2580
ctaaagggtt	agaaaatgtc	catcttctca	aaatgggatg	catttctgaa	acagtccttt	2640
catcccatcc	aggggcacta	cccaggacta	aaggaaggga	gcagttttca	ttattgcagt	2700
agaagcgata	aaaccataaa	tatcttttct	tttcttcaga	gagtagtagg	ggagtctggt	2760
tctgtgaaag	tctggcaata	tgTTTTtatac	actcctttag	tggtccttca	agattacttc	2820
tattctcttc	agaatcaggt	ttcatatact	cccaccagct	agctggaaaa	tcaatctgca	2880
gggtcaccgg	ggatggctga	cttacatccc	acactcctgg	agttatcatt	tctacgggag	2940
gctcactctg	taatgtcatg	ctgaacagca	tagaccgag	aatggatttt	tcttttgtaa	3000
acagtgggaag	acaagtccac	gccagtaa	ttgcattggt	ggttgacag	gcaatcccaa	3060
acagttttac	agttagcatg	gattcccttg	gaagtgaact	tatttcaagg	ggaaaattga	3120
tctgtgcac	ccaggtttct	ggaatgttgt	gtgctgcata	cactgtgaag	ctgaggtggg	3180
aaggaagccc	gggatttaga	taggaagtgc	atctaggtac	atttacaggc	tgaaaatctg	3240
cataaaagct	gttacagtag	acattgatta	gctggtagat	ggatgtggat	agttcagttg	3300
ttaccttctc	tatcaagcct	tttgctgaag	tctctgaact	ttgataaaaa	ttctctcctt	3360
ttctctgaag	aattagactt	agttcattta	ctgcatctgt	aatttgtttg	gtttccacac	3420
accctagaac	actgcatatt	tttttaactt	cttcaataat	attatacacg	ttttcctggg	3480
ttttcaatag	gtatttcagg	tggaagtcat	atTTTctgat	gagtgttaag	agacattgtc	3540
tggaatacttt	ccaaatgatc	ataaattcta	gaagttgatt	cagataaaac	tgactgtggt	3600
cctcttcagt	ctttcgagat	agctttcctg	gagcttcctt	acttttctgc	aggtggagct	3660
gaataacaga	tttatctttt	tgaaacattt	tgtggctccc	caaacagtgg	tcgttttgta	3720
aaaattcttc	agagcccat	acacttagaa	tatgatcttt	ggggagtagc	tggtcatttg	3780
tgcaaaaatg	cagaatttct	gcaattagat	ctttgacaag	ataattagca	catggcataa	3840
aatgaagagg	ttgtgttgag	ttatcaataa	aaatatgtat	attaaaactg	gtcttagaaa	3900
agagctgata	cggaaatgct	gtagtagtgc	tccagatctt	cccagaattg	aaattaacat	3960
cagctgcatg	atatctttct	ctgatttttt	ttactttggt	gcaaaaagag	gccagactcg	4020
tattgtctgt	ttgaggtact	tccactagct	gaatggaaca	acctattgac	tctatattct	4080
tctgccatgt	actttcccat	attccgggtt	gaagagagcc	tttcaaaagc	atcaaagatg	4140
gttccacaat	gttccatgt	ccactccttt	tattctcttc	tttcggcatg	aagtcacttg	4200
agaaggatga	atTTgttgga	ggaatgctac	tttcaaatcc	tatatggtag	ttatgatttt	4260
cattttctaa	ttctttctct	agatttaattt	tatccaaact	tgtgaatgat	ggagctaaaa	4320
tactgaatct	ggaatcatca	gcacatgat	gttttcctat	ggggcttccc	caggagcatt	4380
ctttattcgt	atTTtgaggt	tttggttaaca	cagaaggact	aaaaccaatt	gctggtgctt	4440
tgctaacttg	atgccaggag	agttcacggc	ttttagaagt	gaattcattc	aaggatattt	4500
gggtgtgcttc	atttaatgaa	tgccctgttg	agtcccat	tggtgcagtg	ggcacaaaaa	4560
aggtgttttc	atcaatttca	ctctcgtagt	gtggaatttt	gccactgac	tcatctacta	4620
tctgatcaaa	accagactg	acttggttag	aagaatgggg	ttgatttaca	aagagaaatt	4680
cttggtgttc	atactgcttt	tcgtgtgatt	cattaggatt	tggtccgtt	tgccaagaat	4740
atgccat						4747

&lt;210&gt; 359

&lt;211&gt; 679

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 359

ccagacatca tcttagcact taaggagctg gaagcagagg tatcatttaa actacttcct 60

ctgcttccag	acatcatcct	agcacttaag	gagctggaag	gttgaacaga	aattcttctt	120
ggaatccttg	aagggtttaga	ctccattctt	aaagattgga	ttctgaatat	caggtaacat	180
ttttatttgg	aatatatgta	tacagccttt	ttcaaaatcc	ctagggccac	tcttttgggg	240
gtatttaaaa	aatgtgttag	ctggatctga	ggcatcctgt	aatcaaaacc	aatatatatg	300
tagcaaaatg	aataacattt	ttcaaacttt	ttggacttca	gaattatgga	taacagattg	360
taacctcata	taaaatcata	cttttgcgct	ggggaacggg	cgtcacgcct	gtaatcccag	420
cactttggca	ggctgagact	ggcagatcat	ttgaggtcag	gagttcgaga	ccagcctggc	480
caacatgacg	aaaccccgtc	tcgactaaaa	atacaaaaaa	attagctgga	catggtggca	540
cccattctcta	ctcccagcta	cttgggaggg	cgaagaggga	ggattgcttg	aacccaggag	600
gtggagggtg	cagtgcgctg	agatcatgag	actgcactcc	agcctgggtg	acagagtcca	660
gactccatct	caaaaaaaa					679

<210> 360  
 <211> 2017  
 <212> DNA  
 <213> Homo sapiens

<400> 360	
tttcgtgcgg	gagatcagag
ccgccatggg	ccacacgcac
ggactacctg	cccttccgcc
ggtggccaca	gaggccagtg
ctgtgccctc	atcagcctca
ccatacctat	cctatccaga
agggccagga	ggaatgagt
cgtaagcatg	gacttagggc
gcagggaggc	caccctcgtg
ccttctcctc	cttcttactt
ccgcttcttc	ccctctgtgg
cctgctcggc	tgtggccttg
cagagagttc	aagcccaac
cccctggtgg	tggagtgtgg
catggaccaa	cagatcacag
agctggcttc	cacctggacc
tggactgcct	tggatgtct
gagagagagc	agagcctgtg
gaggctgaca	ggcctggtgg
gctcaagttc	attccaatgc
gctcagcagc	attcagttca
agccagacct	gctactcttg
tcagctttgc	cctgtctggt
cttccccctc	atgttgctgg
accacaggaa	ctcctctggc
gaaggggctg	gagccagaac
gtatcagcca	aaggctccag
gagtggagac	cccaggaaac
ctttggctta	acttocagat
gacctcagtt	acctcctgac
gcacttagga	aaggctggtg
ttaaaaggtc	ctgagccacg
gtttgacaga	atctaagggc
gtctttccag	aataaatatt
gtcccgcctg	gtcccgcctg
ggtgcagcgg	accggcagag
catctgggtg	gctacctttt
ctacttcacc	cgcttcactg
cgatgctgtg	ggcaaaatgc
ctctgcctac	gggtgcctct
aaggacaagg	ccaaaagaca
atccttgctg	ccgccacctg
tcatacagtc	ccagacattg
tgtctatggc	ctcaagtgtg
gctcagcgac	ttctcctcag
gggcctagcc	acaccaaagc
gtgtcacctt	ttggagccaa
gcctgccctg	ctgctgtcta
caaccgcatg	gaatacagac
ggctgtgctg	atgctactca
catctccctg	gctcacatgg
gcgccccaac	ttcctgggta
tacaggagcc	tccatcttcc
tggcatcttc	ctgtatatgg
gaagctgttg	cttgatgcca
ctctgaccag	gggccacctc
gataatcaag	tctacccttg
ggctccgaaag	gcccctggaga
gatgccagag	gaggagagaa
tggaaagtgc	agtgaagatt
ttctgtgaat	tagctggagt
gcttactcag	gaagtccagg
cttggggaag	gactgaaggg
agagtggcag	gaagcaagca
actgatcagg	ccccattcac
cattttgaac	tttctgtcct
ctcttttcat	cttgcaaaga
aaataaa	



<210> 361  
 <211> 2900  
 <212> DNA  
 <213> Homo sapiens

<400> 361  
 atggggctca aggcgcgcag ggcggcgggg gcggctggcg gcggcggcga cgggggcggc 60  
 ggaggcggcg gggcgggctaa cccagccgga ggggacgcgg gcggcgccgg cgacgaggag 120  
 cggaaagtgg ggctggcgcc cggcgacgtg gagcaagtca ccttggcgct cggggccgga 180  
 gccgacaaag acgggaccct gctgctggag ggcggcgggc gcgacgaggg gcagcggagg 240  
 accccgcagg gcatcgggct cctggccaag accccgctga gccgcccagt caagagaaac 300  
 aacgccaaagt accggcgcat ccaaactttg atctacgacg ccctggagag accgcggggc 360  
 tgggcgctgc tttaccacag cgttgggtgtt cctgattgtc ctagggggtgc ttgattctgg 420  
 ctgtcctgga ccacattcaa ggagtatgag actgtctcgg gagactggct tctgttactg 480  
 gagacatttg ctattttcat ctttggagcc gaggtttgcct tgaggatctg ggctgctgga 540  
 tggttgctgcc gatacaaagg ctggcggggc cgactgaagt ttgccaggaa gccctctgtc 600  
 atgttggaca tctttgtgct gattgcctct gtgccagtgg ttgctgtggg aaaccaaggc 660  
 aatgttctgg ccacctccct gcgaagcctg cgcttcctgc agatcctgcg catgtcgcgg 720  
 gatggaccgg gagaaggtgg cacctggaag cttctggggc tcagccatct gtgccacag 780  
 caaagaactc atcacggcct ggtacatcgg tttcctgaca ctcatccttt cttcatttct 840  
 tgtctacctg gttgagaaag acgtcccaga ggtggatgca caaggagagg agatgaaaga 900  
 ggagtttgag acctatgcag atgccctgtg gtggggcctg atcacactgg ccaccattgg 960  
 ctatggagac aagacaccca aaacgtggga aggcctgtct attgccgcca ccttttcctt 1020  
 aattggcgct tcttttttgc cccttcacgc gggcatcctg gggtcggggc tggccctcaa 1080  
 ggtgcagggc caacaccgtc agaagcactt tgagaaaagg aggaagccag ctgctgagct 1140  
 cattcaggct gcctggagggt attatgctac caaccccaac aggattgacc tgggtggcgac 1200  
 atggagattt tatgaatcag tcgtctcttt tcttttcttc aggaaagaac agctggaggc 1260  
 agcatccagc caaaagctgg gtctcttgga tcgggttcgc ctttctaate ctctgtgtag 1320  
 caatactaaa ggaaagctat ttaccctctt gaatgtagat gccatagaag aaagtccctc 1380  
 taaagaacca aagcctgttg gcttaaaca taaagagcgt ttccgcacgg ccttccgcat 1440  
 gaaagcctac gctttctggc agagttctga agatgcgggg acaggtgacc ccatggcgga 1500  
 agacaggggc tatgggaatg acttcccctc cgaagacatg atccccacc tgaaggccgc 1560  
 catccgagcc gtcagaattc tacaattccg tctctataaa aaaaaattca aggagacttt 1620  
 gaggccttac gatgtgaagg atgtgattga gcagtattct gccgggcac tcgacatgct 1680  
 ttccaggata aagtaccttc agacgagaat agatatgatt ttaccccctg gacctccctc 1740  
 cacgccaaaa cacaagaagt ctacagaaagg gtcagcattc accttcccct cccagcaatc 1800  
 tcccaggaat gaaccatatt taggccagac catccacatt cagaaattcg aagaccaaag 1860  
 gcattgatgg gggaagtttg ttaaaagttt gaaaggacag gtttcaggga ctggggagga 1920  
 agctggactt cctcgtggat atgcacatgc aacacatgga acggttgag gtgcaggcca 1980  
 cggagtatta cccaaccaag ggcacctcct cgcagctga agcagagaag aaggaggaca 2040  
 acaggtattc cgatttgaaa accatcatct gcaactattc tgagacaggc ccccggaac 2100  
 caccctacag cttccaccag gtgaccattg acaagtcag cccctatggg tttttgcac 2160  
 atgaccctgt gaacctgccc cgagggggac ccagttctgg aaaggttcag gcaactcctc 2220  
 cttcctcagc aacaacgtat gtggagaggc ccacggctcct gcctatcttg actctctcgc 2280  
 actcccaggt gagctgccac tcccaggctg acctgcaggg ccctactcgc gaccgaatct 2340  
 cccccggca gagacgtagc atcacgcgag acagtgcac acctctgtcc ctgatgtcgg 2400  
 tcaaccacga ggagctggag aggtctccaa gtggcttcag catctcccag gacagagatg 2460  
 attatgtgtt cggcccaaat ggggggtcga gctggatgag ggagaagcgg tacctcgccg 2520  
 aggggtgagc ggacacagac acggaccctc tcacgcccag cggctccatg cctctgtcgc 2580  
 tccacagggg atgggatttc tgattcagta tggacccctt ccaataagcc catttaaaag 2640  
 aggtcactgg ctgaccctc cttgtaatgt agacagactt tgtatagtcc acttactctt 2700  
 acaccgcagc cttaccagcg gggacaccaa tggctgcac aaatgcacgc gtgtgcgtgg 2760  
 tggcccaacc caggcagggg cttcccacag cctcttcctc cccatgtcac cacaacaaag 2820  
 tgcttccttt tcagcatggg ttgcatgact ttacactata taaatggttc ccgctaactc 2880  
 cttctaggat aaaaaaaaaa 2900

<210> 362  
 <211> 5433  
 <212> DNA  
 <213> Homo sapiens

<400> 362

cggacgcgtg	ggatcattga	atttgaccca	aagtatactg	ccttcgaagt	ggaggaagat	60
gttgggctga	tcatgatccc	agtgggtgag	ctacatggaa	cttatggcta	tgtgacagct	120
gatttcattc	ctcagagctc	ctctgccagt	cccgagggtg	ttgattacat	tttgcatggc	180
agtacagtca	cctttcagca	tgggcaaaac	ttaagtttta	ttaaatactc	catcattgat	240
gacaatgaaa	gtgaatttga	ggagcccatt	gaaattctac	tcactggagc	tactggagga	300
gcggtccttg	ggcgccacct	agtgagcaga	atcataatag	ctaagagtga	ctctcccttt	360
ggagttataa	ggtttctcaa	tcaaagcaaa	atttctattg	ctaateccaa	ttccacaatg	420
attttatcac	tgggtctgga	gcggactgga	ggactcttgg	gagagattca	ggtgaactgg	480
gagacagtag	gacccaactc	tcaagaagcc	ttactgccac	agaatagaga	cattgcagac	540
ccagtgaagc	ggttgttcta	ttttggagaa	ggagaaggag	gagtggagaa	cataattctg	600
acaatctatc	ctcatgaaga	aattgaagtt	gaagagacat	tcattattaa	acttcatctt	660
gtgaaaggag	aagctaaatt	agactccaga	gctaaagatg	ttacattaac	catacaagag	720
tttggtgacc	caaatggagt	tgttcagttt	gctcctgaaa	ctttgtctaa	gaagacttat	780
tcagagcctc	tggctctgga	agggcccctg	ctcattacct	tctttgtcag	aagagtcaag	840
ggcacctttg	gagagattat	ggtttactgg	gaattaagta	gtgagtttga	cattactgaa	900
gactttcttt	ccaccagtgg	atttttcacc	attgctgatg	gagagagtga	agctagcttt	960
gatgttcatt	tgctaccaga	tgaggtagct	gagatagagg	aagattatgt	gatccagctt	1020
gtttctgtag	agggaggagc	cgaactggat	ctggagaaga	gtatcacatg	gttctctgtt	1080
tatgcaaatg	atgaccacaa	tggagtattt	gccctgtatt	cggatcgcca	gtcaataactt	1140
attgggcaga	accttattag	atccatccaa	attaacataa	cccggcttgc	tggaaacattt	1200
ggagattgtg	ctgttgggct	tcgaatatca	tcggatcata	aagaacagcc	gattgttacc	1260
gaaaatgcag	agaggcagct	gggtgtcaaa	gatgggtgcca	catataaagt	ggacgtgggtg	1320
ccaataaaga	atcaggtctt	cctatcactg	ggctctaatt	tcactttgca	actggtgact	1380
gtgatgcttg	tcgggtggacg	tttctatgga	atgccaacaa	ttcttcagga	agcaaatct	1440
gctgtccttc	cagtctctga	gaaagctgcc	aattctcagg	tcggatttga	atccactgct	1500
tttcaactca	tgaacatcac	tgtctggcaca	agccacgtta	tgattttctag	gagaggcaca	1560
tatggagctc	tctcggttgc	ctggaccact	ggatatgctc	ctgggttaga	aattcctgaa	1620
ttcattgttg	ttggcaacat	gacccaacaa	ctggggagcc	tttcattttc	ccacggtgaa	1680
caaaggaaag	gagttttcct	gtggacgttt	cctagccctg	gttggccaga	ggcctttggt	1740
cttcacctat	caggagtgc	gagcagtgct	cctggcggag	ctcaactccg	atcagggtttc	1800
attgttgctg	aaattgaacc	aatgggcgtc	ttccaatttt	ccactagctc	aagaaatctc	1860
atagtgtcag	aagatacaca	gatgatcaga	ttacatgtac	aaagactatt	tgggttccac	1920
agcgtcttta	ttaaagtttc	ttatcagacc	actgcaggaa	gcgccaagcc	actggaagat	1980
tttgagcctg	ttcagaatgg	ggaactgttt	tttcaaaaat	tccaaaactga	ggttgatattt	2040
gaaataacaa	ttattaatga	tcagctttct	gagatagaag	aattttttta	cattaacctt	2100
acttcagtag	aaattagggt	attacaataa	tttgatgtta	attggagccc	acgcctgaat	2160
ctagatttca	gtgttgcagt	gattacaata	ttggataatg	atgacctggc	aggaatggat	2220
atttccttcc	ccgagacaac	tgtggctgta	gcagttgaca	caactctcat	tcctgtagaa	2280
actgaatcca	ccacatacct	cagcacaagc	aagacgacta	ccattctgca	gccaaccaac	2340
gtggttgcca	ttgttactga	ggcaactggt	gtatctgcca	tccttgagaa	acttgtcacc	2400
cttcattggca	cacctgctgt	gtctgaaaag	cctgatgtgg	ccactgtaac	tgccaatggt	2460
tccattcatg	gaacattcag	ccttgggcca	tccattgttt	atattgaaga	ggagatgaag	2520
aatggcacat	tcaaacctgc	agaagttcct	atccgaagaa	ctgggtgggtt	tactggcaat	2580
gtcagcataa	cagttaaaac	tttcggtgaa	agatgtgctc	agatggaacc	aaatgcattg	2640
ccctttcgtg	gtatctatgg	gatttccaac	ctaactgggt	cagttgaaga	agaagacttt	2700
gaagaacaaa	ctcttaccct	tatatcccta	gatggagaaa	gagaacgtaa	agtatcagtt	2760
caaatttttg	atgatgatga	gcctgagggg	caggaattct	tctacgtgtt	tctcacaac	2820
cctcaagggg	gagcacagat	tgtggagggg	aaggatgata	ctggatttgc	agcttttgcc	2880
atggttatta	ttacaggggag	tgaccttcac	aatggcatca	taggattcag	tgaggagtcc	2940
cagagtggac	tagaactcag	ggaaggagct	ggtatgagaa	gattgcacct	tattgtcaca	3000
agacagccaa	acagggcctt	tgaagatgtc	aaggtctttt	ggcagtcac	acttaacaaa	3060
acagtcgtcg	tgctccagaa	ggatggggta	aacctgatgg	aggaacttca	gtctgtgtca	3120
gggaccacaa	cctgtacaat	gggtcaaaaa	aatgtcttta	tcagcattga	actcaaacca	3180

gaaaagggtac	cacaggttga	agtgtatattt	tttgtggaac	tatatgaagc	tactgctgga	3240
gcagcaataa	acaacagtgc	cagattcgca	cagattaaaa	tcttagaaag	tgatgaatct	3300
caaagccttg	tgtatattttc	tgtgggttct	cggctggcag	tggtcacaa	gaaggccact	3360
ttaatcagtc	tcgaggtggc	cagagattct	gggacaggac	taatgatgtc	tgtaaacttt	3420
agtaccacag	agttgaggag	tgctgaaaca	attggtcgta	ccatcatatc	tccagctatt	3480
tctggaaagg	atthttgtgat	aactgaaggc	acattgggtct	ttgaacctgg	ccagagaagc	3540
actgtattgg	atgtcatcct	aacgccagag	acaggatctt	taaattcatt	tcctaaacgc	3600
ttccagattg	tcctttttga	cccaaaagg	ggtgccagaa	ttgataaagt	gtatgggact	3660
gccaacatca	ctcttgtctc	agatgcagat	tcgcaggcca	tttgggggct	tcgagatcag	3720
ctacatcagc	ctgtgaatga	tgataattctc	aacagagtgc	tccataccat	cagcatgaaa	3780
gtggccacag	aaaacacaga	tgaacaactc	agtgccatga	tgcatcta	agaaaagata	3840
actactgaag	gaaaaattca	agctttcagt	ggtgccagcc	gaactctttt	ctatgagatt	3900
ctttgttctc	ttattaaccc	aaagcgcaag	gacactaggg	gattcagtca	ctttgctgaa	3960
ttgactgaga	atthttgcctt	ttctctgtctg	actaatgtta	cttgccggtc	tcctgggtgaa	4020
aaaagcaaaa	ccatccttga	tagttgcccc	tatttgtcaa	tattgggtct	tcactgggtat	4080
cctcagcaaa	tcaatggaca	caagtgtgaa	ggaaaggaag	gagattacat	tcgaattcca	4140
gagaggctac	tggatgtcca	ggatgcagaa	ataatggctg	ggaaaagtac	atgtaaat	4200
gtccagttta	cagagtata	cagccaacag	tggtttataa	gtggaaacaa	tccttcctacc	4260
ctaaaaaata	aggtattatc	tttgagtgtg	aaaggtcaga	gttcacaact	cctgactaat	4320
gacaatgagg	ttctctacag	gatttatgct	ctgagccta	gaattattcc	tcagacatct	4380
ctgtgtctcc	tttggaatca	ggctgtctgca	agctgggtgt	ctgacagtca	gttttgcaaa	4440
gtgattgagg	aaactgcaga	ctatgtggaa	tgtgcctgtt	tacacatgtc	tgtgtatgct	4500
gtctatgtct	ggactgacaa	cttgtcttca	tacaatgaag	ccttcttcac	ttctggattt	4560
atatgtatct	caggtctttg	cttggtctgtt	ctttcccata	tcctctgtgc	caggtactcc	4620
atgtttgcag	ctaaacttct	gactcacatg	atggcagcca	gcttaggtac	acagattctg	4680
tttctggcgt	ctgcatacgc	aagtccccaa	ctcgctgagg	agagctgttc	agctatggct	4740
gctgtcacac	attacctgta	tccttgccag	tttagctgga	tgctcattca	gtctgtgaat	4800
ttctggtagc	tgtggtgat	gaatgatgag	cacacagaga	ggcgatatct	gctgttttct	4860
cttctgagtt	ggggactacc	agcttttgtg	gtgattctcc	tcatagttat	tttgaaagga	4920
atctatcatc	agagcatgtc	acagatctat	ggactcattc	atggtgacct	gtgttttatt	4980
ccaaacgtct	atgctgcttt	gttcaactgca	gctctgttcc	ctttgacgtg	cctcgtgggtg	5040
gtgttcgtgg	tgttcatcca	tgctaccag	gtgaagccac	agtggaaagc	atatgatgat	5100
gtcttcagag	gaaggacaaa	tgctgcagaa	attccactga	ttttatatct	ctttgctctg	5160
atttccgtga	ctgggctttg	gggaggacta	cacatggcct	acagacactt	ctggatgttg	5220
gttctctttg	tcattttcaa	cagtctcgac	ctctagtac	cctctgttct	acttttattc	5280
tctatgagat	caacattttt	tagcttccac	acagggactc	tgacttcaag	agagaaagaa	5340
agtacttttg	tacttacatg	cctactgagc	ccagattcca	aaggccttgg	ggttctatgt	5400
ttccttaaca	ctgaatgggc	tttccaagt	cat			5433

<210> 363  
 <211> 3569  
 <212> DNA  
 <213> Homo sapiens

<400> 363	
agcggccggg	gccacgatgg
gggcccggc	gctccccggg
cgctcccag	gcccggggg
ggggaggag	ccgctggaga
taaagtactc	tcgctgggat
tggtttgaaa	ccaagctgtg
aacatttggg	gaactgtcgc
ggattaccag	gggggacgtg
aggtgtgggt	gagaaaagg
ccagggcgga	ctgcctgcca
tggggtagaa	agaacccatg
agcgcgacgg	ctgcgcgggg
ggggaacggc	cgcgatcggg
ggcgcgctcc	ttgctggccc
cgcccgact	gccaaggacc
tgtgttaaca	acaatacttg
taaaagttgc	aaaggctcgt
cctgtgttga	gcttgggaaa
aggaacatat	atgggacttg
cctctgtgcc	tggtcagatg
agttcctgtg	tgccaaggt
ccagattcca	aaggccttgg
cat	
60	
120	
180	
240	
300	
360	
420	
480	
540	
600	
660	

ttgaaacgcc	ctccctaccc	ctccttattt	tcctttggat	ggattcaggg	cagaatattt	720
acacacttgg	ggtggacttc	ttcctgttat	tagcaaaacta	aaaaaatgtg	gaacatatac	780
taaaaacatg	agaccggtat	atccaacaaa	aactttcccc	aatcactaca	gcattgtcac	840
cggattgtat	ccagaatctc	atggcataat	caacaataaa	atgtatgac	ccaaaatgaa	900
tgcttccttt	tcacttaaaa	gtaaagagaa	atttaatcct	gagtgggtaca	aaggagaacc	960
aatttgggtc	acagctaagt	atcaaggcct	caagtctggc	acatttttct	ggccaggatc	1020
agatgtggaa	attaacggaa	ttttcccaga	catctataaa	atgtataatg	gttcagtacc	1080
atltgaagaa	aggatttttag	ctgttcttca	gtggctacag	cttcctaaag	atgaaagacc	1140
acacttttac	actctgtatt	tagaagaacc	agattcttca	ggtcattcat	atggaccagt	1200
cagcagtga	gtcatcaaag	ccttgccagag	ggttgatggg	atggttggta	tgctgatgga	1260
tggtctgaaa	gagctgaact	tgccacagatg	cctgaacctc	atccttattt	cagatcatgg	1320
catggaacaa	ggcagttgta	agaaatacat	atatctgaat	aaatatattg	gggatgttaa	1380
aaatattaaa	gttatctatg	gacctgcagc	tcgattgaga	ccctctgatg	tcccagataa	1440
atactattca	tttaactatg	aaggcattgc	ccgaaatcct	tcttgccggg	aaccaaacca	1500
gcacttcaaa	ccttacctga	aacattttct	acctaaagcgt	ttgcactttg	ctaagagtga	1560
tagaattgag	cccttgacat	tctattttgga	ccctcagtg	caacttgcac	tgaatccctc	1620
agaaaggaaa	tattgtggaa	gtggatttca	tggtctctgac	aatgtatttt	caaataatgca	1680
agccctcttt	gttggctatg	gacctggatt	caagcatggc	attgaggctg	acacctttga	1740
aaacattgaa	gtctataact	taatgtgtga	tttactgaat	ttgacaccgg	ctcctaataa	1800
cggaaactcat	ggaagtctta	accaccttct	aaagaatcct	gtttatacgc	caaagcatcc	1860
caaagaagtg	caccccttgg	tacagtgcct	cttcacaaga	aacccagag	ataaccttgg	1920
ctgctcatgt	aacccttcga	ttttgccgat	tgaggatttt	caaacacagt	tcaatctgac	1980
tgtggcagaa	gagaagatta	ttaagcatga	aactttaccc	tatggaagac	ctagagtctc	2040
ccagaaggaa	aacaccatct	gtcttctttc	ccagcaccag	tttatgagt	gatacagcca	2100
agacatctta	atgccccttt	ggacatccta	taccgtggac	agaaatgaca	gtttctctac	2160
ggaagacttc	tccaactgtc	tgtaccagga	ctttagaatt	cctcttagtc	ctgtccataa	2220
atgttcattt	tataaaaaata	acaccaaagt	gagttacggg	ttcctctccc	caccacaact	2280
aaataaaaaa	tcaagtggaa	tatatcttga	agcttttgct	actacaaata	tagtgccaat	2340
gtaccagagt	tttcaagtta	tatggcgct	ctttcatgac	accctactgc	gaaagtatgc	2400
tgaagaaaga	aatggtgtca	atgtcgtcag	tggtcctgtg	tttgactttg	attatgatgg	2460
accgttgtga	ttccttaaga	gaatctgagg	caaaaaagaa	gagtcocatc	cgtaacccaa	2520
gaaaattttt	ggattcccaa	ctccacttcc	ttttatttgt	gctaacaagc	tgtaaagat	2580
acatctcaga	cgcctttgca	ctgtggaaaa	cctaggacac	cttaggcttt	ccattttgcc	2640
ttcacaggga	ctggattaac	agcgagacgt	gtgggtgcac	gggaagcatg	actcctcatg	2700
gggttgaaga	attcgttaaa	tgtttacaca	gagcaccgga	tcacaggatg	ttgaggcaca	2760
tcacttggac	tcagcttcta	tcaacaaaga	aaagagccag	tttcagacat	tttaaagttg	2820
aaaacacatt	tgccaacctt	tagccaagaa	gactgatatg	ttttttatcc	ccaaacacca	2880
tgaatctttt	tgagagaacc	ttatatttta	tatagtcctc	tagctacact	attgcattgt	2940
tcagaaactg	tcgaccagag	ttagaacgga	gccctcgggtg	atgcggacat	ctcagggaaa	3000
cttgcgta	cagcacagca	gtggagagt	ttcctgttga	atcttgcaca	tatttgaatg	3060
tgtaagcatt	gtatacattg	atcaagttcg	ggggaataaa	gacagaccac	acctaaaact	3120
gcctttctgc	ttctcttaaa	ggagaagtag	ctgtgaacat	tgtctggata	ccagatat	3180
gaatctttct	tactatttgt	aataaacctt	gatgggcatt	ggggcaaaca	gtagacttat	3240
agtaggggtg	gggtagccca	tggtatgtga	ctatctttat	gaggaatttt	aaagtgggtc	3300
tggtatctct	tttaacttga	gtttcatttc	ttttcattgt	aatcaaaaaa	aaaaaattaa	3360
gcagaagcca	aaatactttt	gagaccttgt	ttcaatcttt	gctgtatatc	ccctcgaaaa	3420
tccaagttat	taatcttatg	tgttttcgtt	ttaaattttt	tgattgggag	tttcttttaga	3480
ttttaatggg	tccaaaggag	ttcaactttt	gaggggacga	tctttgaata	tacttaccta	3540
ttataaaatc	ttactttgta	tttgtattt				3560

&lt;210&gt; 364

&lt;211&gt; 832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 364

tcccttctatg	cttattcgga	ggggcggcaa	ggcatgtttc	ccagttttta	agatcttgcc	60
ccccccata	atztatgagg	accgttctgt	gtccgggcat	cagtgatggt	gccctgcat	120
ttcggggtgc	tctttggagg	gcgtgtttgt	tgaaaaacca	cccccaacc	cctgcccgc	180
ggtcccgga	ctggccaaca	tggaaaggtgc	tgcggatggt	ggatccgcgt	gccaggcggc	240
tccgctcccc	tgatgggggt	gccaggctgt	gactggaggg	ggaggcaggg	ggcaccctg	300
gggtgctga	gctgttttct	ttcccatttg	gcaacagtga	cgggcgctca	gccccgggc	360
gttctgtgca	aacgtagggtg	ttcctgcggg	tcatcatgct	aggaggagg	ttgttggggg	420
tgctcgtgct	gtccttccgc	cgctctggga	tctctgcctt	gttgggggtg	tgggcgctgc	480
tgaccatggg	gctgaagggg	gggcagccct	cgactcccac	tccccgcggt	gctgcagctc	540
gccttccggc	ctggcagccg	ctcctccttc	agctccgcct	cccccgctgt	cgctgggctg	600
cgtttgggg	gcaggggtgc	aggggatggg	ccacctgggg	gagggggtac	cgtttagagc	660
tggcatcacc	acggaaacc	agaactgact	ctgggggatc	gttggaaacct	gagaattcct	720
cacgtggggt	gcaatctctg	tgtgggcat	tctgacaata	tctgtcaaaa	ttacctcaag	780
attaccaacg	cacatatact	gacttagaaa	ctccaaatca	atgacatcat	gc	832

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365						
cacacactgc	accacagctc	tcccacctct	gaggccgagg	agttcgtctc	ccgcctctcc	60
accagaact	acttccgctc	cctgccccga	ggcaccagca	acatgacctc	tgggaccttc	120
aacttcctcg	ggggccggct	gatgatccct	aatacaggaa	tcagcctcct	catcccccca	180
gatgccatac	cccgagggaa	gatctatgag	atctacctca	cgctgcacaa	gccggaagac	240
gtgaggttgc	ccctagctgg	ctgtcagacc	ctgtcgagtc	ccatcgtttag	ctgtggacct	300
cctgggcgctc	ctgcttacct	ggccagtcac	cctggggtat	ggacctgtgt	gggggagccc	360
agccctgaca	gctggggagcc	tgcgcctcaa	aaagcagtcg	tgcgagggca	gctgggagga	420
tgtgctgcac	ctgggcgagg	aggcgccctc	ccacctctac	tactgccagc	tggaggccag	480
tgctgcttac	gtcttcaccg	agcagctgag	ccgctatgcc	ctgggtgggag	aggccctcag	540
cgtggctgcc	gccaagcgcc	tcaagctgct	tctgtttgcg	ccggtggcct	gcacctccct	600
cgagtacaac	atactgggtct	actgcctgca	tgacactcac	gatgcactca	acgtagtggg	660
gcagctggag	aagcagctgc	agggacagct	gatccaggag	ccactggtac	tgcacttcaa	720
ggacagttac	cacaacctgc	gcctatccat	ccacgatgtg	cccagctccc	tgtggaagag	780
taagctcctt	tgcagctacc	aggagatccc	cttttatcac	atctggaatg	gcacgcagcg	840
gtacttgcac	tgcaccttca	ccctggagcg	tgtcagcccc	agcactagtg	acctggcctg	900
caagctgtgg	gtgtggcagg	tggagggcga	cgggcagagc	ttcagcatca	acttcaacat	960
caccaaggac	acaagggttg	ctgagctgct	ggctctggag	agtgaagcgg	gggtcccagc	1020
cctgggtgggc	cccagtgccct	tcaagatccc	cttcctcatt	cggcagaaga	taatttccag	1080
cctggaccca	ccctgtaggc	gggtgcccga	ctggcggact	ctggcccaga	aactccacct	1140
ggacagccat	ctcagcttct	ttgcctccaa	gcccagcccc	acagccatga	tcctcaacct	1200
gtgggaggcg	cggcacttcc	ccaacggcaa	cctcagccag	ctggctgcag	cagtggctgg	1260
gactggggcca	gcaggacggg	ggcttctttc	acagtgttcg	gaggctgagt	gctgaggccg	1320
g						1321

<210> 366  
 <211> 777  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 366

gggtccgctg	cagggcaggt	tcagcagcaa	cagcagcggc	gacaccagca	gggaaaagtg	60
acagtgaat	acgatcgtaa	ggagcttcgg	aagcggctgg	tgctggagga	atggatcgtg	120
gagcagctgg	gtcagctcta	cggctgagag	gaagaagaaa	tgccagaggt	agaaattgac	180
attgatgatc	tttttgatgc	atacagtgat	gaacagagag	cttcaaaatt	acaggaagct	240
cttgtagact	gctacaaacc	aacagaggaa	tttatcaaag	agctgctttc	tccgataaga	300
ggcatgagga	aactgagccc	ctccgcagaa	gaagagtgtg	tgattctgga	acagggtgaa	360
actctcccag	agatgaagaa	agagtcctgg	gatttgtact	tcataagac	ttttgtgaaa	420
gaataggtgt	ccttatgaac	aacgtttttg	tttttttttt	ttcttttttg	ggggtaaagg	480
tggtgggggtc	tattagacat	ttattcaaga	gcgttctttt	ttgggtttta	aagggttttg	540
ttaatgtaat	atttaaatac	caaaaatata	ttgacttttag	ccacagccta	cccagggttt	600
atcaaggagg	ggggaccctc	aggggaagggc	ccccccaggt	tgcgtttctt	gcagggactc	660
aaatgttaat	tcccttatga	tcccggaaaa	atagtttttt	tacaagaagt	tgggcaaaat	720
ttttttccta	aagttggaca	ttggactcaa	ttggcaaat	tttcaacctg	gtatttt	777

&lt;210&gt; 367

&lt;211&gt; 2056

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 367

aattatgtta	gatggccggg	tgcggtggct	cacgcctgta	atctcagcac	tttgggaggg	60
cgagatggaa	gacgtcatag	cacggatgca	agatgaaaaa	aatggaattc	ctattcgtac	120
ggtcaaaagc	tttctttcca	agatacctag	cgtcttctct	ggttcagaca	ttgttcaatg	180
gttgataaag	aacttaacta	tagaagatcc	agtggaggcg	ctccatttgg	gaacattaat	240
ggctgcccac	ggctacttct	ttccaatctc	agatcatgtc	ctcacactca	aggatgatgg	300
caccttttac	cggtttcaaa	ccccctat	ttggccatca	aattgttggg	agccggaaaa	360
cacagattat	gccgtttacc	tctgcaagag	aacaatgcaa	aacaaggcac	gactggagct	420
cgcagactat	gaggctgaga	gccctggccag	gctgcagaga	gcatttgccc	ggaagtggga	480
gttcattttc	atgcaagcag	aagcacaagc	aaaagtggac	aagaagagag	acaagattga	540
aaggaagatc	cttgacagcc	aagagagagc	gttctgggac	gtgcacaggc	ccgtgcctgg	600
atgtgtaaat	acaactgaag	tggaacattaa	gaagtcatcc	agaatgagaa	acccccacaa	660
aacacggaag	tctgtctatg	gtttacaaaa	tgatattaga	agtacagtc	ctaccacac	720
accacacca	gaaactaaac	ctccaacaga	agatgagtta	caacaacaga	taaaatattg	780
gcaaatacag	ttagatagac	atcgggttaaa	aatgtcaaaa	gtcgctgaca	gtctactaag	840
ttacacggaa	cagtatttag	aatacgaccc	gtttcttttg	ccacctgacc	cttctaacc	900
atggctgtcc	gatgacacca	ctttctggga	acttgaggca	agcaaagaac	cgagccagca	960
gagggtaaaa	cgatgggggt	ttggcatgga	cgaggcattg	aaagaccag	ttgggagaga	1020
acagttcctt	aaatttctag	agtcagaatt	cagctcggaa	aatttaagat	tctggctggc	1080
agtggaggac	ctgaaaaaga	ggcctattaa	agaagtaccc	tcaagagttc	aggaaatatg	1140
gcaagagttt	ctggctcccg	gagccccag	tgctattaac	ttggattcca	agagttatga	1200
caaaaccaca	cagaacgtga	aggaaacctg	acgatacaca	tttgaagatg	ctcaggagca	1260
catttacaaa	ctgatgaaaa	gtgattcata	cccacgtttt	ataagatcca	gtgcctatca	1320
ggagcttcta	caggcaaaaga	aaagagggga	aatctctcac	gtccaagagg	ttaacaagcc	1380
ttgctcagtc	ttactaaacg	gatcatcttg	tagcatgaat	gcagactgga	gtcactgcac	1440
acactttgta	gctcaatgtt	gtgacctgga	gcagaggaca	ttagaacaag	atgttgcattg	1500
agcaaaggac	ctaaattgtt	atttttgtgt	gtacattcca	tctccaatgg	actcttccgt	1560
ctcaatgcct	ccattccaaa	ctgttgtctg	ctttctttct	ccttctacta	tgctggatct	1620
gtgtctcttc	ctttttaaca	agttcaagtg	aagtaaaacc	ttttcttttt	ttccttcttt	1680
ctctctctct	ctctctcaaa	gcttcagtta	gacacacagt	tcactgaaaa	ttcagtcagt	1740
caaaaactgg	agaactgta	aaagaaaaaa	gtatatatca	ataagtatac	atgtggcttc	1800
acattttatta	aacaataaat	tccgcacaga	aagtttctatt	tcaccaatgt	gtcacagctca	1860
gaaacaaact	catgtcttcg	gtctgttgtc	tgtacattct	ccgttaaatgt	ttctcgcatt	1920
tattttttata	ccatatttaa	agaagaaaca	ccttttactc	caaagtatt	aaagttgatc	1980

ccttctctgt aaatttgtgt atgtttatat tgttgtttta tctttcatta aaagatgtca 2040  
 gaatctcaaa aaaaaa 2056

<210> 368  
 <211> 460  
 <212> DNA  
 <213> Homo sapiens

<400> 368  
 ggcacgaggg actatccacg cattgtgaac cacctggacc acacctatgt cactgcgccc 60  
 caagccttca tgatgttcca gtactttgtg aagggtggtgc ccactgtgta catgaagggtg 120  
 gacggagagg tactgacgac aaatcagatc tatgtgacca gacatgagaa ggctgcctat 180  
 gtgctgatgg gcgaccaagg ccttcccga gtcttcatcc tctatgagct ctgcgccatg 240  
 atggtgaacc tgacggagat acacacgttc ttctctctct tctgacaat tgtgggcgct 300  
 caccataggt ggcatgttct ttgagcattt tgtcattaat tacttaaccc ataagtgggg 360  
 gcttgggttc tatttcaaaa atgaaaactc ttacagggg ggccatagga ctttatatgg 420  
 agtgaacttt tttatgtatt ggagtttacg ggggggctct 460

<210> 369  
 <211> 2355  
 <212> DNA  
 <213> Homo sapiens

<400> 369  
 gtcogtgtgg tggaattcgc agcggcagtt cgtggtgcgg gcctggggct gcgcggggccc 60  
 ttgcggccgg gcagtccttc tggccttcgg gctagggctg ggcctcatcg aggaaaaaca 120  
 ggcggagagc cggcggggcg tctcggcctg tcaggagatc caggcaattt ttaccagaa 180  
 aagcaagccg gggcctgacc cgttggaac gagacgcttg cagggccttc ggctggagga 240  
 gtatctgata gggcagtcga ttgtaaggg ctgcagtgtg gctgtgtatg aagccaccat 300  
 gcctacattg cccagaaacc tggaggtgac aaagagcacc gggttgcttc caggagaggg 360  
 cccaggtacc agtgaccag gagaagggca ggagcgagct ccggggggccc ctgccttccc 420  
 cttggccatc aagatgatgt ggaacatctc ggcaggttcc tccagcgaag ccatcttgaa 480  
 cacaatgagc caggagctgg tcccagcgag ccgagtggcc ttggctgggg agtatggagc 540  
 agtcacttac agaaaatcca agagaggtcc caagcaacta gcccctcacc ccaacatcat 600  
 ccgggttctc cgcgccttca cctcttcctg gccgctgctg ccaggggccc tggctgacta 660  
 cctgatgtg ctgccctcac gcctccaccc tgaaggcctg ggccatggcc ggacgtgtgt 720  
 cctcgttatg aagaactatc cctgtaccct gcgccagtac ctttgtgtga acacaccag 780  
 cccccgcctc gccgccatga tgcgtgtgca gctgctggaa ggcgtggacc atctggttca 840  
 acagggcatc gcgcacagag acctgaaatc cgacaacatc cttgtggagc tggaccaga 900  
 cggctgcccc tggttggtga tcgcagattt tggctgctgc ctggctgatg agagcatcg 960  
 cctgcagttg ccttcagca gctggtacgt ggatcggggc ggaaacggct gtctgatggc 1020  
 cccagaggtg tccacggccc gtccctggcc cagggcagtg attgactaca gcaaggctga 1080  
 tgccctgggca gtgggagcca tcgcctatga aatcttcggg cttgtcaatc ccttctacgg 1140  
 ccagggaag gccaccttg aaagccgcag ctaccaagag gctcagctac ctgcactgcc 1200  
 cgagtcagtg cctccagac tgagacagtt ggtgagggca ctgctccagc gagaggccag 1260  
 caagagacca tctgcccag tagccgcaaa tgtgcttcat ctaagcctct ggggtgaaca 1320  
 tattctagcc ctgaagaatc tgaagttaga caagatggtt ggctggctcc tccaacaatc 1380  
 ggccgccact ttgttgcca acaggctcac agagaagtgt tgtgtggaaa caaaaatgaa 1440

gatgctcttt	ctggctaacc	tggagtgtga	aacgctctgc	caggcagccc	tcctcctctg	1500
ctcatggagg	gcagccctgt	gatgtccctg	catggagctg	gtgaattact	aaaagaactt	1560
ggcatcctct	gtgtcgtgat	ggtctgtgaa	tggtaggggt	gggagtcagg	agacaagaca	1620
gcgcagagag	ggctggttag	ccggaaaagg	cctcgggctt	ggcaaatgga	agaacttgag	1680
tgagagttca	gtctgcagtc	ctgtgtctac	agacatctga	aaagtgaatg	gccaagctgg	1740
tctagtagat	gaggctggac	tgaggagggg	taggcctgca	tccacataga	ggatccaggc	1800
caaggcactg	gctgtcagtg	gcagagtttg	gctgtgacct	ttgcccctaa	cacgaggaac	1860
tcgtttgaag	ggggcagcgt	agcatgtctg	at ttgccacc	tggatgaagg	cagacatcaa	1920
catgggtcag	cacgttcagt	tacgggagtg	ggaaattaca	tgaggcctgg	gcctctcgct	1980
tccaagctg	tgçgttctgg	accagctact	gaattattaa	tctcacttag	cgaaagtgc	2040
ggatgagcag	taagtaagta	agtgtgggga	tttaaacttg	agggtttccc	tcctgactag	2100
cctctcttac	aggaattgtg	aaatattaaa	tgcaaattta	caactgcaga	tgacgtatgt	2160
gccttgaact	gaatatttgg	ctttaagaat	gattcttata	ctctgaagggt	gagaatatatt	2220
tgtgggcagg	tatcaacatt	ggggaagaga	tttcatgtct	aactaactaa	ctttatacat	2280
gatttttagg	aagctattgc	ctaaatcagc	gtcaacatgc	agtaaagggt	gtcttcaact	2340
gaaaaaaaaa	aaaaa					2355

&lt;210&gt; 370

&lt;211&gt; 1333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 370

gccaggccgg	caccaggcac	agacacttat	gcccttgttg	ggagaacaga	gagaggctct	60
cttgtccaact	gcctgtcttc	ggttccaact	gctggttctc	ctagaggcct	ctcctcagac	120
tcgcagagct	gcctgatcat	tgctacagaa	tgaactctag	cccagctggg	accccaagtc	180
cacagccctc	cagggccaat	gggaacatca	acctggggcc	ttcagccaac	ccaaatgccc	240
agccacggga	cttcgacttc	ctcaaagtca	tcggcaaagg	gaactacggg	aaggctcctac	300
tggccaagcg	caagtctgat	ggggcgttct	atgcagtga	ggtactacag	aaaaagtcca	360
tcttaaagaa	gaaagagcag	agccacatca	tggcagagcg	cagtgtgctt	ctgaagaacg	420
tgcggcaccc	cttcctcgctg	ggcctgcgct	actccttcca	gacacctgag	aagctctact	480
tcgtgctcga	ctatgtcaac	gggggagagc	tcttcttcca	cctgcagcgg	gagcgccggt	540
tcctggagcc	ccgggccagg	ttctacgctg	ctgagggtggc	cagcgccatt	ggctacctgc	600
actccctcaa	catcatttac	agggatctga	aaccagagaa	cattctcttg	gactgccagg	660
gacacgtggg	gctgacggat	tttggcctct	gcaaggaaagg	tgtagagcct	gaagacacca	720
catccacatt	ctgtggtacc	cctgagtact	tggcacctga	agtgtctctg	gaaagagcct	780
tatgatcgag	cagtggactg	gtggtgcttg	ggggcagtc	tctacgagat	gctccatggc	840
ctgccgccct	tctacagcca	agatgtatcc	cagatgtatg	agaacattct	gcaccagccg	900
ctacagatcc	ccggaggccg	gacagtggcc	gcctgtgacc	tcctgcaaag	ccttctccac	960
aaggaccaga	ggcagcggct	gggctccaaa	gcagactttc	ttgagattaa	gaaccatgta	1020
ttcttcagcc	ccataaactg	ggatgacctg	taccacaaga	ggctaactcc	acccttcaac	1080
ccaaatgtga	caggacctgc	tgacttgaag	cattttgacc	cagagttcac	ccaggaagct	1140
gtgtccaagt	ccattggctg	taccctgac	actgtggcca	gcagctctgg	ggcctcaagt	1200
gcattcctgg	gattttctta	tgcgccagag	gatgatgaca	tcttgattg	ctagaagaga	1260
aggacctgtg	aaactactga	ggccagctgg	tattagtaag	gaattacctt	cagctgctag	1320
gaagagctgt	att					1333

&lt;210&gt; 371

&lt;211&gt; 2457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



<400> 371

agcggcgcga	gacctgaag	ggacaccagg	agaagattcg	gcagcggcag	tccatcctgc	60
ctcctcccca	gggcccggcg	cccatccctt	tccagcaccg	cggcggggat	tccccggagg	120
ccaagaatcg	cgtgggcccc	caggtgccac	tcagcgagcc	aggtttccgc	cgtcgggagt	180
cgcaggagga	gccgcggggc	gtgctggctc	agaagataga	gaaggagacg	caaatcctca	240
actgcgcctt	ggacgacatc	gagtggtttg	tggcccggct	gcagaaggca	gccgaggctt	300
tcaagcagct	gaaccagcgg	aaaaagggga	agaagaaggg	caagaaggcg	ccagcagagg	360
gcgtcctcac	actgcgggca	cggccccccc	tctgaggcg	agttcatcga	ctgcttccag	420
aaaatcaagc	tggcgattaa	cttgctggca	aagctgcaga	agcacatcca	gaaccccagc	480
gccgcggagc	tcgtgcaactt	cctcttcggg	cctctggacc	tgatcgtcaa	cacctgcagt	540
ggcccagaca	tcgcacgctc	cgtctcctgc	ccactgctct	cccagatgc	cgtggacttc	600
ctgcgcggcc	acctgggtccc	taaggagatg	tcgctgtggg	agtcactggg	agagagctgg	660
atgcggcccc	gttccgagtg	gccgcgggag	ccacaggtgc	ccctctacgt	gccccagttc	720
cacagcggct	gggagcctcc	tgtggatgtg	ctgcaggagg	ccccctggga	ggtggagggg	780
ctggcgtctg	cccccatcga	ggaggtgagt	ccagtgaacc	gacagtccat	aagaaactcc	840
cagaagcaca	gcccacttcc	agagcccacc	cccccggggg	atgccctacc	accagtacgc	900
tccccacata	ctcacagggg	ctaccagcca	acaccagcca	tggccaagta	cgtcaagatc	960
ctgtatgact	tcacagcccc	aaatgccaac	gagctatcgg	tgctcaagga	tgaggtccta	1020
gaggtgctgg	aggacggccg	gcagtgggtg	aagctgcgca	gccgcagcgg	ccaggcgggg	1080
tacgtgcctt	gcaacatcct	aggcgaggcg	cgaccggagg	acgccggcgc	cccgttcgag	1140
caggccggtc	agaagtactg	gggccccgcc	agcccgaccc	acaagctacc	cccaagcttc	1200
ccgggggaaca	aagacgagct	catgcagcac	atggacgagg	tcaacgacga	gctcatccgg	1260
aaaatcagca	acatcagggc	gcagccacag	aggcacttcc	gcgtggagcg	cagccagccc	1320
gtgagccagc	cgctcaccta	cgagtccggg	ccggacgagg	tccgcgcctg	gctggaagcc	1380
aaggccttca	gcccgcggtt	cgtggagaac	ctgggcatcc	tgaccggggc	gcagctcttc	1440
tccctcaaca	aggaggagct	gaagaaagtg	tgcggcgagg	agggcgtccg	cgtgtacagc	1500
cagctcacca	tgcagaaggc	cttcttgagg	aagcagcaaa	gtgggtcgga	gctggaagaa	1560
ctcatgaaca	agtttcatct	catgaatcag	aggagggggg	aggacagcta	ggcccagctg	1620
ccttgggctg	gggcctgcgg	aggggaagcc	caccacacat	gcattggagta	ttatttttat	1680
atgtgtatgt	attttgtatc	aaggacacgg	agggggtgtg	gtgctggcta	gaggtccctg	1740
cccctgtctg	gaggcacaac	gccatcctt	aggccaaaca	gtaccaagg	cctcagccca	1800
caccaagact	aatctcagcc	aaacctgctg	cttgggtggg	ccagcccctt	gtccaccttc	1860
tcttgaggcc	acagaactcc	ctggggctgg	ggcctcttcc	tctggcctcc	cctgtgcacc	1920
tgggggggtcc	tggcccctgt	gatgctcccc	catccccacc	cacttctaca	tccatccaca	1980
ccccaggggtg	agctggagct	ccaggctggc	caggctgaac	ctcgcacaca	cgcagagttc	2040
tgtcctctga	ggggggggccg	ggaggggctc	cagcaggagg	ccgtgggtgc	cattcggggg	2100
aaagtggggg	aacgacacac	acttcacctg	caagggccga	caacgcaggg	gacaccgtgc	2160
cggcttccaga	cactcccagc	gccactctt	acaggcccag	gactggagct	ttctctggcc	2220
aagtttccag	ccaatgatcc	cgcattgggt	ttgggggtgc	tgggtgtgtc	tgggtcctgg	2280
acttgagtct	caccctacag	atgagaggtg	gctgaggcac	cagggtctaa	caattaaacc	2340
agttaagtct	caaaaaaaaa	aaaaaggggg	ggccgtttta	aagaaccctt	ggggggggcc	2400
aagttaacgc	gggctggcaa	ggtaaaagtt	ttttccttat	agggagccgt	ataaaac	2457

&lt;210&gt; 372

&lt;211&gt; 1333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 372

aagcttggca	cgagggtctt	gtcagcagcc	cggccattgg	agcatatctt	tctgccagtt	60
acggagacag	cctcgttgtg	ctgggtggcca	cagtgggtggc	tcttctggac	atctgcttca	120
tcttagtggc	tgttccagaa	tctctgcctg	agaaaatgag	accggtttcc	tggggagctc	180

agattttcttg	gaaacaagca	gacccttttg	cgctcgttgaa	gaaagttgga	aaagattcta	240
ctgtcttact	aaatctgcat	caccgtgtgt	ctttcatacc	ttcctgaagc	tgggacagta	300
ttcaagtttt	ttttctctat	ctcagggcag	gtcataggg	ttgggatctg	ttaaaattgc	360
agcattcata	gctatggtag	gaattctgtc	tattgtggct	cagacggcct	ttcttagcat	420
cttgatgaga	tcattaggaa	ataagaatac	tgtcctcctt	ggcttgggct	tccagatgct	480
ccagttagcc	tggtagggtt	ttggatcaca	ggcctggatg	atgtgggcag	cagggaccgt	540
ggctgccatg	tccagcatca	cgtttccggc	aatcagtgcc	ctcgtctctc	ggaatgcaga	600
gtcagatcag	caaggagttg	cccaggggat	cataactgga	ataagaggac	tatgcaatgg	660
cctggggcca	gcactgtatg	gcttcatatt	ctacatgttc	catgtggaac	tgactgagtt	720
gggcccga	ttgaattcta	acaacgttcc	cctgcaggga	gctgtcatcc	caggcccgcc	780
gtttttat	ggggcatgta	tagtccttat	gtcttttctg	gctgccttat	tcattcctga	840
atacagtaaa	gccagtggag	ttcaaaaaca	cagtaacagc	agcagcggca	gcctgacca	900
cacccagaa	cggggcagtg	atgaggacat	tgagccacta	ctgcaagaca	gcagcatctg	960
ggagctctct	tcatttgagg	agcctgggaa	tcagtgcact	gagctgtaaa	ctcggcagaa	1020
agtgggat	tgcatacgcc	atctctgaga	gccatggagg	gagccacacc	cctggtgact	1080
tcattggtgct	ggatgggaga	cgctagcggc	atccttcagg	gccaaagttg	ataaaatacca	1140
ccgccatcat	tctgtctatc	ctcctcctgt	tttttttttt	ctcttacatt	cttttttttt	1200
tcccggttaa	tccttaaaac	cagaaaaaaa	ttggaaaaac	ttctttgcaa	aaagggggca	1260
actcccagg	ggaacctcaa	ataaaaaaag	cattcttttg	tgaaaaaagg	agggcttcct	1320
tgaaggaca	aaa					1333

<210> 373  
 <211> 2578  
 <212> DNA  
 <213> Homo sapiens

<400> 373						
atggcggcag	gcctggccac	gtggctgcct	tttgctcggg	cagcagcagt	gggctggctg	60
cccctggccc	agcaacccct	gccccgggca	ccgggggtga	aggcatctcg	aggagatgag	120
gttctggtg	tgaacgtgag	cggacggcgc	tttgagactt	ggaagaatac	gctggaccgc	180
taccagaca	ccttgctggg	cagctcggag	aaggaattct	tctacgatgc	tgactcaggc	240
gagtacttct	tcgatcgca	ccctgacatg	ttccgccatg	tgctgaactt	ctaccgaacg	300
gggcggctgc	attgcccacg	gcaggagtgc	atccaggcct	tcgacgaaga	gctggctttc	360
tacggcctgg	ttcccagact	agtccgtgac	tgctgccttg	aagagtatcg	ggaccgaaag	420
aaggagaatg	ccgagcgctt	ggcagaggat	gaggaggcag	agcaggccgg	ggacggccca	480
gccctggccg	caggcagctc	cctgcggcag	cggctctggc	gggccttcga	gaatccacac	540
acgagcacgc	cagccctcgt	tttctactat	gtgaccggct	tcttcacgcg	cgtgtcggtc	600
atcgccaatg	tggtaggagc	catcccatgc	cgcggctctg	cacgcaggtc	ctcaagggag	660
cagccctgtg	gcgaacgctt	cccacaggcc	tttttctgca	tggacacagc	ctgtgtactc	720
atattcacag	gtgaatacct	cctgcggctg	tttgccgccc	ccagccgttg	ccgcttcctg	780
cggagtgtca	tgagccctcat	cgactgggtg	gccatcctgc	cctactacat	tgggcttttg	840
gtgcccaga	acgacgatgt	ctctggcgcc	tttgtcacc	tgctgtgttt	ccgggtgttt	900
cgcatcttca	agttctccag	gcactcacag	ggcttgagg	ttctgggcta	cacactcaag	960
agctgtgcct	ctgagctggg	ctttctcctc	ttttccctaa	ccatggccat	catcatcttt	1020
gccactgtca	tgttttatgc	tgagaagggc	acaaaacaaga	ccaactttac	aagcatccct	1080
gcggccttct	ggtataccat	tgtcaccatg	accacgcttg	gctacggaga	catggtgcc	1140
agcaccattg	ctggcaagat	tttcgggtcc	atctgtctac	tcagtggcgt	cttgggtcatt	1200
gccctgcctg	tgccagtcac	tgtgtccaac	tttagccgca	tctaccacca	gaaccagcgg	1260
gctgacaagc	gccgagcaca	gcagaagggtg	cgcttgccaa	ggatccgatt	ggcaaagagt	1320
ggtaccacca	atgccttctt	gcagtacaag	cagaatgggg	gccttgagg	cagcggcagt	1380
ggcgaggaa	aggctgtttg	tgtcaggaa	cgttctgcct	ttgaacagca	acatcaccac	1440
ttgtgcact	gtctagagaa	gacaacgtgc	catgagtcca	cagatgagct	caccttcagt	1500
gaagccctgg	gagccgtctc	gccgggtggc	cgcaccagcc	gtagcacctc	tgtgtcttcc	1560
cagccagtgg	gacccggaag	cctgtgtctt	tcttgctgcc	ctcgcagggc	caagcgccgc	1620
gccatccgcc	ttgccaaactc	cactgcctca	gtcagccgtg	gcaggcatgc	aggagctgga	1680
catgctggca	gggcttgccg	aggagccatg	ccccttcaga	gccgctccag	ccttcaatgc	1740

caagcccat	gacagccttg	acctgaactg	cgacagcggg	ggacttcgtg	gctgccatta	1800
tcagcatccc	taccctcct	gccaacaccc	cagatgagag	ccaaccttcc	ccccctggcg	1860
gcggtggcag	ggccggcagc	accctcagga	actccagcct	gggtaccctt	tgccctcttc	1920
ccgagactgt	caagatctca	tccctgtgag	gggtaggcct	gctgattcag	agggctcctt	1980
tcatttttgg	gaactccttt	ccaaagccat	atttttggga	ggcagagagg	ggcaggcttg	2040
ggcaccctt	ctgccccccc	cactgagaac	tatgcaatgg	agtttcatga	aatgggtccac	2100
atagtgggga	agtagccagg	aaatgagaaa	cttcctccca	ccccagacat	ttttcctggg	2160
gggagctgaa	gcactgggct	tccacaggcc	cctggcctcc	ttgccctagc	acactgggac	2220
tggccccact	ctcccagctg	gactcctgca	tgctcctccc	cttgggctct	cagatgaagg	2280
caaaactttg	atccgacatc	tgagctctag	cctaagaagg	agagttgaga	tttcctcctc	2340
cctctggctg	ggatatggag	ctttggaggt	tcagagaaga	gaacctctac	ctctgatctg	2400
gcctctacga	gaggtcctca	tctccatctg	gcccaacaat	tcccagattc	tgaagcttgg	2460
gaatgcaaac	acaggcttca	tggggctgtg	gccttctggc	aggcgacctg	ccatccccag	2520
ggccttgcc	gagggggttc	aggcttgctt	tttcccaaca	cacactcaga	taggcaca	2578

<210> 374  
 <211> 664  
 <212> DNA  
 <213> Homo sapiens

<400> 374						
tgaggtggg	gcaagccttt	taaggactgg	accacgggtg	ggcaggatac	cgggggagaa	60
cccgcctgt	tagttggggc	tggggagggc	cgcgaccga	gactaaattg	tccttccggg	120
cagatccgct	caccaggccc	tggcgacctg	agcatctacg	acaactggat	ccggtacttc	180
aaccgcagca	gcccgtgtga	cggcctggtc	cccagagcaa	gacttcagcc	aggatctacc	240
ccacctacca	cacagccttt	gacacctttg	actatgtgga	caagtttttg	gaccggggtg	300
aggagggaga	caaggggcat	cctgagacca	ggacaggaga	ggctgaagac	tgagccctgg	360
ccttgtcacc	ttgccgcagg	cttcagcagc	catcaggctg	tggcccggac	agcggggagt	420
gtgattctcc	ggctcagtga	cagcttcttc	ctgcccctca	aagtcagtga	ctacagttag	480
acactccgca	gcttcctgca	ggcagcccag	caagatcttg	gggccctgct	ggagcagcac	540
agcatcagcc	tggggcctct	ggtgactgca	gtggagaagt	ttgaggcaga	agctgcagcc	600
ttgggccaac	gcataatcaac	actgcagaag	ggcagccctg	accccctgca	ggtccggatg	660
ctca						664

<210> 375  
 <211> 1495  
 <212> DNA  
 <213> Homo sapiens

<400> 375						
ggaattcgag	gcgggggcag	cctcgccagc	gggggccccg	ggcctggcca	tgctcactg	60
agccagcgcc	tgcgccctta	cctcgccgac	agctggaacc	agtgcgacct	agtggctctc	120
acctgcttcc	tcctgggcgt	gggtgcccgg	ctgaccccg	gtttgtacca	cctgggcccgc	180
actgtcctct	gcacgcactt	catgggttttc	acgggtcggc	tgcttcacat	cttcacggtc	240
aacaaacagc	tggggcccaa	gatcgtcatc	gtgagcaaga	tgatgaagga	cgtgttcttc	300
ttcctcttct	tcctcggcgt	gtggctggta	gcctatggcg	tggccacgga	ggggctcctg	360
aggccacggg	acagtgactt	cccaagtatc	ctgcgcggcg	tcttctaccg	tccctacctg	420
cagatcttct	ggcagattcc	ccaggaggac	atggacgtgg	ccctcatgga	gcacagcaac	480

tgctcgtcgg	agccccgctt	ctgggcacac	cctcctgggg	cccagggcgg	cacctgcgtc	540
tcccagtatg	ccaactggct	ggtaggtgctg	ctcctcgtca	tcttcctgct	cgtggccaac	600
atcctgctgg	tcaacttgct	cattgccatg	ttcagttaca	cattcggaac	agtacagggc	660
aacagcgatc	tctactggaa	ggcgagcgt	taccgcctca	tccgggaatt	ccactctcgg	720
cccgcgtgg	ccccgccctt	tatcgtcatc	tcccacttgc	gcctcctgct	caggcaattg	780
tgcaggcgac	cccggagccc	ccagccgtcc	tccccggccc	tcgagcattt	ccgggtttac	840
ctttctaagg	aagccgagcg	gaagctgcta	acgtgggaat	cgggtgcataa	ggagaacttt	900
ctgctggcac	gcgctaggga	caagcgggag	agcgactccg	agcgtctgaa	gcgcacgtcc	960
cagaagggtg	acttggcact	gaaacagctg	ggacacatcc	gcgagtacga	acagcgcctg	1020
aaagtgcctg	agcgggaggt	ccagcagtgt	agccgcgtcc	tgggggtggg	ggccgaggcc	1080
ctgagccgct	ctgccttgct	gccccaggt	gggccgccac	cccctgacct	gcctgggtcc	1140
aaagactgag	ccctgctggc	ggacttcaag	gagaagcccc	cacaggggat	tttgcctcta	1200
gagtaaggct	catctgggcc	tcggccccc	cacctgggtg	ccttgctcct	gaggtgagcc	1260
ccatgtccat	ctgggccact	gtcaggacca	cctttgggag	tgatcctcct	acaaagacca	1320
gcatgcccg	ctcctcccag	aaccagtccc	agcctgggag	gatcaaggcc	tggatcccgg	1380
gccgttatcc	atctggaggc	tgcagggtcc	ttggggtaac	agggaccaca	gacccctcac	1440
cactcacaga	ttcctcacac	tggggaaata	aagccatttc	agaggaaaaa	aaaaa	1495

&lt;210&gt; 376

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 376

gcctcataaa	actctgcaaa	tctaaggcca	aaagctgtga	aatgacctt	gaaatgggca	60
tgtgaaattc	caaattcaag	aagactcgct	accaggctgg	catgaggaa	tctgaaaatc	120
tgacagcaaa	taacactttg	agcaagccca	ccagatacca	ggcgagctga	aggaaatcaa	180
gcaagatata	tcagccctgc	gctatgagct	tcttgaggaa	aatctcaag	ctactgggtga	240
gctggcagac	ctgattcaac	aactcagcga	gaagtttgga	aagaacttaa	acaaagacca	300
cctgaggggtg	aacaagggca	aagacattta	gcagcccaca	tcggcgtctg	tgactttctac	360
cagcattcca	agg					373

&lt;210&gt; 377

&lt;211&gt; 2867

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 377

cttcctcttc	tccacgcagg	cttcaacagg	agatttatgg	agaatagcag	cataattgct	60
tgctataaat	aactgattca	aatagaacat	ggggaagtcc	gctcccagtt	caaattacgg	120
gcctgtaatt	cagtgtttac	agcattagat	cactgtcatg	aagccataga	aataacaagc	180
gatgaccacg	tgattcagta	tgtcaaccca	gccttcgaaa	ggatgatggg	ctaccacaaa	240
ggtgagctcc	tgggaaaaga	actcgtgat	ctgccccaaa	gcgataagaa	ccgggcagac	300
cttctcgaca	ccatcaatac	atgcatcaag	aagggaagg	agtggcaggg	ggtttactat	360
gccagacgga	aatccgggga	cagcatccaa	cagcacgtga	agatcacccc	agtgttggc	420
caaggaggga	aaattaggca	ttttgtctcg	ctcaagaaac	tgtgtgttac	cactgacaat	480
aataagcaga	ttcacaagat	tcacgtgat	tcaggagata	attctcagac	agagcctcat	540
tcattcagat	ataagaacag	gaggaaagag	tccattgacg	tgaaatcgat	atcatctcga	600

ggcagtgatg	caccaagcct	gcagaatcgt	cgctatccgt	ccatggcgag	gatccactcc	660
atgaccatcg	aggctcccat	cacaaagggt	ataaatataa	tcaatgcagc	ccaagaaaac	720
agcccagtc	cagtagcgga	agccttgga	agagttctag	agattttacg	gaccacagaa	780
ctgtactccc	ctcagctggg	taccaaagat	gaagatcccc	acaccagtga	tcttggtgga	840
ggcctgatga	ctgacggcct	gagaagactg	tcaggaaacg	agtatgtgtt	tactaagaat	900
gtgcaccaga	gtcacagtca	ccttgcaatg	ccaataacca	tcaatgatgt	tcccccttgt	960
atctctcaat	tacttgataa	tgaggagagt	tgggacttca	acatctttga	attggaagcc	1020
attacgcata	aaagggcatt	ggtttatctg	ggcttaaagg	tcttctctcg	gtttggagta	1080
tgtgagtttt	taaactgttc	tgaaaccact	cttcgggcct	ggttccaagt	gatcgaagcc	1140
aactaccact	cttccaatgc	ctaccacaac	tccaccatg	ctgccgacgt	cctgcacgcc	1200
accgctttct	ttcttgga	ggaaagagta	aagggaagcc	tcgatcagtt	ggatgaggtg	1260
gcagccctca	ttgctgccac	agtccatgac	gtggatcacc	cgggaaggac	caactctttc	1320
ctcctgcaat	gcaggcagtg	agcttgctgt	gctctacaat	gacacctgct	gttcctggag	1380
agtcaccaca	ccgccctggc	cttcagcct	cacggtcaag	gacaccaaaa	tgcaacattt	1440
tcaagaatat	tgacaaggga	accattatcg	aacgctgcgc	caggctatta	ttgacatggt	1500
tttggaaca	gagatgacaa	aacactttga	acatgtgaat	aagtttgtga	acagcatcaa	1560
caagccaatg	gcagctgaga	ttgaaggcag	cgactgtgaa	tgcaaccctg	ctgggaagaa	1620
cttccttgaa	aaccaaattc	tgatcaaacg	catgatgatt	aagtgtgctg	acgtggccaa	1680
cccatgccgc	cccttgga	tgtgcattga	atgggctggg	aggatctctg	aggagtattt	1740
tgacagact	gatgaagaga	agagacaggg	actacctgtg	gtgatgccag	tgtttgaccg	1800
gaataacctgt	agcatcccca	agtctcagat	ctcttccatt	gactacttca	taacagacat	1860
gtttgatgct	tgggatgcct	ttgcacatct	accagccctg	atgcaacatt	tggctgacaa	1920
ctacaaacac	tgggaagacac	tagatgacct	aaagtgcaca	agtttgaggc	ttccatctga	1980
caggctaaag	ccaagccaca	gagggggcct	cttgaccgac	aaaggacact	gtgaatcaca	2040
gtagcgtaaa	caagaggcct	tcctttctaa	tgacaatgac	aggtattggt	gaaggagcta	2100
atgtttaata	tttgaccttg	aatccattcc	aagtcccca	aatttccatt	ccttagaaag	2160
ttatgttccc	atgaagaaaa	atatatgttc	cttttgaata	cttaaatgac	agaacaaata	2220
cttgggcaaa	ctccctttgc	tctgcctgtc	atccctgtgt	acccttgtca	atcccatggg	2280
ggctggttca	ctgtaactag	caggccacag	ggaaggcaaa	gccttgggtg	cctgtgagct	2340
catctcccgg	gatgggtgac	taagtaggct	taggctagg	gatcagctca	tcctttacca	2400
taaaagtc	cattgctgtt	tagcttgact	gttttccctca	agaacatcga	tctgaaggat	2460
tcataaggag	cttatctgaa	cagattttatc	taagaaaaaa	aaaaaaccca	cttaaaatag	2520
gggaagcaac	taggaccaaa	ttacagataa	actagttagc	ttcacagcct	ctatggctac	2580
atggttcttc	tggccgatgg	tatgacacct	aagttagaac	acagccttgg	ctgggggggtg	2640
ccctctctag	actggtatca	gcagcctgtg	taaccccttt	cctgtaaaag	gggttcattct	2700
taacaaagtc	atccatgatg	agggaaaaag	tggcatttca	tttttgggga	atccatgagc	2760
ttcctttatt	tctggctcac	agaggcagcc	acgaggcact	acaccaagta	ttatataaaa	2820
gccattaaat	ttgaatgccc	ttggacaagc	ttttcttaaa	aaaaaaa		2867

&lt;210&gt; 378

&lt;211&gt; 8053

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 378

gctttccttt	ctaaagtaga	agaggatgat	tatccctctg	aagaactact	agaggatgaa	60
aacgctataa	atgcaaaacg	gtctaaagaa	aaaaaccctg	ggaatcaggg	caggcagttt	120
gatgttaatc	tgcaagtccc	tgacagagca	gttttaggga	ccattcatcc	agatccagaa	180
attgaagaaa	gcaagcaaga	aactagtatg	attttgata	gtgaaaaaac	aagtgagact	240
gctgccaaaag	gggtcaacac	aggaggcagg	gaaccaaata	caatggtgga	aaaagaacgc	300
cctctggcag	atagaaagc	acagagacca	tttgaacgaa	gtgacttttc	tgacagcata	360
aaaattcaga	ctccagaatt	aggtgaagtg	tttcagaata	aagattctga	ttatctgaag	420
aacgacaacc	ctgaggaca	tctgaagacc	tcagggcttg	caggggagcc	tgagggagaa	480
ctctcaaaag	aggaccatga	gaacacagag	aagtacatgg	gcacagaaag	ccaggggtct	540
gctgctgcag	aacctgaaga	tgactcgttc	cactggactc	cacatacaag	tgtagagcca	600
gggcatagtg	acaagaggga	ggacttactt	atcataagca	gcttcttta	agaacaacag	660

tctttgcagc	ggttccagaa	gtactttaat	gtccatgagc	tggaagcctt	gctacaagaa	720
atgtcatcaa	aactgaagtc	agcgcagcag	gagagcctgc	cctataatat	ggaaaaagtc	780
ctagataagg	tcttccgtgc	ttctgagtc	caaattctga	gcatagcaga	aaaaatgctt	840
gatactcgtg	tggctgaaaa	tagagatctg	ggaatgaacg	aaaataacat	at ttgagag	900
gctgcagtg	ttgatgacat	tcaagacctc	atctat tttg	tcaggtacaa	gcactccaca	960
gcagaggaga	cagccacact	ggtgatggca	ccacctctag	aggaaggctt	gggtggagca	1020
atggaagaga	tgcaaccact	gcatgaagat	aatttctcac	gagagaagac	agcagaactt	1080
aatgtgcagg	ttcctgaaga	acccacccac	ttggaccaac	gtgtgattgg	ggacactcat	1140
gcctcagaag	tgtcacagaa	gccaaatact	gagaaagacc	tggaaccagg	gccagttaca	1200
acagaagaca	ctcctatgga	tgctattgat	gcaaacaagc	aaccagagac	agccgcccga	1260
gagccggcaa	gtgtcacacc	tttggaaaaac	gcaatccttc	taatatattc	at tcatgttt	1320
tatttaacta	agtgcgtagt	tgctacattg	cctgatgatg	ttcagcctgg	gcctgatttt	1380
tatggactgc	cattggaacc	tgtattttat	actgccttct	tggaattg	ttcgtttg	1440
at tttcttat	ggagaactgt	cctgtgtgtg	aaggatagag	tatatcaagt	caggaacag	1500
caaatttctg	agaagttgaa	gactatcatg	aaagaaaata	cagaacttgt	acaaaaattg	1560
tcaaattatg	aacagaagat	caaggaatca	aagaaacatg	ttcaggaaac	caggaaacaa	1620
aatatgattc	tctctgatga	agcaattaaa	tataaggata	aaatcaagac	acttgaaaaa	1680
aatcaggaaa	ttctggatga	cacagctaaa	aatcttctgt	ttatgctaga	atctgagaga	1740
gaacagaatg	tcaagaatca	ggacttgata	tcagaaaaca	agaaatctat	agagaagtta	1800
aaggatgtta	tttcaatgaa	tgctcagaa	ttttcagagg	ttcagattgc	acttaattgaa	1860
gctaagccta	gtgaagagaa	ggtgaagtct	gaatgccatc	gggttcaaga	agaaaatgct	1920
aggcttaaga	agaaaaaaga	gcagttgcag	caggaatacg	aagactggag	taaattacat	1980
gctgagctca	gtgagcaaat	caaatacttt	gagaagtctc	agaaagattt	ggaagttagct	2040
cttactcaca	aggatgataa	tattaatgct	ttgactaact	gcattacaca	gttgaatctg	2100
ttagagtgtg	aatctgaatc	tgagggtcaa	aataaagggt	gaaatgattc	agatgaatta	2160
gcaaatggag	aagtgggagg	tgaccggaat	gagaagatga	aaaatcaa	taagcagatg	2220
atggatgtct	ctcggacaca	gactgcaata	tcggtagttg	aagaggatct	aaagctttta	2280
cagcttaagc	tcaagagcct	ccgtgtccac	taaatgtaaa	cctggaagac	caggtaaaga	2340
aattgggaaga	tgaccgcaac	tcactacaag	ctgccaaagc	tggaactgga	gatgaatgca	2400
aaaccttgag	gcagaaagtg	gagattctga	atgagctcta	tcagcagaag	gagatggctt	2460
tgcaaaagaa	actgagtcaa	gaagagtatg	aacggcaaga	aagagagcac	aggctgtcag	2520
ctgcagatga	aaaggcagtt	tcggctgcag	aggaagtaaa	aacttacaag	cggagaattg	2580
aagaaatgga	ggatgaatta	cagaagacag	agcggctcatt	taaaaaccag	atcgtacacc	2640
atgagaagaa	agctcatgaa	aactggctca	aagctcgtgc	tgcaagaa	gctatagctg	2700
aagagaaaag	ggaagctgcc	aatttaagac	acaaattatt	agatttaaca	caaaagatgg	2760
caatgtctga	agaagaacct	gtgattgtaa	aaccaatgcc	aggaaaacca	aatacacaaa	2820
accctccacg	gagaggtcct	ctgagccaga	atgggtcctt	tgcccctacc	cctgtgagtg	2880
gtggagaatg	ctcccctcca	ttgacagtgg	agccaccctg	gagacctctc	tctgtactct	2940
tcaatcgaag	agatatgcct	agaagtgaat	ttggatcatt	ggacgggcct	ctacctcatc	3000
ctcgatggtc	agctgaggca	tctgggaaac	cctctccttc	tgatccagg	tctggtacag	3060
ctaccatgat	gaacagcagc	tcaagaggct	cttcccctac	cagggtactc	gatgaaggca	3120
aggttaatat	ggctccaaaa	gggccccctc	ctttcccagg	agtcctctc	atgagacccc	3180
ccatgggagg	ccctgtacca	ccaccctatc	gatatggacc	accacctcag	ctctgcggac	3240
cttttggg	ctggccactt	cctccacctc	ttggcccttg	tatgcgtcca	ccactaggct	3300
taagagaatt	tgaccaggc	gttccaccag	gaagacggga	cctgcctctc	cacctcggg	3360
gatttttacc	tggaacagca	ccatttagac	cttttaggtt	acttggccca	agagagtact	3420
ttattcctgg	taccgatta	ccaccccaaa	cccatggctc	ccaggaatac	ccaccaccac	3480
ctgctgtaag	agacttactg	ccgtcaggct	ctagagatga	gcctccacct	gcctctcaga	3540
gcactagcca	ggactgttca	caggctttta	aacagagccc	ataaaactat	gacctctgag	3600
gtttcattgg	aaagaaagtg	tactgtgcat	tatocattac	agtaaaggat	ttcattggct	3660
tcaaaatcca	aaagtttatt	ttaaaaggtt	tgttgtttaga	actaagctgc	cttggcagtg	3720
tgcat tttt	agccaaacaa	ttcaaaaatg	tcattttctc	cctaaataaa	aatcaccttt	3780
taagctagag	cgtccttaca	actttgaaat	tgcaataaaa	gaataacctg	gttttagcta	3840
atgtagcata	tgtaattgca	aaatgattta	gaatgtcatg	aaaaatatga	acatttctctg	3900
tggaatgct	ttaagaacat	gtattttccat	tatcctat t	ttagtgtaca	ccagctgaat	3960
acggagcaat	ggtgtttata	agcgtttttt	taaactatct	ggtcacaaag	actgttacgc	4020
taaaaatgtt	tactaaaaga	tcactaaact	atctcccctc	ttgctgaagt	tctttgtagt	4080
aatagctcat	aaaaatttgt	ttattaatat	ttoccaagt	tctgttgact	cattggactg	4140
ttatgggct	tgtgccattt	ggggaacatg	taaactcagg	ctcccagaac	tgaagatgg	4200
ggctgggtgg	acacttcgg	ctgcctctcc	gtcacctgtg	aactctacaa	gtgacgtctt	4260
tttatttcaa	agaagtttta	tttcccact	tgtaatagca	ttocacatgc	ctttccttta	4320
cgatcctcat	tgtcctat t	gagaatgggt	ttcctgagag	tgagtttacc	attagtagcc	4380
aagagttgtt	tgaccctgat	gttcccattg	tttttacc	ttcctgttag	aaaaagggtg	4440
ccacaacaga	aaaatgaaaa	tgatgtgtca	tgcccgtaaa	agtatagaaa	tctttaaaaa	4500

ttttaaaatg	tacagtcctt	tatctatctt	tcccatccct	tgccactgat	ttttgaggaa	4560
tataataaaa	agattggaag	agtataatgc	catgagaaag	aatgatttag	gactgtgagg	4620
gttataacat	gccctaggtc	agcaaccaag	ggttgaaatc	agttctgttt	tagggggaaa	4680
tggggggggc	gacagatatt	attccaaaat	taatattaat	taatatttaa	acgttggtgt	4740
ttttatttta	aaatcagtaa	ctaaccatct	ggaattgcac	cataacttaa	gtcttatcca	4800
ttactacact	gtctttaaaa	caatgtttct	ttaaatactc	tacaacgttt	ctaagaacga	4860
acttcagaca	ttttaattac	agtaataata	gcactccttt	taaggagttt	cagatccaca	4920
ctaaaactaa	aatcataaaa	ggctgatact	tttgtttgct	gctaggctat	attcttccat	4980
tctttgaagt	cctatgatgt	aatatTTTTg	aaacctagt	tatgtcttgt	cactgttgtg	5040
atatttaatc	gattaagaat	accttgtaaa	aaggagcaaa	agcttcaatg	tgaacaatt	5100
ttctctcttt	atactaaaca	actgaagata	gatagtttag	aaagataagg	acctttgaaa	5160
gaagacaact	ctgtcaaagt	tcataaggaa	tataaaaatt	cttcaggaaa	agagaattca	5220
atctatatgt	cctcccgttt	aatatcaaga	atagaagaaa	ttaaggaggaa	aactccacag	5280
aagagcatag	gccactttta	gccatgtaaa	aataagatta	agtcacaaat	acaacttttg	5340
aatttacctg	tcaatatctc	tttaggacac	aaaacaatgc	tgaagttaat	ataatttcta	5400
attttaaatg	tcatttaagt	gtagattatg	ccatctagga	aggtaagtag	gaaaggtaaa	5460
ttaaatctat	ttttaaaatt	caaaatatta	gagtattttt	ccccctctaa	gccttttttg	5520
gtgattatct	tgatctgac	ataattgaga	aactggtaag	ctgtaaagat	tccagtgtag	5580
cttctctgag	aagttgtgag	ccagtcata	actgcttctt	cacatccatc	tgatttgcac	5640
ccatttctctg	cagcaaaccc	cccaaacgag	gggtgcccaa	tatgcccagat	gggccatagg	5700
ggagtatcat	cccctcagcc	caaatcacct	tttcccatcc	tcctaaagtt	tccatccctat	5760
tttggaagt	catctccaac	taattgtgtc	tggatttagt	tgctaaaatt	gtcttattta	5820
tttatgaagc	agcaatatct	agcctgaaag	catttctgcc	atagttgttg	tagttatatc	5880
gccaatggct	gatttttttc	attggaaagt	aaattttaagt	aattcgtggg	atgtggtata	5940
ttctgtgtca	acttcaagat	aatcactcat	tttctcgtta	tattcaggtc	tgaattaaag	6000
ttaagttaat	caccagtggt	tcaatttaag	cttctttaat	gttgatgaaa	ggtatttcta	6060
gttcataata	actatactta	tgtgaaggat	agcagatgct	tcatataaat	tatcattttg	6120
atatacatat	cttatggttt	atgagaaaag	agaaaaata	atacatcggt	tttgctacac	6180
tttaatgggt	ttttttttta	agggattttt	tttcagggtct	tgtcagcaac	atcaaacaaa	6240
aggtactgag	tactccacag	ggtacagagt	gctgccaaag	accttagaaa	aattacatga	6300
cacggagaaa	atgcgctctt	tgctccttga	agagcttaca	gtctagggat	ttgacaactc	6360
acagtcttag	gaactgggca	aagtaaggca	aattcttcat	cccctagagc	tattgtggac	6420
tgaatcattt	tagaatttgg	aattaatcca	atcaagatga	gagacaagac	taaatttggc	6480
tgagaattca	ttcaggctcg	catagttttt	attaacatcc	gtctagtaaa	cagaatggac	6540
ctaacagaca	actgaaagta	aagactagat	ctcttgaagt	gcaagggcta	caacaactta	6600
attgtggtta	cttattttta	aaagcaaaaca	tactgaatgg	tatgactagg	gtgattacac	6660
tagtttaaaa	ataggccagg	tactgacact	gcattccctt	catgcattgc	tcatttaaaa	6720
tagtgaatat	taaaatatgt	gggctttaca	tctaaccac	agaaagccca	ccgcaaatgt	6780
tctgtgtatc	aaatatccac	ctcatgtgta	ctatgaaagt	tttatttatg	ccccattaag	6840
tcaaaagtaa	attatagtaa	gctaattgac	tgcatatttt	catatggatg	aatgtcagta	6900
tatctaaata	ggaaataaat	ggcgatccta	tctacctata	taaaaaaat	agaatatctt	6960
tccagatttt	gcatactcct	cactgtaaga	agaggtatgc	aggttttaag	gtttcacaa	7020
cagttgtcag	aaaaacagca	gttatgcctg	cagtatctcg	ttagcatctg	actcaattat	7080
tttttagatta	cattgttttag	aagacattgt	aaacctatct	aaaactttgt	aattattttg	7140
agatggttcc	aatgttaacc	ctagaatcat	catcagaaag	agtaacaatg	tgatgtagaa	7200
gaacagctaa	tcgacatgac	taaaatatgt	ctcattttca	gaaaaacaat	ctggctcatc	7260
ggaaacaatc	acagctacaa	cctagggaac	actcccatgt	gggatactga	tctggccaag	7320
gcacactttc	taagcaggaa	aactatcaga	tcagggtgaa	tttaggccac	ttcagagggtg	7380
ctgcctataa	acatccagac	agaccttctt	aggcagcaga	actggtccca	ttcctctcaa	7440
agcagtttga	cactacccta	cccacatcaa	cccaaagctt	gacgttaagt	caaaagagca	7500
tattggagca	aaagtgaaca	gatgtgtaaa	ctctagcaca	ttcttattgc	tgtattaagt	7560
ctgaagatga	gcacatccta	cccacaacag	tattgttcca	ggaagcaggg	taggagtagt	7620
ggtaaattag	aaaatagact	attaattgca	caattaatag	aaaagtaaaa	acatgtttca	7680
aaatctacaa	taaacctgta	tccaaggag	tcctatacgt	cagtgtgatg	tgctggactc	7740
tgaattctgt	ggtacagctt	tgcatgggac	tcctgcccgc	ctactggtct	gggtacggct	7800
tgcttccctg	ctgttgaagg	gtgaatatgc	tacacagagc	tatgatgggt	tctactgagt	7860
ggtaaaatc	acagaagttc	caggttcac	atgtcaggat	cattccttgt	gcaaagtttg	7920
atgtagatga	agataaagt	gtttcttggt	caataattgc	aatttctttc	ttttaaagtc	7980
agtggttttc	ttgtatagtt	ctattacaat	tggcccagggt	ttaatttcat	ccatctccat	8040
gaaagcaaaa	cac					8053

<210> 379  
 <211> 4455  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 agatggctgc cgacagtgcg cccgaatccg aggtatttga gatcacggac ttcaccactg 60  
 cctcggaatg ggaaagggtt atttccaaag ttgaagaagt cttgaatgac tggaaactga 120  
 ttggaaactc tttgggaaag ccactcgaaa agggatatatt tacttctggc acatgggaaag 180  
 agaaatcaga tgaaatttcc tttgctgact tcaagttctc agtcaactcat cattatcctg 240  
 tacaagagtc cactgataaa gaaggaaagg atgagttatt agaggatgtt gttccacaat 300  
 ctatgcaaga tttgctgggt atgaataatg actttcctcc aagagcacat tgcctggtaa 360  
 gatggtatgg gctacgtgag ttcgtggtga ttgcccctgc tgcacacagt gacgctgttc 420  
 tcagcgaatc taagtgcacac cttcttctga gttctgtttc tattgccttg ggaaacactg 480  
 gctgtcaggt gccactcttt gtgcaaattc accacaaatg gcgaagaatg tatgtaggag 540  
 aatgtcaagg tcctggtgta cgaactgatt tcgaaatggg tcatcttaga aaagtgccaa 600  
 atcagtacac tcacttatca ggtctgctgg atatcttcaa atcaaagatt ggatgtcctt 660  
 taactccatt gcctccagtt agtattgcta ttcgatttac ctatgtactt caagattggc 720  
 agcagtattt ttggcctcag caacctccag acatagatgc ccttgttaga ggagaagtgt 780  
 gaggcttgga gtttgcaag ttaccatttg gtgcctgcga agatcctatt agtgaactcc 840  
 atttagctac tacatggcac tcatctgacc gaagggatca ttgtggataa tgatgtttat 900  
 tctgatttgg atcctattca agctccacat tggctgttta gagttcgaaa agctgagaat 960  
 cctcagtggt tgcctaggtga ttttgcact gaatttttta aaatttgccg tcgaaaggag 1020  
 tcaactgatg agattcttgg acgatctgca tttgaggaaag aaggcaaaga aactgctgat 1080  
 ataactcatg ctttgtcaaa attgacagag cgggcatcag ttccaattca taaattatca 1140  
 gtttcaataa tggtagacac tgcaaagaag aaaatccgaa aacacagagg tgtagaggag 1200  
 tcaccgctaa ataatgatgt tcttaatact attctcctgt tcttattccc tgatgctgtt 1260  
 tctgagaaac cattagatgg aactacttca acagataata ataatcctcc atcagagagt 1320  
 gaagactata atctctacaa tcagttcaag tctgcacat ctgacagttt aacatacaaa 1380  
 ctggctttgt gtctctgtat gatcaatttt taccatggag ggttgaaagg agtggcacac 1440  
 ctctggcagg aatttgttct tgaaatgcgt ttccgatggg aaaacaactt tctgattcca 1500  
 ggattagcaa gtggaccccc agatctgagg tgttgtttac tgcacagaa actacagatg 1560  
 ttaaattgtt gtattgaaag aaagaaggca cgtgatgagg ggaaaaagac aagtgttca 1620  
 gatgtcacta atatatatcc aggggatgct ggaaaagcag gagaccagtt ggtgccagat 1680  
 aatctaaaag aaacagataa ggaaaaggga gaggtaggaa aatcttggga ttcttgagat 1740  
 gacagcgaag agaatttttt tgaatgccta agtgatactg aagaacttaa aggaaatgga 1800  
 caagagagtg gcaagaaagg aggacctaaag gagatggcaa atttaaggcc ggaaggacgg 1860  
 ctctatcagc atgggaaact tacactgtcg cataatggag aacctctcta cattccagta 1920  
 acccaggaac cagcacctat gacagaagat ctgtcagaag agcagtctga agtttttagct 1980  
 aaattaggta catcggcaga gggggctcac cttcagcac gcatgcagag tgcctgtctg 2040  
 ctctcagata tggagtcttt taaggcagct aatccaggtt gctccctgga agattttgtg 2100  
 aggtggtatt caccocggga ttatattgaa gaggaggtga ttgatgaaa gggcaatgtg 2160  
 gtgctgaaag gagaactgag tgcccggatg aagattccaa gcaatatgtg ggtagaagcc 2220  
 tgggaaacag ctaagccaat tcctgctaga aggcaaaggga gactcttcga tgatacacgg 2280  
 gaagcagaaa aggtgctgca ctatctggca atccagaaa ctgcagacct tgctcggcac 2340  
 ctgttacctt gtgtgattca tgcagctgta ctcaaggtaa aggaagaaga aagtctcgaa 2400  
 aacatttctt cagttaagaa gatcataaag cagataatat ccattccag taaagttttg 2460  
 cacttcccca atccagaaga caagaaattg gaagaaatca ttcaccagat tactaattgt 2520  
 gaagctctca ttgccagagc tcggctcacta aaagccaagt ttggaactga gaaatgtgaa 2580  
 caggaggagg aaaaggaaga tcttgaaagg tttgtgagtt gcctgctgga gcagcctgaa 2640  
 gtgttagtca ccggtgcagg aagaggacat gctggcagga tcattcaca gctgtttgtg 2700  
 aatgcccaga gggctgcagc tatgactcca ccagaggagg aattgaagag aatgggctcc 2760  
 ccagaggaaa gaaggcagaa ctccgtgtca gacttcccac cccctgctgg ccgggaattc 2820  
 attttgcgca ccactgtgcc gcgccctgct cctactcca aagctctgcc tcagcggatg 2880  
 tacagtgttc tcaccaaaga ggactttaga cttgcaggtg ccttttcac agataacttc 2940  
 ttcttctgat tcttctagca ttactcgttg gtggcttcag agacagtgtc gcctcctcct 3000  
 gagggaggga aggtaccagg gagaacctgg gaggtcctgg agagggccct gtccagttgg 3060  
 gtgatcagga atcaaacag catcggaag acttcccagc accaagcttg agctgtgtcg 3120  
 tttcgtggag ggggcagcga ggatgggctt gagctgttga gagatttctg ccctagagat 3180



ggcctttgta	tatggggggg	tgggtggggg	acacaaacac	atcagacact	ccgtcctcac	3240
actggcagga	cgggtgtcat	cgcattctct	tctgtgacca	gcctctaggc	tagcggtgc	3300
attcgtggtc	tgtgcaaaca	cttcgtgggt	ctatatatca	gcagcaagt	tgcaaaataa	3360
aggacctgtt	aactcagatt	tctggatatt	ttgggtggtag	cttctagtcc	cagaatctgt	3420
gtttttaaaa	tactacatga	cattctgtct	attcaatcac	ctgggtggta	tctttcttgt	3480
actaattaac	tgttgatgag	cattttggat	attctaggag	aaagcctata	atttcacata	3540
gtttctcttt	ttcatgtaac	tgtaacctaa	atgtattact	tctgataaaa	ctatatatca	3600
aatgtcactg	caaattagtt	ttatatctgt	catgtgagat	ttgtcttact	tatttttctt	3660
ttggttgcca	tggaagttat	ggccctgaaa	atcgtctccc	tccccttctc	ttgctgtaca	3720
gcatgcgttc	tctttttgtg	gttgctggct	gggtactgta	tttaatgaag	tagagaatag	3780
cacttgcaaa	aatacagtct	tggtagctag	agactgtcat	gcagatagta	taatttggtg	3840
tatgtgctaa	tgcattgagt	agaggattat	tttaacacac	tatttttgctt	ttgtatttta	3900
gttaaaataa	tcgatgggga	tgtgtagccc	ccccgtgtga	ggatgacatc	accacatttc	3960
tagtttcatg	gagctcaaga	tgtcttgtgt	ctgtgtggct	agatggcctc	tgcttggtaa	4020
tcttattttt	aggcctaaaa	ttcccactta	aatccaaagt	aaaaatgggt	atactgaagc	4080
ataaaccttg	cctgtgtaat	tttaaaaaat	taatagagct	gtgcaaacc	tgttattttt	4140
gtaaaaaaa	aaaaaataca	tatctatata	taatatgtgt	gtgtgtgtga	cataatgcaca	4200
cgtctctgtg	tatgtgaagt	aggggaggcc	ctgggggatg	acctcccagc	ctttatgaat	4260
ctttctctta	tgctgctgga	cttcattctt	actgggtcacg	cgatgcaggc	ggcctgaggc	4320
cagtgtgtga	ccaagtagaa	gacggttcct	aaggacagag	tttgtctgtt	ttctaacaaa	4380
gaaaaattct	acaaggagt	ggttaaagtt	acaaaggcat	tgtgaatcta	ataaaaggaa	4440
aggtgtcgtc	taaaa					4455

<210> 380  
 <211> 2333  
 <212> DNA  
 <213> Homo sapiens

<400> 380						
tttttttttt	ttctattttt	aatcaaattt	cttttttaatg	aaaactaatt	tttaaggggca	60
agataaccaca	gcagaagaaa	aacgtcttgc	aagaaaagac	ttcatgggtt	acaacgatca	120
aatgtatggg	ctatttgctt	gattgggtggc	ctggactcag	caagagattc	ctttgcagca	180
gaggttgggc	acacatctgg	gggctgcaac	accactgaaa	agacagcttt	ctaagcatta	240
gtgtaaggga	aaaagcagag	tgccctaaact	tggccatttc	caccaagaaa	aaaagtttca	300
tagcaacctt	ccttcaccag	aaaggcttac	tttatgatat	gctaacagaa	cagaaaagca	360
ggttgggaca	agatacagac	tttgttgcat	ttagctatga	cccttctctc	ccctctgtgg	420
atgtgggcag	ggtggggaga	ggcaggaaga	ggcagtagag	ggaaatgaca	tttgcactca	480
ggcttcccgc	ccctaccac	ccctaccctt	cgcccagaca	gacgtcggat	ctatgctgca	540
ccaggggtgg	gtcatggagt	ccagctaatt	gccaggagct	gaggcgtgta	caagccatga	600
aaagagctgc	cccacggcct	ccccacatca	ctgtccttca	tgcacttgca	tctttaaggc	660
tgccagcttc	agagctccct	ggacattccc	tggccaagt	tcateccctgt	gtcaaatgga	720
tgggatgccca	ggtaatcctt	gtactccccg	tcaatcagtt	tggcggcatt	gttccctggca	780
aaccagcagt	ctatctgtct	ttccccgttg	taaatcttcc	tttgcttcca	gaccactggg	840
acttggtggc	ctttcactgt	taggacggcc	tcaggccctt	ctcccactg	aaggagcaga	900
gggtgagtga	ggttctggct	gggccctgca	gggtcttctg	tgagtctggc	atcctgattc	960
aggaaactgac	ccagcagtcc	gtggcagttg	ctggaaaggc	cctcgctgtt	ggcaatgtag	1020
aaaccaggt	ggtgtcgtcg	gaaggcgccc	ggctttttgt	agagggtggat	gaggatgaca	1080
aaggctatgg	agccctggat	ggtgacggtg	acattggcgt	tggcagacac	ggacacctcc	1140
agccccagc	gtccccacc	cacactctgg	ttgcagggga	gcaccagtct	gtccccacca	1200
tccaagatga	ctctgctcgg	tgtgatctcg	agataagatc	tctctggctt	gttgatgagg	1260
atggtgatag	tgcgcaagta	agtgcgctgt	ttcttgtggc	catttgaggg	ggcgggtgcc	1320
ccaattaact	ctccgttcac	tgtgacacca	gagtcctgt	gatcagagac	cagcctgagg	1380
atgtccccgg	gctgcccac	aatgttgaag	cacacggtga	gtctgctcag	ggggaaatcc	1440
acaacaaagt	gggatcacc	atccactgat	gttttagaga	ttttaattct	tggctgggtat	1500
ggcttcttga	gcaaaggctc	tggctgcgtg	ccagctcctc	gcacgctctg	caccaccggt	1560
tcgggtccca	tggcagccga	catgccgtgg	gcctcctcca	ggccatccat	gcgtgggacc	1620

ggccccctca	gcttcatgga	ggtgaaggga	gtgaggaagc	ggtagctcac	agccagggcc	1680
tgggcccgc	gccgcagccg	ctccttctcc	ggttcatcgt	cactttgcag	ccaggagctc	1740
agcagctcct	ttgtggtgag	gtagctccag	agacgctcga	tgtggttggt	gtccccctct	1800
ccatcgccctc	caggcctggg	gcttcctgtg	acatctttcc	ctgccttctg	aggccgcaca	1860
ggcacatctg	tcttcaggat	gatgaatttc	ttactgttgc	tggcgggtgac	ctccacgtgc	1920
aggtgatcca	gcttcctgtc	caccagcttc	cccgcaatga	tgatctccga	gccgttgaag	1980
tagttggggg	acagggtctt	ggtggcctgc	accactgagc	tgggggggata	atcgatgcgg	2040
atgtcagaga	ggagcggggg	cctgatttca	tcgtagaacc	cgatgagctg	cgagcctgcg	2100
tcctcctcct	cgtgcacgcg	ccgtgtgagg	ccacagttct	ccagcgacag	tttctccagc	2160
agcctgaagt	ccacgtcgtt	gccgatgcca	atggtgaaga	tgcagacttg	gcctcggggc	2220
gcctctcggg	tgttgttgag	gatcttgagg	gtgtgcgtct	ccccgaccgt	gggcttgcct	2280
tccgtcagga	agacgatgag	ggacacgctc	cggctctccc	tacgcgtggg	cga	2333

<210> 381  
 <211> 607  
 <212> DNA  
 <213> Homo sapiens

<400> 381	
cctggggcgtg	ctcccccg
caccaagctc	agccccct
cttgctccca	tgcagaca
tgccctgtgga	gtttggggg
agatcaacta	tgggggtgag
agtatgagca	cacgaggtcc
tgttcccggg	ctgtgtgctc
tctaaacgca	tcagctacac
atggagaaat	tctaggtgaa
acaatgagtt	cacagccttc
tacaaca	

<210> 382  
 <211> 4197  
 <212> DNA  
 <213> Homo sapiens

<400> 382	
gcctgtctgc	ccctgagcac
ccctgtctgc	gggactgtcc
accctaacaa	ggccatcttc
acaaagcttg	cgggctcctg
agttctttct	gaggtcagat
ccgacggcca	cgctgcgggtg
agaagattcc	agtgtctgtg
tggtggctct	ggagcccgtg
ccgtcacgtc	atgtgacagt
tggtggggca	gcataatcaca
acatcccaaa	gaatctcaag

tccctctgag	cttaaagctg	aaatcccaac	ccagcagcga	ggaggcgacc	accggtgagg	720
cggccccctgt	gagcggctac	cgggcatctg	tctgggtgtt	ctgcaccatc	agtggcctca	780
tcaccctcct	gccggatggg	accatccacg	gcatcaacca	cagcttcgcg	ctgacactgt	840
ttgggttacgg	aaagacggag	ctcctgggca	agaatatcac	tttcctgatt	cctggtttct	900
acagctacat	ggaccttgcg	tacaacagct	cattacagct	cccagacctg	gccagctgcc	960
tggacgtcgg	caatgagagt	gggtgtgggg	agagaacctt	ggacctgtgg	cagggccagg	1020
accagctga	ggggggccag	gatccaagga	ttaatgtcgt	gcttgctggt	ggccacgttg	1080
tgccccgaga	tgagatccgg	aagctgatgg	aaagccaaga	catcttcacc	gggactcaga	1140
ctgagctgat	tgctggaggg	cagctccttt	cctgectctc	acctcagcct	gctccagggg	1200
tggacaatgt	cccagaagga	agcctgccag	tgacgggtga	acaggcgctg	cccaaggacc	1260
agcaaatcac	tgcttgggg	agagaggaac	ctgtggcaat	agagagcccc	ggacaggatc	1320
ttctggggaga	aagcaggtct	gaaccagtgg	atgtgaagcc	atttgcttcc	tgogaagatt	1380
ctgaagctcc	agtccagct	gaggatgggg	gcagtgtatg	tggcatgtgt	ggcctgtgtc	1440
agaaggccca	gctagagcgg	atgggagtca	gtgggtccag	cgggtcagac	ctttgggctg	1500
gggctgccgt	ggccaagccc	caggccaagg	gtcagctggc	ggggggcagc	ctcctgatgc	1560
actgcccttg	ctatgggagt	gaatggggct	tgtgggtggc	aagccaggac	ttggccccc	1620
gccccctctgg	gatggcaggg	ctctcgtttg	ggacacctac	tctagatgag	ccgtggctgg	1680
gagtggaaaa	cgaccgagaa	gagctgcaga	cctgcttgat	taaggagcag	ctgtcccagt	1740
tgagccttgc	aggagccctg	gatgtcccc	acgccgaact	cgttccgaca	gagtggcagg	1800
ctgtcaccgc	tcctgtgtcg	tcctgcgac	tgggaggcag	agacctgtgc	ggtggctgca	1860
cgggcagctc	ctcagcctgc	tatgccttgg	ccacggacct	ccctgggggc	ctggaagcag	1920
tggaggccca	ggaggttgat	gtgaattcgt	tttcctggaa	cctcaaggaa	ctctttttca	1980
gtgaccagac	agaccaaacg	tcatacaatt	gttcctgtgc	tacgtctgaa	ctcagagaga	2040
cacctctctc	cttggcagtg	ggctccgatc	cagatgtagg	cagtctccag	gaacaggggt	2100
cgtgtgtcct	ggatgacagg	gagctgttac	tactgaccgg	cacctgtgtt	gaccttggcc	2160
aaggccgacg	gttccgggag	agctgtgtgg	gacatgatcc	aacagaaccg	cttgaggttt	2220
gtttggtgtc	ctctgagcat	tatgcagcaa	gcgacagaga	aagcccagga	cacgttcctt	2280
ccacgttgg	tgctggccct	gaggacacgt	gcccatacag	agaggagcca	aggctgaacc	2340
tccaggtcac	ctccacgccc	gtgatcgtga	tgcgcggggc	tgctggcctg	cagcgggaga	2400
tccaggaggg	tgctactctc	gggagctgct	accatcgaga	tggtttacgg	ctgagtatac	2460
agtttgaggt	gaggcgggtg	gagctccagg	gccccacacc	tctgttctgc	tgctggctgg	2520
tgaaagacct	cctccacagc	caacgcgact	cagccgccag	gacccgcctg	ttccttgcca	2580
gcctgcccg	ctccacccac	tctaccgctg	ctgagctcac	cggaccacgc	ctgggtggaag	2640
tgctcagagc	cagaccctgg	tttgaggagc	cccccaaggc	tgtggaactg	gaggggttgg	2700
cggcctgtga	ggcgagtag	tcccaaaagt	accataccat	gagcccgctg	ggcagtgagg	2760
ccttcggctt	cgtgtggact	gctgtggaca	aggaaaaaaa	caaggagggtg	gtgggtgaagt	2820
ttattaagaa	ggagaaggtc	ttggaggatt	gttggattga	ggatcccaaa	cttgggaaag	2880
ttacttttaga	gatcgcaatt	ctatccaggg	tggagcacgc	caatatcatc	aaggtatttg	2940
atatatttga	aaaccaaggg	ttcttccagc	ttgtgatgga	gaagcacggc	tccggcctag	3000
acctcttcgc	tttcatcgac	cgccacccca	ggctggatga	gcccctggcg	agctacatct	3060
tccgacaagt	gagagcaggg	ccagagccgt	ctagtgtcag	cagtgggata	cctgcgcttg	3120
aaggacatca	tccaccgtga	catcaaggat	gagaacatcg	tgatcgccga	ggacttcaca	3180
atcaagctga	tagactttgg	ctcggccgcc	tacttggaaa	ggggaaaatt	attttatact	3240
ttttgtggga	ccatcgagta	ctgtgcaccg	gaagtctctc	tggggaatcc	ctacagaggg	3300
cgggagctgg	agatgtggtc	tctgggagtc	actctgtaca	cgtgtgtctt	tgaggagaac	3360
cccttctgtg	agctggagga	gacctgtggg	gctgccatac	acccgccata	cctggtgtcc	3420
aaagaactca	tgagccttgt	gtctgggctg	ctgcagccag	tccttgagag	acgcaccacc	3480
ttggagaagc	tgggtgacaga	cccgtgggta	acacagcctg	tgaatcttgc	tgactataca	3540
tgggaagagg	tggttcgagt	aaacaagcca	gaaagtggag	ttctgtccgc	tgcgagcctg	3600
gagatggggg	acaggagcct	gagtgatgtg	gccaggctc	aggagctttg	tgggggcccc	3660
gttccaggcg	aggctcctaa	tggccaaggc	tgtttgcata	ccggggatcc	ccgtctgctg	3720
accagctaaa	caccaatttc	ttcctgcttt	tctccacttg	gtttggaaaa	tcacacagtt	3780
ttcaggctcc	atctgttttg	agaaaataca	ttctgaagca	tcccaatttc	accttctaaa	3840
aactcatgtg	caggtttgat	aaacaccaga	acagaagaca	gtgatgctgt	attatttttag	3900
atttattaca	tagattttgga	attcactttt	ttcatgacct	agaaaaaac	attccagtgt	3960
tcaactgttt	tatattatta	aagggttttt	aatttgtgaa	cttctgaagg	catgagtgtt	4020
ttctctttct	acttttgtat	atgtgcatgt	tttgtttcct	ctgacttggg	atatgctcat	4080
ctgagtgacg	gatattgtgaa	atttgtagaa	ctggttagtc	aaatggccag	actatttcat	4140
taattttattt	cctcaaatgc	ttttcaaat	aaagcacctt	tgttagtaaa	cagttaa	4197

<210> 383  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<400> 383  
 ctggtattca tacagtgaca gagggagtggt ttttagaaat ttatagctgt ttctaggtga 60  
 aaacactggg tgatttagct cccttggttaa gagcactgag cagaaagaag ttccctatca 120  
 aatgggtgtg tggagcagcc ctgttctccc catcccgtag agctccagga agttaaccag 180  
 ggacttcagc tgcgacctgc agatttctaa gccccctgt tatttctctg tcttttacgg 240  
 gcctgtgtat ttcagacttg gtgggtggcag tcaacgggggt ctggatcctc gtggagacat 300  
 ttatgctgaa aggtgggaac ttcttctcca agcacgtgcc ctggagttag ctctctttc 360  
 taactatcta tgggggtggag ctgttcctga aggttgccgg cctgggccct gtggagtact 420  
 tgtcttccgg atggaacttg tttgacttct ccgtgacagt gttcgccttc ctgggactgc 480  
 tggcgctggc cctcaacatg gagcccttct atttcatcgt ggtcctgcgc cccctccagc 540  
 tgctgaggtt gtttaagtgt aaggagcgt accgcaacgt gctggacacc atgttcgagc 600  
 tgctgccccg gatggccagc ctgggcctca cctgtctcat cttttactac tccttcgcca 660  
 tcgtgggcat ggagtcttc tgcgggatcg tcttcccaa ctgctgcaac acgagtacag 720  
 tggcagatgc ctaccgtgg cgcaaccaca ccgtgggcaa caggaccgtg gtggaggaag 780  
 gctactatta tctcaataat tttgacaaca tctcaacag ctttgtgacc ctgtttgagc 840  
 tcacagttgt caacaactgg tacatcatca tgggaaggct cacctctcag acctccact 900  
 ggagccgct ctacttcatg accttttaca ttgtgacct ggtggtgat acgatcattg 960  
 tcgcctttat cctcgaggcc ttcgtcttcc gaatgaacta cagccgcaag aaccaggact 1020  
 cggaggttga tgggtggcat acccttgaga aggaaatctc caaagaagag ctggttgccg 1080  
 tcttgagct ctaccgggag gcacgggggg cctcctcgga tgtcaccagg ctgctggaga 1140  
 cctctccca gatggagaga taccagcaac attccatggt gtttctggga cggcgtatcaa 1200  
 ggaccaagag cgacctgagc ctgaagatgt accaggaga gatccaggag tggatagagg 1260  
 agcatgccag ggagcaagag cagcagcgac aactcagcag cagtgcagcc ccgcgcgcc 1320  
 agcagcccc aggcagccgc cagcgtccc agaccgttac ctagcccagc gccgaaaagc 1380  
 cgtctcttct atgcaataac acaatagtat tactctactg cgatgtacgg aactgcggtg 1440  
 tgtgtacaca tactcacgta tatgcacata tttatataca ggaagaaaaa agacagacaa 1500  
 gatggggctt ggtttataac caccttgccc tgtcttctt aactccagaa gccagtttg 1560  
 tgaggggtgg ggtgctggcc accaggtctg agctcttct actgtggaag gctccagaag 1620  
 gcccttcaca aggagacccc tcacctggat ccagtcgact ggggggcttg cccctcatgt 1680  
 gggctggcct ccatcgcca cgtccaaagc tgtcactgct actgcttcag gctcacatcc 1740  
 ccccgacctg atggcgtgcc cgtccctct cctgcgggc catgccacag gtttctgtgt 1800  
 tttgctttag ggacagaacc acttaggaag gaaagaactc ccg 1843

<210> 384  
 <211> 1459  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 ctggcgggctg tgggaaccca gggccggccg aggcggccag gaggtgagat ggcagctggg 60  
 caaaatgggc acgaagagtg ggtgggcagc gcatacctgt ttgtggagtc ctgctggac 120  
 aaggtggtcc tgtcggatgc ctacgcgcac cccagcaga aggtggcagt gtacagggtc 180  
 ctgcaggctg ccttggcaga gagcggcggg agcccgagc tgcctcagat gctgaagatc 240  
 caccgcagcg accgcagct gatcgtgcag ctgcgattct gggggcgga gccctgtggc 300  
 cgcttctctc gcgcctaccg cgagggggcg ctgcgcgcg cgtgcagag gagctggcg 360  
 gcgcgcctcg cccagcactc ggtgcgctg caactgggtat ctgcgcgcg gcgcgcagcg 420  
 gctggaggct ttgctggcgg acgaggagcg ctgtttgagt tgcatacctag cccagcagcc 480

cgaccggctc	cgggatgaag	aactggctga	gctggaggat	gcgctgcgaa	atctgaagtg	540
cggctcgggg	gcccggggtg	gcgacgggga	ggtcgcttcg	gcccccttgc	agcccccggt	600
gcctctctcg	tcggagggtga	agccgcccgc	gccgcccga	cctgcccaga	cttttctgtt	660
ccagggtcag	cctgtagtga	atcgcccgct	gagcctgaag	gaccaacaga	cgttcgcgcg	720
ctctgtgggt	ctcaaatggc	gcaagggtgg	gcgctcactg	cagcgaggct	gccgggcgct	780
gcgggacccg	gcgctggact	cgctggccta	cgagtacgag	cgcgagggac	tgtacgagca	840
ggccttccag	ctgtgcggc	gcttcgtgca	ggccgagggc	cgccgcccga	cgctgcagcg	900
cctggtggag	gcactcgagg	agaacgagct	caccagcctg	gcagaggact	tgctgggcct	960
gaccgatccc	aatggcgggc	tggcctagac	caggggtgca	gccagctttt	ggagaacctg	1020
gatggcctta	gggttccttc	tgcggctatt	gctgaacccc	tgtccatcca	cgggaccttg	1080
aaactccact	tggcctatct	gctggacctg	ctggggcaga	gttgattgcc	ttccccagga	1140
gccagaccac	tgggggtgca	tcattgggga	ttctgcctca	ggtaacttga	tagagtgtgg	1200
ggtggggggg	acctgctttg	gagatcagcc	tcaccttctc	ccatcccaga	agcggggcct	1260
acagccagcc	cttacagttt	cactcatgaa	gcacctgat	ctttggtgtc	ctggacttca	1320
tcctgggtgc	tcagataact	gcagtgaagt	aaaacaggaa	tcaatcttgc	ctgccccag	1380
ctcacactca	gcgtgggacc	ccgaatgtta	agcaatgata	ataaagtata	acacggattt	1440
tgatgtgaga	aaaaaaaa					1459

&lt;210&gt; 385

&lt;211&gt; 2408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2408)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 385

tttttttttt	ttcgagataa	acctttttat	ttatttatgc	ttctccattt	tgtttaaaac	60
aacaacaaca	accaccttaa	tgtaactgac	agcccttccc	cctcaccctg	cctcgggctg	120
ggggtagtta	atggggaaat	ggccccagg	gtggggctga	ccagaagagc	ccctcaaggga	180
gctcatggag	cccaaattccc	ctgccctggg	gaggggacct	gtagtgtgtg	acgggagcct	240
ctcccagagc	tctgcttgta	ccatcaaaga	tgcccttggc	caacaagggt	caggaagcat	300
ggggggaggga	tttcggcctc	ctctgtccct	accagcccca	atctcacgag	cagggctggg	360
gggtttaaaa	agggtggagc	gggtgggggt	ggctcacacg	aaggagtact	ggttgttaaa	420
tggccccctg	ggtggcccc	ttcctctcca	tcacccccct	agtggtgact	gctgcagctg	480
caccaattgg	gggcaccccc	gcgtcccac	caggacccag	gcgcccttgg	gcctcttgag	540
cctggggcct	atggccctct	cccaattcac	ccacggggac	cagctaaacc	acggggacca	600
gcctcttccg	ggacccctcc	acccgcccgc	tttctcttcc	tcttgccctc	ctttggctgc	660
tgcggctgcc	tnttgcccgc	cacttccctg	cgcctctoga	cgccctcttc	ttccccaggc	720
tgtgggggat	ctgtccatga	aggggggttca	gggggctggg	gtgggtcatg	ggaggtggtc	780
ggttacacag	tcactcgctc	cgaagggcac	gaggggtgcag	gaggcattcg	gggtggcatc	840
catctccctc	gcacaccccc	gcatggctcc	cagcctgctc	ccggcctcac	ttcttgggtg	900
cacgggcacc	tcctcccctg	cagacctgct	ctgctcacc	tgtgtcgcct	gggaggatgg	960
gacatagctg	acaaggacaa	catcactgga	gcctcccagc	tccaaaggga	tggggtgcac	1020
ccggaagtgc	tcgagcatat	cgaaaatgga	ctggaaccac	aggtgctgga	cccggcactg	1080
accctcctcg	ttcagcgaca	aacgcagggt	cttggccttg	ccctggaagt	tgaagggtgag	1140
gacgtattca	ccccgccttg	tctcactctg	gcgcaccagg	aagacaccgt	gggagccagt	1200
gccgccagtc	agcaccaact	gtgcagcctt	gagccgagag	agcatcccgt	ggaaccaagg	1260
ataccctgag	aggggctggg	ccccctcacc	gcctctggc	tcccccttgg	aacagggaag	1320
accctgtggc	tgtttccgga	gtgtccaagg	gagggtaggg	ggctgagagg	ggatgaactg	1380
tccttgcctg	gggtccctct	tcaatgggga	tgcggggggg	caactctggg	ggaagcagtt	1440
ccatcgagtc	aaaatgggag	gcggcaatgg	aggcagagct	gggggagatg	gatgccgagg	1500
ggcggctctg	gagggcccca	tatgccccct	gcgacaggcg	gtcattgctc	tcgctgggtc	1560
caagcagcag	gtcctggctg	ggtagactct	ccgagtgtat	caggcaggac	agctccaggc	1620

tgtctgtgtt	ctcccttgta	aggaatgagg	tcccaggggc	cagagggagg	gtcatggggc	1680
ggggactggt	agcagggcag	ggtcctgggc	tcaggcattc	ttggatgtca	gacacccagg	1740
ccttcacatg	ctgggcatcc	actgtctcca	tgataatact	ggatggacct	tccaccttaa	1800
ccacaaacgt	gttctcccgg	tcaggcatct	ccagggctgt	ggttgtccgg	acgtctgtga	1860
tagaagagca	ggggatgctg	agtccggggc	gagaggcctt	gggtggtaca	aagaactcca	1920
ggcgacttcg	tcctctctct	tctccttcac	ttcgaagcag	caggcgacac	ttctgccact	1980
gaggctgccc	tcctccccct	gaaggaggcc	cagccacccc	tcctccccgg	cccactccgg	2040
ctgggtcagg	ggctgcctcc	tcagccccc	tgaaactcag	cagctcttcc	ctctgcacca	2100
tccctgctcc	atccttcaag	gcgccccctc	cccactgag	tctcagctc	tcaaaacggt	2160
gagtcacatc	ttccccagg	gacgttccat	cactgaccag	tcccctacca	acggtcccag	2220
ccccgccaga	ggagtggag	ttgctgtttc	cacctaagac	tggggggcct	gacgaggtct	2280
ccaggggccc	agcggaggag	ggaggggtcaa	cggctccccg	ccactgcagg	atgccacgga	2340
ctgagcctcg	gacagagcga	cccactgaac	gcagggaaaa	gcgcttcttg	agcttcggct	2400
tggaggag						2408

&lt;210&gt; 386

&lt;211&gt; 2204

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 386

ttgggggaacc	cccagggttt	tcccatcccc	ccggtgtaaa	accgcggccc	aggaaatgga	60
ttttgggggc	cccataaaaa	aactttttgcg	ttgccagccc	ccggacgtta	acctggatcc	120
tttaaaacgg	cccccccttt	tttttttttt	tctttaacaa	aatttttatt	taataaatgg	180
ttaaaatcgc	agtgccaaaa	atacattgac	atttagcaat	ttcactgaaa	ggaagaaact	240
acagaatgca	cggtttcaga	aagctatttt	aagttatttta	caaataaagt	atctaaaact	300
caaaaacagg	ctctgtatgc	tatatctagt	ttatcccttc	ccgaacaaaa	tttctgttat	360
ttgggcaaat	tcttaaacca	tggttttaac	cgtaatgggt	acaaaccaca	aacacatcca	420
tccagagact	gaaaccgttt	ctatccggtc	agtggcaaaa	ctgttgaaag	ggcaatagtt	480
gaagctgttg	ggttttatat	agtgtgaact	ctgataaata	ttcctaccag	gactaaaaca	540
cagcacgctt	tgcgggcatg	gctgactcac	aaagggttga	acaaacaaga	actactcttc	600
actcgacacc	atggctcaga	ggccaccgag	aagcacgagt	gactgacagc	tcctctgctt	660
acaaacgaat	gaaacccaaa	gtggatgtcg	ttctcacagc	actgaaagtg	cttcaggact	720
caactgac	caatactaac	tttcttccct	attttacaca	tatttttcta	ctgtccagtg	780
gaaatcattt	ctgttttgg	ctaaacaaca	aatactagtt	tataacagga	atggtaaaat	840
ctgtgagaat	tctgtcaat	ttaatacaag	atcactactt	tctttagaat	ggtttctgcg	900
tgtttctacg	tcacctctg	tatttttagc	ttccagtttc	ctggtaagga	ataagttctc	960
cttcccagtc	acactcgggg	tcatttacac	gtttctggga	tgcccttgct	cgtccatgga	1020
ggccaggtgc	gtgcagtgc	tcactctgcc	tcttccctct	tctcaggacc	agtccccgaa	1080
ccttctgcct	tgcagatcct	cctgtttccg	ccacactctc	gcgctcggaa	gcgagctcct	1140
ggatcataca	gctgcaaggc	tggccggctc	ttgtttgcc	gtcgtctctt	tctgggtgct	1200
ggactgtcgt	cacacctctg	cgtcttcccc	agtctctcca	tggcctcccc	cggagccccg	1260
ctgtcctggc	tccccttctt	ccctctgtct	tggccaggtc	ctttccccc	tctctgctca	1320
tctcactcc	ttctggaag	ccgttcaggc	tcgtggtgag	ctctgtgcct	cctgcgctca	1380
tccacatggt	atctttgtgc	ttcagattct	tgttcttgag	atctctccac	atccctgtgc	1440
tctttatcac	tgcgctgtg	tgacgtctcc	tggggctcct	ccagcgagcc	ttccatgggc	1500
ctggctttta	cgactgcacc	gggggcacag	gattcctgct	tgccacctcc	agtatcaatc	1560
tctctcctc	tttcttttgg	tttctctgtg	gttggttcct	ctcccttttc	tggtttctta	1620
agaagcttaa	tccttacttc	tttctctgca	atttctctct	gtttatctgt	ctcttttttt	1680
tgcactcttt	cttctctctt	tcttctctct	tcttctctct	ccgcgaacg	tttcttttct	1740
aactctctcc	tcctccgttc	ttctcgcttc	tcttctcgaa	ttctctgctt	ttctaatctt	1800
ctatttttaa	tatatccaa	aagaggtgtg	gttcttctag	caatgagctc	tcttgctctc	1860
gcctccatct	cccccagcag	agtctcagg	tggcactgg	tcttctcttc	ctccacacag	1920
taggtttcta	aaaacttctt	atattctgga	tctttgctgt	caaggaagat	atatccatca	1980
aaacgatctc	taaaaagaag	gatgtcatca	ggattcctaa	aattaatgta	tgtctcttgag	2040
tagagatgag	gataaagact	caggctcggc	gcgaagaact	cgaagtagtc	gtgtgctggc	2100

agcgggcgca gctgctcctc cagctgctcc ttggtgaggc ccggaggcag gcggcggatg 2160  
accacctgcg gggagcgcg cggcgttccc accggggcac gaaa 2204

<210> 387  
<211> 798  
<212> DNA  
<213> Homo sapiens

<400> 387  
tttcgtagca aacaggtttc acgaccactg ctctctggag tcttattcct cagagtatga 60  
gcccttgacc aaggagcatg gaatgcatca cctatgtttg aacaagggcg ccagatgacc 120  
tctgcggacc caggggtttg gaagtgtgta tgtggagcca caggacttgt tttagggcgt 180  
gtggggcggtg tgtgtgagtg ggcttctgca ggtgggcagc cagcgggcac aggcgtggag 240  
agcatgggtca cccatggaga caccgctcac ggggactttc ctttggcccc acatcccga 300  
gggtctcttc ttcgatgatt cctatggctt ctaccaggc caggtgctca ttggccctgc 360  
caagatcttc tccagcgtcc agtggtgtgc aggtgtcaag cccgtgctca gcaccaagag 420  
caagtccga gtggtggtgg aagaggtgca ggtgtgtagg ttgaaagtta catggattac 480  
caagagtttc tgtccagggg gcacggacag cgtcagcccc ccacgtctgt catcaccag 540  
gaaaacctag gcagggtgaa gcgtctcgga tgctttgacc atgctcagcg gcagcttggg 600  
gagcgtgtc tgtatgtctt cccagccaag gtagagccag ccaagattgc ctgggaatgt 660  
ccagaaaaaa actgcgcca gggggagggc tctatggcca agaagtgaa gcgcctgttg 720  
aagaagcagg ttgtgcggat catgtcatgc tcccagaca ccagtggtc ccgggaccat 780  
tccatggaag acccagac 798

<210> 388  
<211> 4530  
<212> DNA  
<213> Homo sapiens

<400> 388  
tttcgtgaca gtagccctg ctcgcccttc gaggttccact gcctaagtgg cgagtgcac 60  
cactccagct ggcgctgtga tgggtggccc gactgcaagg acaaactga cgaggaaaac 120  
tgcgctgtgg ccacctgtcg ccctgacgaa ttccagtgtc ctgatggaaa ctgcatccat 180  
ggcagccggc agtgtgaccg ggaatatgac tgcaaggaca tgagcgatga agttggctgc 240  
gttaatgtga cactctgca gggaccacaac aagttcaagt gtcacagcgg cgaatgcac 300  
accctggaca aagtctgcaa catggctaga gactgcggg actggtcaga tgaacccatc 360  
aaagagtgcg ggaccaacga atgcttgga aacaacggcg gctgttcca cgtctgcaat 420  
gaccttaaga tgggtacga gtgcctgtgc cccgacggct tccagctggg gccccagcga 480  
agatgcgaag atatcgatga gtgtcaggat cccgacacct gcagccagct ctgctgaac 540  
ctggagggtg gctacaagtg ccagtgtgag gaaggcttcc agctggacc ccacacgaag 600  
gcctgcaagg ctgtgggctc catcgccctac ctcttcttca ccaacggca cgaggtcagg 660  
aagatgaacg tggaccggag cgagtaacac agcctcatcc ccaacctgag gaacgtggtc 720  
gctctggaca cggaggtggc cagcaataga atctactggg ctgacctgtc ccagagaatg 780  
atctgcagca cccagcttga cagagcccac ggcgtctctt cctatgacac cgtcatcagc 840  
agagacatcc agggccccga cgggctgggt gtggactgga tccacagcaa catctactgg 900  
accgactctg tcctgggcac tgtctctgtt gcgatacca agggcgtaga gaggaaaacg 960  
ttattcaggg agaacggctc caagccaagg gccatcgtgg tggatcctgt tcatggcttc 1020  
atgtactgga ctgactgggg aactcccgc aagatcaaga aagggggcct gaatggtgtg 1080

gacatctact	cgctggtgac	tgaaaacatt	cagtggccca	atggcatcac	cctagatctc	1140
ctcagtggcc	gcctctactg	ggttgactcc	aaacttcact	ccatctcaag	catcgatgtc	1200
aatgggggca	accggaagac	catcttgagg	gatgaaaaga	ggctggccca	cccttctccc	1260
ttggcgtct	ttgaggacaa	agtatttttg	acagatatca	tcaacgaagc	catttttcagt	1320
gccaaccgcc	tcacaggttc	cgatgtcaac	ttggttgctg	aaaacctact	gtccccagag	1380
gatatggtcc	tcttcacaa	cctcaccag	ccaagaggag	tgaactgggtg	tgagaggacc	1440
accctgagca	atggcggtg	ccagtatctg	tgcttccctg	ccccgcagat	caacccccac	1500
tcgcccaggt	ttacctgcgc	ctgcccggac	ggcatgctgc	tggccaggga	catgaggagc	1560
tgctcacag	agggttgagg	ctgcagtggc	caccaggag	acatccaccg	tcaggctaaa	1620
ggtcagctcc	acagccgtaa	ggacacagca	cacaaccacc	cggcctgttc	ccgacacctc	1680
ccggtgcct	ggggccaccc	ctgggctcac	cacggtggag	atagtgacaa	tgtctcacca	1740
agctctgggc	gacgttgctg	gcaagaggaa	attgagaaga	agccagtag	cgtgagggct	1800
ctgtccattg	tcttccccat	cgttgctcct	cgtcttccct	tgctggggg	tcttccctct	1860
atggaagaac	tggcggctta	agaacatcaa	cagcatcaac	tttgacaacc	ccgtctatca	1920
gaagaccaca	gaggatgagg	tgacatttg	ccacaaccag	gacggctaca	gtaccctctc	1980
gagacagatg	gtcagtctgg	aggatgacgt	ggcgtgaaca	tctgcttga	gtcccgctcc	2040
tgcccagaac	ccttctctgag	acctcgccgg	ccttgtttta	ttcaaagaca	gagaagacca	2100
aagcattgcc	tgccagagct	ttgttttata	tattttattca	tctgggaggc	agaacaggct	2160
tcggacagtg	cccatgcaat	ggcttggtt	gggatttttg	tttcttccct	tctcgtgaa	2220
ggataagaga	aacaggcccg	gggggaccag	gatgacacct	ccatttctct	ccagggaagt	2280
ttgagtttct	ctccaccgtg	acacaatcct	caaacatgga	agatgaaagg	gcaggggatg	2340
tcaggcccg	agaagcaagt	ggctttcaac	acacaaccagc	agatggcacc	aacgggaccc	2400
cctggccctg	cctcatccac	caatctctaa	gccaaacccc	taaactcagg	agtcaacgtg	2460
tttacctctt	ctatgcaagc	cttgctagac	agccagggtta	gcctttgccc	tgtcaacccc	2520
gaatcatgac	ccaccagtg	tctttcgagg	tgggtttgta	ccttccctta	gccaggaaag	2580
ggattcatgg	cgtcggaaat	gatctggctg	aatccgtggt	ggcaccgaga	ccaactcat	2640
tcaccaaagt	atgccacttc	ccagaggcag	agcctgagtc	actggtcacc	cttaatattt	2700
attaagtgcc	tgagacaccc	ggttaccttg	gccgtgagga	cacgtggcct	gcacccagggt	2760
gtggctgtca	ggacaccagc	ctggtgcccc	tcctcccgac	ccctaccac	ttccattccc	2820
gtggctcct	tgactttct	cagttcagag	ttgtacactg	tgtacatttg	gcatttgtgt	2880
tattattttg	cactgttttc	tgtcgtgtgt	gttgggatgg	gatcccaggc	cagggaaagc	2940
ccgtgtcaat	gaatgccggg	gacagagagg	ggcagggtga	ccgggacttc	aaagccgtga	3000
tcgtgaatat	cgagaactgc	cattgtcgtc	tttatgtccg	cccacctagt	gcttccactt	3060
ctatgcaaat	gcctccaagc	cattcacttc	cccaatcttg	tcgttgatgg	gtatgtgttt	3120
aaaacatgca	cggtagggcc	gggcgcagtg	gctcacgcct	gtaatcccag	cactttggga	3180
ggccgaggcg	ggtggatcat	gaggtcagga	gatcgagacc	atcctggcta	acaagggtgaa	3240
acccgctctc	tactaaaaat	acaaaaaatt	agccgggcgt	ggtggcgggc	acctgtatgc	3300
ccagctactc	gggaggctga	ggcaggagaa	tgggtgaac	ccgggaagcg	gagcttgacg	3360
tgagccgaga	ttgcgccact	gcagtccgca	gtctggcctg	ggcgacagag	cgagactccg	3420
tctcaaaaaa	aaaaaccaa	aaaaaccctt	gcttggggca	tcagcagccc	ttggcctctg	3480
gccaggcatg	gcgaggctga	ggtgggagga	tggtttgagc	tcaggcattt	gaggctgtcg	3540
tgagctatga	ttatgccact	gctttccagc	ctgggcaaca	tagtaagacc	ccatctctta	3600
aaaaatgaat	ttggccagac	acagggtgcct	cacgcctgta	atcccagcac	tttgggaggc	3660
tgagctggat	cacttgagtt	caggagttgg	agaccaggcc	tgagcaacaa	agcgagatcc	3720
catctctaca	aaaaccaa	agttaaaaat	cagctgggta	cgggtggcacg	tgctgtgtat	3780
cccagctact	tgggaggctg	aggcaggagg	atgcctgag	cccaggaggt	ggaggttgca	3840
gtgagccatg	atcgagccac	tgactccag	cctgggcaac	agatgaagac	cctattttcag	3900
aaatacaact	ataaaaaaat	aaataaatcc	tccagtctgg	atcgtttgac	gggacttcag	3960
gttctttctg	aaatcgccgt	gttactgttg	cactgatgtc	cggagagaca	gtgacagcct	4020
ccgtcagact	cccgcgtgaa	gatgtcacaa	gggattggca	attgtcccca	gggacaaaac	4080
actgtgtccc	ccccagtga	gggaaccgtg	ataagccttt	ctggtttcgg	agcacgtaaa	4140
tgctccctg	tacagatagt	ggggattttt	tgttatgttt	gcactttgta	tattggttga	4200
aactgttatc	acttatatat	atatatacat	atacacacat	atatataaaa	tctattttatt	4260
tttgcaaaacc	ctggttgctg	tattttgttca	gtgactattc	tccgggcccct	gtgtaggggg	4320
ttattgcctc	tgaatgcct	cttctttatg	tacaaagatt	atgtgcacga	actggactgt	4380
gtgcaacgct	ttttgggaga	atgatgtccc	cgttgtatgt	atgagtggct	tctgggagat	4440
gggtgtcact	ttttaaacca	ctgtatagaa	gggttttgta	gcctgaatgt	cttactgtga	4500
tcaattaaat	ttcttaaatg	aacaaaaaaa				4530



<211> 2343  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1) ... (2343)  
 <223> n = a,t,c or g

<400> 389

tttttttttt	ttatgtggat	aatattttatt	tgtatcttat	ctatagaaca	aatattttaca	60
gatacaaacg	gaatcacagc	aaagttgcta	taaaaccatc	cagacctctc	gatggccact	120
tctgaaaaca	tccacgggtga	agggcagggc	caggcctggc	tgtggagtgg	gccagctgag	180
tacctgggcg	tcagccaagg	gaaatggttg	gggattatgg	cttcagcact	ctgccggagc	240
acattcctga	gcgtgacaa	cgtggagccc	tcaccgcccc	caacctaccc	aacctcaatg	300
gggaaggaaa	ggggcctgag	ctgggcaggg	ctgcccgggc	tcactatgtg	cctgctccag	360
gagtcctcgg	cccctgtgct	ggcaggagca	tccttgagct	ggaccgggag	gcctctctgg	420
cctggggctg	ctccctgccc	ggcaggctgc	tgtttggcag	ctggaggtgg	caagagctgc	480
tgggtgctgcc	agggcgtgtt	ggccaggaat	gagctcccag	ggcagccctg	aggaaagggg	540
cttaggaagc	gcctcccagc	tcactactag	gagctgggga	ctgtcagtcg	tgagtggggc	600
tggggtacag	gagcacctgc	ctctcctttc	tttggccttag	aagtggggaa	ggaagggcca	660
ggaaaaggga	ccaaagccgc	cccagccttg	gcccctaggc	cgccctgggga	ctgtgtgtgt	720
gctgaggggg	cagtgggagg	tgggcagctc	tggagttccc	tgcaccctgg	gatccttggg	780
ctgctctcac	tcccggggtc	ccagcagggc	aaggcctctg	cttgggacca	gtgctgctct	840
tcctcgctgc	ttactccagg	aggtgaaggt	gacagggcgg	caaggagagg	taaccacagc	900
atggctgggg	acaggcgcta	cactgggccc	cggaccacgc	acagggatca	cagtgtcggg	960
ctcgcgaca	cacctctggc	cacatgtgca	caccacatac	atccacacgc	acctccctcc	1020
tgctctggcg	gaggctcatt	ctctctcgca	gccactcgcc	ctctctgcct	ctcacatatg	1080
cggtcacaga	gtgaatccga	gcattcttatt	gctgcagggg	gcaggggctg	cggcatcagg	1140
gaaagttaat	ccacgaagag	cgagaacagc	accattacca	cgatgcccgc	acagagcaga	1200
agcagctgct	gcagggagcg	ccacgggtcc	tcttcttcca	agaggtcagg	gagcagcttc	1260
accaaggcga	tgtagagaaa	gccgccagag	gtgaaggcca	ggaccagggc	tgccgtctcc	1320
tctactccct	tgggggactg	ggtacagatg	gcgaagccag	cgcccagtag	gccccccagc	1380
gctgttgaga	gttgcagctt	ggctgcgctc	catcggtcaa	agccggcccg	gagcaggatg	1440
gcaaagtgcg	ccacctcatg	ggggatctca	tgcaggagga	tggccatggg	tgctcaggagc	1500
ccgatcttct	tgctcacaag	gaagctggca	gccacagcca	gcccgtgggt	gaagttatcg	1560
atggtgttgg	ccagcaggtt	gaggtagccg	ctgactttga	tgctccggac	cacggcacccg	1620
aggccggggc	ctgcagccgg	ctgggcccaga	cagtggcctc	cattgagcgc	ggcggcagca	1680
gcagtggggt	cttgttggg	ggcctggctg	gtcccctcct	ccttgctgtc	caggaacatc	1740
ttctccaacg	ccaggaaggt	caggatgcca	gcaatgacct	acagccccag	ctgttgctgc	1800
tgctgcaggc	tctgcccctc	accaccaggg	ctggcgctgc	acgtgtaggc	ccaggcttcg	1860
ggcagcagat	gcagaaacac	attgcccaag	agtcccccca	gggcgaagct	gagcagctgc	1920
ttcaggcgcc	aggccccagc	ttctgagcgc	agcatggtcc	ccatctctag	gggaatgaca	1980
agcaacggga	agaccccact	gagccccacc	atgagggaac	ccaggaggga	gcagatccag	2040
gtgtccagcc	gctctccgct	cagcagagcc	ccccaggact	cgctttcctt	gttgtccagg	2100
cgacaggccc	tcgcagtccc	ccggctccgg	agggccggct	gggaaccccc	agcccttccc	2160
aagagctcca	gggcaagggc	agtgaggaag	aggagccttg	ggcccgccat	gccacagcca	2220
gggcagggac	atccaggcat	gccacgtacg	tgcggcgccg	gcggcgccga	tccggggcgc	2280
cccagcccgg	gaattcggtg	ncggctcgctg	tgcgtacggc	ttcaatnatc	aaannngggc	2340
acg						2343

<210> 390  
 <211> 1325  
 <212> DNA  
 <213> Homo sapiens

<400> 390

gggaaaagtga	gtgctgggcca	ggctggggcgc	gacagaacac	ttcgacgggc	tccggagccc	60
agattcagcc	aggaaccac	aggcaactcg	gcctaccccc	agctgaggcc	ctttttggac	120
ccgcagggga	gagatcttaa	accagcgct	ttggtccac	ccaccgctc	ccacactggg	180
aggagaccat	ggctccacac	acagcccctg	ccaggccac	aggggcgggc	atgggggccc	240
acctgcctcc	tgcatgtgtg	gacaggggtcc	tgagagtgga	ggagggccgc	agggagtacc	300
tggcgtttcc	caccagcaag	agctcggggc	agaaggggcg	gaaggagctg	ctgaagggca	360
acggccggcg	catcgactac	atgctgcatg	cagaggagg	gctgtgccc	gactgggaag	420
ccgaggtgga	agaattcagt	tttatcacc	agctgtccgc	cctgacggac	cacctgccag	480
tagccatgcg	actgatggtg	tcttcggggg	agga'ggaggc	atagaccgtc	cggagcagtg	540
gggcctctgc	cagcccttgc	agctgcagcc	catccctggg	ccatgtccc	tccatcgagt	600
gcccgggtgct	tgggggagga	gggcagggac	agggagggag	ccacagtcag	tgcccgggaa	660
cctggaagct	gcgctgctct	gcgcctctgg	gcctcactgt	ggacagagga	gtcaggcccgc	720
cccaggagc	ctccagctgc	ctaaccagt	ccattctttc	acaacacgat	tttctacaaa	780
tctacagcac	aaccgagttt	gtaaccctg	ggtagtatg	aggaccgggt	tcgtgtactc	840
tctgtatctc	ctcttaagct	tcgtccagg	ttctttattt	ttgtctgctg	ccaatgtcgt	900
ctcgcatgcc	tgacccctcg	catgcacgct	gcccgcctgc	cacgtgccac	gctgtagcca	960
cagaccctt	gctcgggcct	cacccaaggc	caaactccaa	acacaatcag	aaccagccaa	1020
agaagcactt	cctgggcacg	gccaccagct	ctcccgctc	cagtgtgggc	cggctcctgc	1080
agggtccgag	ggctgcatct	ctaccagcca	gccagggct	cttcccagg	tctcgcatte	1140
aagggaatt	acatttttaa	aagaaaaaca	gaaaaagggt	aatcacaaaa	ccaaccctca	1200
cttcacagg	tctgtaagtc	actcatagaa	ctttgctctt	cccagagacag	ggtcccttcc	1260
ccagctcagg	cacaacagag	tctggcaggc	tctggcacc	tgggcctcct	ccgggagcct	1320
cccat						1325

<210> 391  
 <211> 1458  
 <212> DNA  
 <213> Homo sapiens

<400> 391

tttttttttt	ttcaggctta	aataacaaaa	tatatattcag	atatgcacag	ttttaactga	60
ggactacaca	agccttcctc	gggctgcagg	cccgccgccc	tcccagtggg	attcacagcc	120
cctgcggagt	ttgtcctcac	gcacaccaca	cacgatcggg	tataaaacac	attctataaa	180
cacgttctga	tgcaaaactgt	gtgtccataa	atatatatatt	atgcaagtgc	ctcccaccca	240
ctgcagggcc	gtacagctct	ggggacagga	ggtcacagcc	gactttaaac	cacagggttaa	300
gtagaagggt	gcaggtcaaa	tagaagttcc	cgtgtgattg	catcacccaa	cggcactggt	360
ctgtcatcag	gaaatgctga	gtgcccgcgc	tggccgggtg	ggcgcgggcg	gtggtcagac	420
gctgctctgg	agctggctat	ctgtggcact	gtcaggggct	gaggactggc	tgggcagaca	480
agtttccagg	ccatctgaag	actccgacag	gggcttgtat	aagaagcagg	ctatggcaaa	540
gaagaggacg	cccagcacct	gttacaggag	cccctgatg	agtatgtagc	ggctcatggc	600
cgaattctgg	tacaccaagc	aggagccctg	ctggccacac	tggctcctgcc	acagcagaca	660
ggccttgtcg	atcaccacagc	cgaaggcgat	gggccccggg	atgcccccta	gtattctaac	720
tacaatccac	tggattccca	gggcaaagga	tctctgaggg	tcacggacac	atcgtagagt	780
tgccgttagt	gcagggaatgc	tgctgaggaa	tgtaaagaaa	attacaacga	atatgaaaac	840
cagaaggagg	ggctttctct	gacaagtga	agtgcatctt	cctgcagtgg	catggccaaa	900
accagaggaa	agattctgag	ggatacagct	acagtctcgg	tacacctggg	aagcccaaca	960
atagctccga	ttacaagggg	aaggcacggg	ggccccttcc	caggggtccag	gggaggacag	1020
gggcggtagg	cagcggtcc	actcaccttc	tggcgtcca	cattcgtctc	cgtggctgca	1080
gggcaccctg	cgtggcacag	tgagaagtac	atgagccgt	ccgagccgca	cacagggctg	1140
tagtgttctg	gctggcagct	gcaggcagcg	ttgcagggag	ccgttaggtt	caggtggcct	1200
tcgggcagga	ggctcccgc	gtagctggct	gtgacgccc	ccatgggcac	actggggcag	1260

tgcagtgaga	agacgaggat	gcccagcagg	ctgacaacgg	tgcagaacag	gcagaacttg	1320
atgaccgcgg	agccccggag	cctgagcttg	ttcacaaaaga	agccgcccag	gaaggtgccg	1380
ccaccacccg	ctggcaccac	caggtaccca	aacaaggtgg	cagcttctga	ggcactcagg	1440
cgaattccac	cacacgga					1458

<210> 392  
 <211> 1667  
 <212> DNA  
 <213> Homo sapiens

<400> 392

tttttttttt	ttctatgtac	aaaaacattt	taattgaaat	acctgtataa	aaaaatatga	60
tctccagaca	tctcactttt	gaactgaaag	aacccccatc	tgcatgcct	gcacacaccg	120
cattcacaca	aacacaggta	ctgaataaat	ttaacgctca	ggctctggcc	ccaccccagc	180
tttcagagcc	cacaagcaga	ctgtacaaag	tcaataattt	aaaacccaaa	ccctgggcac	240
agtgcctgga	agtgtcaggg	tcacccactc	cccttaagtt	agccactata	catgttcac	300
ttctgacagg	cggggccagg	acagacgcca	ggcacaggaa	tcagggcctg	gggtccctgg	360
accacagcca	ccccctcccc	tgctcccca	ctgtccctg	gggcttgga	gaggcagact	420
gctcagagga	aataacctca	acaaataaat	ttaacaataa	atagcccgg	tgggccgagg	480
gcacctccag	ggggtcacac	cataaataac	agagttggcg	gcgggtacgg	ctcgctggg	540
cgggcggggc	cggaggccag	gacttgcatt	gtgtgtgcag	gacgtgcca	gacgcacacc	600
gcaggactga	gggcgggagg	tgggcttggg	accctgcgcc	ggcggaaga	gctccgggtg	660
ggcaggcaga	tgggaaggcc	gcctccggac	acagcagcac	agagggcggt	ctggggttca	720
agtatccacc	cagggcaggc	gggacctcga	ccggagcgtc	tttggaaga	cagagcttga	780
gaaaaccaag	tcccgcggga	ccagcgttca	aaaggcactc	aaagcgaagg	tcaccagggg	840
tcagagggtca	ctgcttccgc	aggaggagac	ggcccacgca	ggaaaaagtc	agggctctggg	900
ggcgtcccag	gtctggccaa	ggcagggtgg	cccctagctc	ccagtcagggt	gcagctcctc	960
acaagctctc	gctgctggac	gtggtgctgg	ccacgtcatc	agggtcgagg	gtgcacagcc	1020
gcaggtcaca	gctctccggg	gcgcccccg	cagccccag	catccaggga	tgggccgcaa	1080
tctgatccag	cgacggccgc	tctgaggggc	gcaggacag	gcaccaccgg	atcagctgct	1140
ggcactctgg	agagaccctc	ctccggaaga	gcaggcgggc	tcggaggatc	tcctcgtcct	1200
gctcgaaagg	gatgtcccca	cacaccatat	cgtagagaag	cacgcccagc	gaccacacgg	1260
tggccgagcg	cccgtggtag	cgggtgtagc	ggatccactc	cggggggctg	tacactcggg	1320
tgccgtcgaa	ctcgggtgtag	accgtgtcct	tgagcagcgc	acccgaaccg	aagtcgatga	1380
gcttgagctc	tccggagcgc	agggtccaaa	gcagattttc	gtccttaatg	tcgcggtgca	1440
cgaccccgca	gctgtggcag	tggcgacagg	cggccagcac	ctgcgcgaag	aaagcggcgc	1500
gccagcggct	cgtccagggc	gccgcgctcc	gtgataaagt	cgaagatggg	cctagcgcgc	1560
gctcggggcg	ctccagcacc	agcaggaagc	cgtcggggcg	ctcgaaccag	tccagcaggc	1620
ggatgacgcc	gcgcgcgcgc	cccggcgcg	ccaccttgcg	cagcagc		1667

<210> 393  
 <211> 1938  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1938)  
 <223> n = a,t,c or g

&lt;400&gt; 393

gtggaagaa	cagtcagaaa	gcctctcctg	tggatgatga	acagctgtca	gtctgtcttt	60
ctggattcct	agatgaggtt	atgaagaagt	atggcagttt	ggttccactc	agtgaaaaag	120
aagtccttgg	aagattaaaa	gatgtcttta	atgaagactt	ttctaataga	aaaccattta	180
tcaataggga	aataacaaac	tatcgggcca	gacatcaaaa	atgtaacttc	cgatatcttc	240
ataataaaca	catgctggat	atggacgacc	tggcgactct	ggatggtcag	aactggctga	300
atgaccaggt	cattaatatg	tatggtgagc	tgataatgga	tgcagtccca	gacaaagtgc	360
acttcttcaa	cagctttttt	catagacagc	tggtaaccaa	aggatataat	ggagtaaaaa	420
gatggactaa	aaaggtggat	ttgtttaaaa	agagtcttct	gttgattcct	attcacctgg	480
aagtccactg	gtctctcatt	actgtgacac	tctctaactc	aattatttca	ttttatgatt	540
cccaaggcat	tcattttaag	ttttgtgtag	agaatataag	aaagtatttg	ctgactgaag	600
ccagagaaaa	aaatagacct	gaatcttcag	ggttggcaga	ctgctgttac	gaagtgtatt	660
ccacaacaga	aaaacgacag	tgactgtgga	gtctttgtgc	tccagtactg	caagtgcctc	720
gcccttagag	cagcctttcc	agttttcaca	agaagacatg	ccccgagtgc	ggaagaggat	780
ttacaaggag	ctatgtgagt	gccggctcat	ggactgaaac	tcagcagggg	ctctgggaag	840
tctgaccaag	ttggagcaga	tggtttgtaa	cttgaatctc	caaacactta	gttgaatttt	900
tacagatatt	tcagatcagt	gggtgttggg	gccactattg	ttacctccaa	atttttatttt	960
ttgcccttaa	ttccatttct	cccagctacc	atgtactatt	gttttaagt	cagtttggtt	1020
tcatttttaa	ttttatgggt	ctgtgcgtcc	cccataattt	atatttatta	ttcaaacgca	1080
tgcatataga	cagagcatgc	agtgaagagt	attaaaaaaa	aaagcttagt	agatttggtg	1140
cagcttttga	aacttagggt	agacgtgaaa	ctgaaataca	ggtttcaaat	ttacttcccc	1200
agaacctaaa	aatgcaagat	gtttttgata	ccaaccataa	cctcctgaga	atagtaagt	1260
ttcccccg	gcattaagg	taagcctggg	gggtgttttt	gaccaaattc	cagtccctgt	1320
tttaccttta	cccagcggca	actttcacc	aacttcccct	ctcccaagt	agtcttagag	1380
agtgcagtcc	cattcctttt	tgaaggggtg	gatggaagt	gtcgtaaact	gactgggtgc	1440
ttctgtttct	gggaggcaca	cttghtaagg	acagtggctg	ctttggggag	agtaagggtg	1500
gagaaaaagc	aaccttggag	gccagtaaca	atgacagatt	tcaatcgtgg	tttttaggaat	1560
tataatacgt	ggcatacatc	tcataaaggc	ttttgctggg	atattgaatt	ccctgaattt	1620
ttctgttttc	gacctgttaa	aaaaatctta	acatccatca	aactagtgg	caaacaaatg	1680
agaatgcagc	tgttctcaga	gtaattttta	agttgtcatt	tccctgtgtt	gcctcccaat	1740
tggaagaagt	taagggtttac	caaatgcatt	tctatttcaa	gggtatctga	aacgtaacaa	1800
ttcaaaactg	aaggctgact	gacttnagat	gttttgagg	tggctggaga	gaacagggaa	1860
ggtaatagag	acacacttag	tcccatggga	agcgcagcac	cgttgtaggt	tctttctcct	1920
gtcccattag	cgacctca					1938

&lt;210&gt; 394

&lt;211&gt; 1283

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1283)

&lt;223&gt; n = a,t,c or g

&lt;400&gt; 394

gatttcagtt	gcctgaaagc	tgtaagtctg	ctttttttaa	agagaaattg	gagttaagca	60
gacttttcat	tttttgatca	tgacctgga	aagagaaata	tatttgacat	caaaactcag	120
cacatatcct	tggtctatat	atacacatga	aagtttcata	aaacaataca	ctgatatttt	180
ccatgctgta	ttctatttca	ttttttaaaa	tgctgggtgt	atcccattaa	actggtttca	240
aaataaatat	aacatgtaca	caacaacaac	actggggttag	agggccagta		300
agctcagcga	gtatcagcaa	ctgagacttc	atccttgtct	cacaaggact	aaaaagagaa	360
taatgttctc	attatgtggt	tcaatgccac	acccatgtat	ctgagatata	catgtcacia	420
tctgggagaa	gcctgtcctc	aattttacttt	aaatacccaa	ttctgcctag	aacatgaatt	480

agacacatag	taagctcttg	agtgaagtgc	agatgataat	gacacgatca	cataccactt	540
aaaaatatct	taacaccttt	acttagatct	catctcatac	ttgtagcatt	tcttcaaatt	600
tactttgaaa	aaagagcttc	actgtgtgtg	gttgtcatac	acattcttct	acccaacat	660
ggacctcttt	tttctctca	ggcgcacttc	atctaatttt	tttagcactg	gcttggcctt	720
tttgaggag	gtggagtagc	tcttcagaaa	ggcttcaaac	acagtttcag	tggtgggatg	780
ggtactgagg	aaggccttct	ccaggacata	gaggtctact	cccttatcct	ctggaagtgc	840
tgaaatgaaa	ctcagcccaa	agtctatgag	cacaatgttc	agctgttcca	gggggggttt	900
caggagcatg	ttggagggtg	tgagatcacc	atgaatgagg	tcttcacgt	gcattcgagc	960
caaaacctgc	ccaattgtct	tggctaagtt	ggagagaccc	tggggagtgt	ttttcagtct	1020
ccatagtgga	ctgaatataa	tctcgaacag	tactgagcc	ttcaatttct	tccatatata	1080
agcagttgga	agcatagtcc	acaaaaaga	caactggggc	agatattcca	gcgcggcgac	1140
agcgaggagg	cgcccgggcc	tcctgcaccg	tccgcgtct	gccaagccgc	gcctccagcg	1200
ccgggtgcgc	gtagccttgg	gaagcgggtg	ttnttncnn	ggccttgcta	gccccctggc	1260
tcattnnccc	cggcccggtc	tcc				1283

&lt;210&gt; 395

&lt;211&gt; 2149

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 395

acgagcctgc	gttttcgggc	cagaggacat	gatgcagggg	gaggcacacc	ctagtgtctc	60
ccttattgac	agaaccatca	agatgagaaa	agaaacagag	gctaggaaag	tggtcttagc	120
ctggggactc	ctaaatgtat	ctatggctgg	aatgatata	actgaaatga	ctggaaaatt	180
gattagttca	tactacaatg	tgacatactg	gccccctctg	tatattgagc	ttgcccttgc	240
atctctcttc	agccttaatg	ccttatttga	tttttgga	tatttcaa	atactgtggc	300
accaacaagt	ctgggtgtta	gtcctggaca	gcaaacactt	ttaggggtga	aaacagctgt	360
tgtacagact	acgcctccac	atgatctggc	agcaacccaa	atccctcccg	ctccaccttc	420
cccttcaatt	cagggtcaga	gtgtgttgag	ttatagccct	tctcgttcgc	ccagtaccag	480
tcccaagtgc	accaccagct	gtatgactgg	ttacagccct	cagctgcaag	gtctgtcctc	540
aggtggcagt	ggttcttata	gccctggagt	gacctaactg	cccgtcagtg	gttataataa	600
gttggcgagc	tttagccctc	ctcctccttc	tccgtaccct	accactgttg	gaccagtggg	660
gagcagtggg	ttgagatctc	gctaccgttc	ttcacctacc	gtctacaact	cacctactga	720
caaagaagac	tacatgaccg	acctaogaac	tttggatact	tttctcagaa	gtgaagagga	780
gaaacagcat	agggttaagc	tggggagccc	agattctacc	tctccttcca	gcagctctac	840
tttctggaac	tatagtctgt	ctatggggga	ttatgcacaa	actttaaaga	agtttcagta	900
tcagcttgcc	tgtaggtctc	aggccccatg	tgctaaacaa	gatgaagccg	atctcagctc	960
taaacaagcc	gcagaagagg	tctgggcaag	agtggctatg	aatagacaac	ttcttgatca	1020
tatggattca	tggacagcta	aattttagaaa	ttggatcaat	gagacaatat	tagtgccact	1080
tgttcaagag	attgagtctg	tcagcacaca	gatgagacga	atgggttggtc	cagagctaca	1140
gataggagag	gctagtatta	ctagcttgaa	acaagctgcc	ctgggttaaag	cgcctctcat	1200
tccgactttg	aacacaatcg	ttcagtatct	agaccttact	ccaaatcagg	aatacttggt	1260
tgaaaggatc	aaagaactat	ctcagggagg	ttgtatgagc	tcatttcgat	ggaacagagg	1320
tggcgacttc	aaaggacgaa	agtgggatac	agacctgccc	accgattctg	ctatcatcat	1380
gcattgtatt	tgcacctacc	ttgattccag	attacctcca	catccgaagt	atcccgacgg	1440
aaaaactttt	acttctcagc	actttgttca	gacaccaa	aaaccagatg	ttacaaatga	1500
gaatgttttt	tgcattttatc	agagtgtctat	caacctctcc	cattatgagc	tcattctacca	1560
gogtcatgta	tacatacctg	ccaaagggca	gaaataatat	gtttcataca	ttgttgatgt	1620
ttctctacat	cataaagacc	aaagagtcag	gaatgcttgg	gagagttaat	cttggtctat	1680
ctggtgtgaa	tatattgtgg	atctttggcg	agtgaagc	catatattta	attctgacat	1740
ttagactatt	tactgaacc	agaagtcgaa	actaaacatc	tctgagccac	tgactcttct	1800
gaaataaaat	acacatgggt	gtatgttaca	gactcttttag	atttaacaga	aaatgtagct	1860
gttatgaaat	gtaattgtaa	aaatatgtcc	cgtatcttct	atatcgagac	attgccttta	1920
attttatatc	gcttttcaga	aatttcagtt	gactacaaaa	ctgcaaccct	tcggattttt	1980
attgactcaa	aatagtgcc	ttccccctaa	tgaaatagat	tttgagtctt	tttttcattg	2040
taacccccaa	atgagaatca	tctacctgat	tcttgtagca	aaaaaaaa	tttttcagtc	2100

tttttttttt ttaaagaggg tttttgccaa cccaaactgg agggcaggg

2149

<210> 396  
 <211> 1895  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 actgtagacc attagtccag tgcggtggaa ttcatacaacc gaaacaacag tgtggtacag 60  
 gtccctgcttg ctgctggggc tgatccaaac cttggagatg atttcagcag tgtttacaag 120  
 actgccaaagg aacaggaat ccattctttg gaagtcctga tcaaccgaga ggatgacttc 180  
 aacaacaggg tgaacaaccg cgccagtttc aagggctgca cggccttgca ctatgctgtt 240  
 cttgctgatg actaccgcac tgtcaaggag ctgcttgatg gaggagccaa cccctgcag 300  
 aggaatgaaa tgggacacac acccttgatg tatgcccag aaggggaagt gatgaagctt 360  
 ctgaggactt ctgaagccaa gtaccaagag aagcagcgga agcgtgaggc tgaggagcgg 420  
 cgccgcttcc ccctggagca gcgactaaag gagcacatca ttggccagga gagcgccatc 480  
 gccacagtgg gtgctgcgat ccggaggaag gagaatggct ggtacgatga agaaccacct 540  
 ctggtcttcc tcttcttggg atcatctgga ataggaaaaa cagagctggc caagcagaca 600  
 gccaaatata tgcacaaaga tgctaaaaag ggcttcatca ggctggacat gtccgagttc 660  
 caggagcggc acgaggtggc caagtattat gggctctcac caggctacgt tggccatgag 720  
 gagggtggcc agctgaccaa gaagtgaag cagtgcacca atgctgtggt gctctttgat 780  
 gaagtagaca aggcccatcc agatgtgctc accatcatgc tgcagctgtt tgatgagggc 840  
 cggctgacag atggaaaagg gaagaccatt gattgcaagg acgccatctt catcatgacc 900  
 tccaatgtgg ccagcgacga gatcgacag cagcgctgc agctgaggca ggaagctttg 960  
 gagatgagcc gtaaccgtat tgccgaaaac ctgggggatg tccagataag tgacaagatc 1020  
 accatctcaa agaacttcaa ggagaatgtg attcgcccta tccagaaagc tcaattccgg 1080  
 agggatgagt ttctgggacg gatcaatgag atcgtctact tccctccctt ctgccactcg 1140  
 gagctcatcc aactcgtcaa caaggaacta aacttctggg ccaagagagc caagcaaagg 1200  
 cacaacatca cgtgctctg ggaccgcgag gtggcagatg tgctggtcga cggctacaat 1260  
 gtgcactatg gcgcccgtc catcaaacat gaggtagaac gccgtgtggg gaaccagctg 1320  
 gcagcagcct atgagcagga cctgctgccc agggggctgt actttgcga tcacggtgga 1380  
 ggactcagac aagcagctac tcaaaagccc agaactgccc tcaccccagg ctgagaagcg 1440  
 cctccccaag ctgctctgag agatcatcga caaggacagc aagactcgca gactggacat 1500  
 ccgggcacca ctgcaccctg agaagggtgt caacaccatc tagcagccac ctgcctgctc 1560  
 ctatgtgccc tcaccatcca ataaaggccc cttgctgtg gcattggcaa aaaaaaaaaa 1620  
 agggggggcc gtttaaaaga acccttgggg ggcccaaat taaccggggc gggcaaggaa 1680  
 aaattttttt ccttatgggg gccgaataa aaaccaacct gggaattttg ggaaagaacc 1740  
 cttatttttg gggggggaca aattgggcca acctccctac aaaaatttaa ggctttaggg 1800  
 aaaaaaaaaa tttttaagg gaaaagggg aaaaacaacc ggcataccct ggcggttggg 1860  
 aagttttgtt tacggagtat gatttagaaa aattt 1895

<210> 397  
 <211> 2416  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(2416)  
 <223> n = a,t,c or g

<400> 397

tttttttttt	tttttttttca	caagttatat	tttatttttaa	cacgaggatt	aacatatagt	60
tacaaggtca	atacaagcct	ccagtgggaag	ctcttttattt	ggttttaattc	catctccaga	120
gacaaacagg	caactctagg	accttttacag	tggcgatcgg	cctccacnac	agcaaaatgc	180
ctccaaagtt	tagaattagt	gcaacacaca	tacgaacggt	ttaaagggtgc	tcaacatcag	240
gttaaaatag	aattctggac	cttttttaaaa	agttttttgga	tgatataaagc	acaggaggca	300
gagccaataa	gaaacatgaa	accaatattt	ctggaaaaaac	acttagcatg	aacgtcactt	360
tttgacgtcg	tgtaaacttt	cttctgcaat	gacggatggt	acaaaaggc	attgagacct	420
ttgcgtgctg	ctgggttagac	aagccgcagg	cttatctcca	cgggtgagcag	gataaaaacc	480
cccaaggaac	agcccatgac	aacctctctgt	gccttttttat	actttcccat	cctacaaagg	540
aaaaactggg	taaaggacaa	gttctctcct	ttcattgcgt	ttctaagaac	ttttcagggc	600
aggttctttt	aaaattagtc	atcttacaaac	acaacagtat	tctagcacgg	tggcgaagtg	660
acaggcggca	gatacggggg	aggaaggaga	cgttcacggg	aaattccaca	ttctactcta	720
tgtgaactgc	tccagaaaaa	tacagacatg	atttcacagt	aggattccca	gagtaaataga	780
tgatacatag	gacaactgac	ctcctctaag	aagcccggct	ggggcagcag	tgagcttttc	840
atggagccac	ctagactggc	ccggaagcaa	caccaggtt	caacatttaa	gagcatcgc	900
tataacattc	tttttgacg	caggtggtgg	aaaagttaa	aaaacaggcg	gaggagtgc	960
gggggggatac	aagcatatcc	tatactgggg	gtgacggtca	ttcaaagagc	aaattactgc	1020
agcttatatc	ttttccacta	tggtgcaaga	aatgaatcta	tcctgaccca	taatatgaaa	1080
gatgcgacgc	acatgcattc	ccgaggctct	aaaatcccat	tttaaagaac	cgtttcacat	1140
cctcgtggag	tggagagtgg	tccacttgac	ttggtgaggt	cagaagttcc	tgaagatccc	1200
tgctgtcccc	gttggcgggg	gagcccatg	tggagctgtg	gggactgcca	cactcaccat	1260
gcacctgttg	gtttgcaggg	acagaggtgc	ggccttgact	cttctcacc	tgtgtcatcc	1320
gggcttgctc	ttcgtctgtc	aagtcagtcc	tcctgcgtga	ctgatgggtg	caccacgctt	1380
aggtcacccg	ttgcaggga	cgggaagtcca	tggctctgcc	gcaaccctga	gcgggttgca	1440
gtcccccccg	gggaagaagc	agtcagagag	gctcacgctc	acctacttta	aaaacccaaa	1500
gccacttcct	cttcacctgc	ctgggcctca	gcgtctctgc	gcttggtggt	tctcgtcccc	1560
gagggctgac	tgagctgctc	cgggaagggtg	gtgtgtgggc	aaccttggtt	ggctgagagg	1620
agcaatttcc	tggtttccac	aagtaaagac	agcccatcc	cttgggacct	gtcctttccg	1680
tccctgtccc	tttggtctct	ataggacttc	cttgtcttag	attcataaac	agcaagagga	1740
actgaggatg	cttgaggga	ccacctagtt	accaaagcca	agcaaagaat	aaagctgccc	1800
gacatcatcc	ccaggcttcc	gtggcgctct	cggtcacagg	agctttaggc	caatggttcc	1860
tcttgactgt	ttttgcccc	aatgagagga	ggggctgctt	tgctttaagg	cgtggcggcg	1920
gggggggggt	ggtggccaca	gattagggga	cctcaggttt	tcctcaaaaa	cccacacagg	1980
gaaagaaact	tggctctaaa	agcaaaactca	acgaattcca	catgccctga	agagcacgtg	2040
ataaaataca	aggggtggtg	cggcgggatc	cctcaaagga	ccacgagagg	cacggggtct	2100
ttggtgatga	aagtgtctaac	ctcggcgggg	tgcggtagct	cacacctgta	atctcagcac	2160
tttgggaggc	tgaggcgggc	ggatcacctg	aggtcaggag	tttgagacca	gcctgaccaa	2220
cacggtgaaa	ccctgtctct	actaaaaata	caaacattag	ccgggcgtgg	tggtgcacgc	2280
ctgtaatcac	agctatttgg	gaggctgagg	caggagaatc	gctggaacct	aggaggtgga	2340
ggttgtagt	agccgagatc	atgccactgc	actccagctc	gaacaataga	gcgagactcc	2400
cgtctcaaaa	aaaaaa					2416

<210> 398

<211> 1495

<212> DNA

<213> Homo sapiens

<400> 398

tggccattta	ggaaaaattg	tccttgggga	tcctctaaaa	aatccttttg	tgtccaatag	60
caccttaaaa	aacctgggcc	ccagataatt	gttgaacctc	agatttagga	aggaaaaattt	120
ccaagctgtc	agctaaaggc	agtttcccc	atttcacaga	atatgtggta	gaagttccga	180
gtaaggaatt	ttttcagcag	ccatgaaagc	tcctgcata	aggaagactc	agtgtgcaac	240

atctgaaagc	agtattgccca	gagcatgact	gtggcaatga	agcaaaatgt	tccctccacc	300
tatccctccc	tcccattgat	aatgcttgaa	gggtcagtc	ctgaaataag	tagagagaaa	360
agtgtttgct	gaaagagcta	atacataagt	caaccttcac	tggtagcaat	gaaggcttcc	420
cagttcaaaa	ttcaacaccc	agaaaaggca	gaaattttag	ctttaaatta	agtttaaatt	480
ttcagttatc	ccagtggact	aggcatttaa	atctgaggag	ttccctgaga	ttccatatga	540
ggaaatgaaa	aacattagct	tgtggattaa	atttaaagag	actgtaagga	gaaaaacata	600
ttttatgaca	tgcctcttaa	ggactcctat	tatttcaatg	aatttggtac	agttataata	660
tgcttgtgat	aaaaaggcat	tatttattaa	gaaatctaaa	atgtaataat	atttcaatta	720
tatagtttta	gagaaccttt	cttgcccaac	acttttctga	tagcaagttg	gacatccttg	780
tttctgaggc	tataaacat	ggggtttagt	aatggagtga	caatcgtgta	tgtagccgtc	840
accagcctgt	ctttgttgga	cacatagttt	gctgtaggcc	tcaggtagat	gaagggaagca	900
cagccataat	gaacaataac	aacactgagg	tgagaggcgc	aggtggaaaa	cgctttccgt	960
ctgccctcag	ctgagggaat	cttcaggata	gtcctcagaa	tgagaaata	agaaacacag	1020
ataaacagaa	agggaaaccac	aagtacaaga	actccacaaa	tgaatatcac	aaatccgtta	1080
acatctgtgt	tggtagaagc	cagaagaatg	actgctgaga	tgtagacagaa	gtaatgattg	1140
actttgttgg	tgtagacaaa	agggaggctg	aaaactaaat	ttactactgt	aagagaggcc	1200
aagaagccac	caattgcaca	ggcagctgcc	agttttccac	acacctgcca	gctcataaga	1260
gtggggtaat	gcagagggtg	acaaatggca	gcatacgcat	cataacccat	cacacccaat	1320
agcaggcagt	tggtaatggc	aaaaccaagg	aagaagaaca	tttgaagagc	acaacagttg	1380
aaggagattg	tcctggccac	agaaagtaga	ttgatgagca	tcctgggtag	aatgacaaaag	1440
gtgtagaagt	ctcagatggt	gagagaaaagc	caggaagagg	ccattggtgt	gtgga	1495

&lt;210&gt; 399

&lt;211&gt; 2752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 399

gcgaccgccca	gcggctacac	ggtaccgcgc	tgagaagctc	aagtccatga	cgtcccggga	60
caactataag	gcgggcagcc	gggagggcgc	gcgcgcgtgc	cgagccgcgc	gtagccgcgc	120
cagccgcagc	cgccgcgtgc	gccgaacctt	accctgtgtc	cggggccaag	cgcaagtatc	180
tggaggactc	ggaccccgag	cgcagcgact	atgaggagca	gcagctgcag	gaggaggagg	240
agggcgcgaa	ggtgaagagc	ggcatccgcc	agatgcgcct	cttcagccag	gacgagtgcg	300
ccaagatcga	ggcccgcat	gacgaggtgg	tgtcccgcgc	tgagaagggc	ctgtacaacg	360
agcacacggt	ggaccgggccc	ccactgcgca	acaagtactt	cttcggcgaa	ggctacactt	420
acggcgccca	gctgcagaag	cgcgggcccgc	gccaggagcg	cctctaccgc	ccgggcgacg	480
tggtagagat	ccccgagtg	gtgcaccagc	tggtgatcca	aaagctgggtg	gagcaccgcg	540
tcacccccga	gggcttcgtc	aacagcgccg	tcacaaacga	ctaccagccc	ggcggctgca	600
tcgtgtctca	cgtggacccc	atccacatct	tcgagcgccc	catcgtgtcc	gtgtccttct	660
ttagcgactc	tgcgctgtgc	ttcggctgca	agttccagtt	caagcctatt	cggtgtctcg	720
aaccagtgtc	ttccctgccg	gtgcgcaggg	gaagcgtgac	tgtgctcagt	ggatatgtctg	780
ctgatgaaat	cactcactgc	atacggcctc	aggacatcaa	ggagcgccga	gcagtcacga	840
tcctcaggaa	gacaagatta	gatgcacccc	ggttggaaac	aaagtccctg	agcagctccg	900
tgtagccacc	caagctatgct	tcagatcgcc	tgtagcagaa	caacagggac	cctgtctctga	960
aacccaagcg	gtcccaaccgc	aaggcagacc	ctgatgctgc	ccacaggcca	cggatcctgg	1020
agatggacaa	ggaagagaac	cggcgctcgg	tgctgctgcc	cacacaccgg	cggagggggt	1080
gcttcagctc	tgagaactac	tggcgcaagt	catacgagtc	ctcagaggac	tgctctgagg	1140
cagcaggcag	ccctgcccga	aaggtagaaga	tgccgcggca	ctgagctctac	ccgcgcgcct	1200
cctgggaact	ctggctcatc	cttacgtagt	tgccctcctc	tttgttttga	gggttttgtt	1260
tttgttcatt	gggggggtttt	tgttttttgg	tttttgtttt	ttttgattct	atatattttt	1320
ccttggtttt	gttgccctgtt	aaggctgaac	aatagaattg	gccaggacct	aggttctcat	1380
attcctggta	ttcctcctgg	atggaaaaggc	tggtggcatc	aataggggac	agaggctgat	1440
gctggagtgg	ccagtagagg	tggtggagca	gagcaccat	cttttaagt	gggctgtatc	1500
aggtgggtt	tattttaaag	caacaaaatg	ttttggttaa	gaaaattatt	ttgctttcag	1560
tgtaaatctt	cgcagtgttc	taaacaaaagt	tcagtcttct	gcttgccctc	ttccctcact	1620
gatgtctgca	cttggttgag	gtctcctgga	gcctcacagg	ctctgctgtt	ctccacttct	1680